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Trophallactic optimization algorithm with markov random field refinement for stroke lesion segmentation

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ABSTRACT

Cerebrovascular accidents (strokes) represent a critical medical emergency requiring rapid and accurate diagnosis. Automated segmentation of stroke lesions from computed tomography (CT) images remains challenging due to low contrast, image noise, and high anatomical variability between ischemic and hemorrhagic subtypes. This paper introduces a novel hybrid approach combining the trophallactic optimization algorithm (TOA), inspired by cooperative nectar exchange in bee colonies, with markov random fields (MRF) for spatial coherence modeling. The proposed TOA-MRF method operates semi-automatically from a single user-defined seed point, leveraging bio-inspired collective intelligence to progressively explore and refine regions of interest. The algorithm simulates the enzymatic transformation of nectar into honey through iterative information exchange between virtual bees, followed by MRF-based regularization to ensure anatomical consistency. Evaluated on a clinical CT dataset from [Hospital Name], the method achieves a Dice similarity coefficient of 87.3% for ischemic strokes and 91.2% for hemorrhagic strokes, with an overall detection accuracy exceeding 89%. Comparative analysis demonstrates the complementary strengths of TOA exploration and MRF refinement, offering a robust and efficient solution for clinical stroke assessment with minimal user intervention.

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1. INTRODUCTION

Stroke represents one of the leading causes of mortality and morbidity worldwide, with approximately 15 million people affected annually according to the World Health Organization (WHO). Early and accurate detection, followed by proper classification between ischemic and hemorrhagic forms, is essential to ensure rapid therapeutic intervention and improve patient outcomes. The critical “golden hour” following stroke onset necessitates immediate medical imaging analysis, typically through computed tomography (CT) scans, to guide treatment decisions such as thrombolytic therapy for ischemic strokes or surgical intervention for hemorrhagic cases.

However, automated segmentation of stroke lesions from CT images remains a significant technical challenge. The complexity arises from multiple factors: low tissue contrast between pathological and healthy regions, presence of imaging artifacts and noise, high inter-patient anatomical variability, and subtle intensity differences between different stroke subtypes. Classical segmentation approaches based on intensity thresholding, active contours, or region growing methods often demonstrate limited robustness, suffering from sensitivity to initialization parameters and difficulty handling the heterogeneous nature of cerebrovascular lesions.

To overcome these limitations, bio-inspired optimization approaches have gained considerable attention in medical image analysis. These methods, inspired by collective behaviors observed in natural systems such as ant colonies, bird flocking, or bee swarms, exploit distributed intelligence mechanisms to efficiently explore complex solution spaces. Among these, the artificial bee colony (ABC) algorithm has demonstrated particular promise due to its balanced exploration-exploitation strategy through cooperative interactions between different bee roles: scouts for exploration, foragers for local exploitation, and onlookers for information sharing.

Complementary to bio-inspired optimization, markov random fields (MRF) provide a powerful probabilistic framework for modeling spatial dependencies in image segmentation tasks. MRFs enable regularization of segmentation results by imposing local coherence constraints between neighboring regions while preserving significant discontinuities at lesion boundaries, making them particularly suitable for medical imaging applications where anatomical structure and spatial continuity are critical.

In this context, we propose a novel hybrid approach termed trophallactic optimization algorithm with markov random field refinement (TOA-MRF), which synergistically combines bio-inspired exploration with probabilistic spatial modeling. The method draws inspiration from the trophallaxis mechanism in bee colonies—the process of food exchange and enzymatic transformation that converts collected nectar into mature honey. This biological analogy translates into a computational framework where virtual bees progressively explore the image space from an initial user-defined seed point, exchange intensity information, and collectively refine regions of interest through iterative transformation mechanisms. The resulting candidate segmentation is then refined through MRF-based regularization to produce a spatially coherent and anatomically plausible lesion mask.

The proposed TOA-MRF approach offers several distinctive advantages over existing methods:

- Semi-automatic operation requiring only a single user-defined seed point, minimizing manual intervention while maintaining clinical control.
- Adaptive exploration through cooperative bee behavior enabling robust segmentation of heterogeneous regions with varying intensities.
- Integrated classification capability distinguishing between ischemic (old and recent) and hemorrhagic stroke types based on intensity characteristics.
- MRF-based spatial regularization ensuring anatomical continuity and suppressing isolated false detections.

Experimental validation conducted on clinical brain CT images demonstrates the model's capability to effectively detect and classify stroke lesions, achieving high segmentation accuracy while maintaining computational efficiency suitable for clinical deployment.

The remainder of this paper is organized as follows: Section 2 reviews related work in stroke segmentation and bio-inspired optimization. Section 3 presents the detailed method of the TOA-MRF approach. Section 4 describes the experimental setup and presents quantitative and qualitative results. Section 5 discusses the findings and limitations, followed by conclusions and future research directions in section 6.

To contextualize TOA–MRF within current medical image analysis trends, recent work can be grouped into three complementary directions. First, interactive and weakly-supervised segmentation has gained traction to reduce annotation costs while keeping a clinician "in the loop"; scribble- or prompt-driven strategies have demonstrated that sparse user input can guide accurate delineation without full pixel-level labels [1]–[4]. Second, as deep models increasingly enter clinical workflows, explainability and trustworthy deployment have become central research themes, with surveys emphasizing limits of saliency-only explanations and the need for governance frameworks and regulatory alignment in radiology [5]–[7]. Third, hybrid pipelines that combine learning-based cues with probabilistic refinement (e.g., MRF variants) continue to be studied as a way to enforce spatial coherence and control false positives, especially in heterogeneous CT protocols [8], [9]. In parallel, stroke lesion segmentation on CT and CT perfusion remains an active topic where recent deep networks report strong accuracy but still depend on data quality, domain calibration, and careful validation across centers [10], [11].

2. RELATED WORK

2.1. Stroke segmentation techniques

Automated stroke lesion segmentation has been extensively studied using diverse methodological approaches. Traditional methods based on thresholding and region growing offer computational efficiency but struggle with intensity heterogeneity and noise sensitivity. Active contour models (snakes) and level set methods provide more sophisticated boundary detection but require careful initialization and parameter tuning.

Deep learning approaches, particularly convolutional neural networks (CNNs), have achieved state-of-the-art performance in medical image segmentation. U-Net architectures [12] and their variants have been successfully applied to stroke lesion detection, achieving high accuracy on large annotated datasets [13]. However, these methods require substantial labeled training data, significant computational resources for training, and may face generalization challenges across different imaging protocols and patient populations.

2.2. Bio-inspired optimization in medical imaging

Bio-inspired algorithms have found successful applications in various medical imaging tasks. The ABC algorithm [14], introduced by Karaboga in 2005, has been applied to image segmentation, feature selection, and optimization problems [15]. Particle swarm optimization (PSO) [16] has been used for multilevel thresholding and registration tasks. Ant colony optimization (ACO) [17] has shown promise in edge detection and path planning for surgical navigation. The TOA [18], represents a more recent bio-inspired approach that models the food exchange and transformation processes in bee colonies. Unlike standard ABC, TOA emphasizes the enzymatic transformation aspect of nectar maturation, providing a natural mechanism for progressive refinement of candidate solutions. This characteristic makes TOA particularly suitable for image segmentation tasks where gradual region refinement is desired.

2.3. Markov random fields for spatial regularization

MRF provide a principled probabilistic framework for incorporating spatial context in segmentation [19]. The MRF energy minimization approach, typically solved through graph cuts [20] or iterated conditional modes, balances data fidelity with spatial smoothness constraints. In medical imaging, MRFs have been extensively used for brain tissue classification [21], tumor segmentation, and multi-modal image fusion.

Recent hybrid approaches combining optimization algorithms with MRF refinement have shown promising results. However, most existing methods either focus purely on optimization without spatial modeling or apply MRF in isolation without adaptive exploration mechanisms. The integration of TOA with MRF presented in this work addresses this gap by combining bio-inspired adaptive exploration with probabilistic spatial modeling.

Beyond algorithmic accuracy, several contributions highlight practical considerations for translation to routine care. Interactive systems are increasingly accompanied by public implementations and benchmarks that facilitate reproducibility and rapid prototyping [22], [23]. At the same time, ethical and regulatory discussions stress requirements for transparency, data governance, auditability, and human oversight when AI is used as decision support in radiology [24]–[26]. These trends reinforce the relevance of interpretable, training-free segmentation approaches that can complement learning-based models, particularly when data are limited or heterogeneous across acquisition settings. Finally, PhysioNet remains a widely used public repository for validated physiological and imaging data, supporting reproducible research and external evaluation [27].

3. PROPOSED METHOD

The proposed TOA-MRF method integrates bio-inspired collective intelligence with probabilistic spatial modeling to achieve robust semi-automatic stroke lesion segmentation. The complete processing pipeline consists of six interconnected stages: image preprocessing, seed-based initialization, bee colony modeling and exploration, trophallactic exchange mechanism, MRF-based refinement, and automatic classification with visualization. Figure 1 illustrates the overall workflow of the approach.

Figure 1 illustrates the overall pipeline of the proposed TOA–MRF framework. It summarizes i) preprocessing steps that enhance CT contrast and suppress noise, ii) interactive seed-based initialization, iii) global optimization using the TOA to delineate candidate lesion regions, and iv) MRF-based refinement to enforce spatial coherence and produce the final lesion mask. The stages of the method and representative outputs are further detailed in Figure 2.

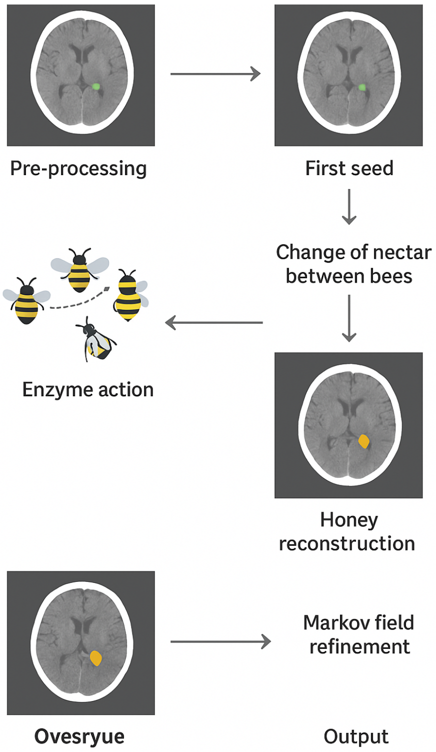


Figure 1. Workflow of the proposed TOA-MRF approach for stroke detection and segmentation in CT imaging. The pipeline illustrates the progression from preprocessing and seed selection through bee colony exploration, enzymatic transformation, honey reconstruction, and MRF-based refinement to the final segmentation output

3.1. Image preprocessing

The input brain CT scan undergoes standardized preprocessing to enhance image quality and prepare data for subsequent analysis:

- Grayscale conversion and intensity normalization to the range [0, 255].
- Noise reduction through median filtering (kernel size 3×3) to suppress imaging artifacts while preserving edge information.
- Optional contrast enhancement via adaptive histogram equalization (CLAHE) to improve discrimination between healthy and pathological tissue.
- Skull stripping or brain extraction when necessary to focus analysis on cerebral tissue.

The preprocessed image serves as the exploration domain for the virtual bee colony in subsequent stages.

3.2. Seed point selection and initial classification

The user initiates the segmentation process by selecting a single seed point within the suspected lesion region. The intensity value at this seed location, denoted I_{seed}, provides preliminary classification of stroke type according to empirically established intensity ranges derived from clinical CT imaging characteristics:

$$\begin{aligned} \text{If } 20 < I_{\text{seed}} < 70 &\Rightarrow \text{Old ischemic stroke (chronic hypodense region)} \\ \text{If } 70 < I_{\text{seed}} < 100 &\Rightarrow \text{Recent ischemic stroke (acute hypodense region)} \\ \text{If } I_{\text{seed}} > 130 &\Rightarrow \text{Hemorrhagic stroke (hyperdense blood)} \end{aligned}$$

This seed point serves as the initial nectar source from which the bee colony begins exploration of neighboring regions exhibiting similar intensity characteristics.

3.3. Bee colony modeling and roles

The virtual bee colony consists of N bees, each represented by a spatial position $p_i(x, y)$ and associated local intensity value I_i. Three distinct bee roles collaborate to explore and refine the region of interest:

- Scout bees (30% of population): Perform random exploration at varying distances from the seed to discover new potentially relevant regions.
- Forager bees (50% of population): Conduct local exploitation in the immediate vicinity of the seed, harvesting pixels with intensity values similar to I_{seed}.
- Onlooker bees (20% of population): Follow high-quality nectar sources identified by scouts and foragers, reinforcing promising regions through focused exploration.

Each bee evaluates the quality of its current position using a fitness function that combines intensity similarity with spatial proximity to the seed:

$$f(p_i) = \omega_1 \cdot \frac{1}{1 + |I_i - I_{\text{seed}}|} + \omega_2 \cdot \frac{1}{1 + d(p_i, p_{\text{seed}})} \tag{1}$$

where ω_1 and ω_2 are weighting parameters controlling the relative importance of intensity similarity versus spatial proximity (typically $\omega_1 = 0.7$, $\omega_2 = 0.3$), and $d(\cdot, \cdot)$ denotes Euclidean distance. Higher fitness values indicate more promising locations for lesion membership.

3.4. Trophallactic exchange and enzymatic transformation

The trophallactic mechanism models the biological process of nectar exchange and enzymatic transformation in bee colonies. In each iteration, bees exchange intensity information with their neighbors, simulating the gradual maturation of nectar into honey through progressive refinement:

$$I_i^{(t+1)} = \alpha \cdot I_i^{(t)} + (1 - \alpha) \cdot \frac{1}{|N(i)|} \sum_{j \in N(i)} I_j^{(t)} \tag{2}$$

where $I_i^{(t)}$ represents the intensity value at bee position i during iteration t, $N(i)$ denotes the neighborhood of bee i (typically 8-connected neighbors), and α is the enzymatic transformation rate ($\alpha = 0.6$ provides balanced refinement). This exchange process ensures gradual homogenization of intensity values within coherent regions while maintaining sensitivity to true boundaries.

After convergence (typically 50–100 iterations), pixels visited by bees with fitness values exceeding a threshold τ ($\tau = 0.5$) are marked as candidate lesion members, forming the initial "honey mask" H_0.

3.5. MRF-based spatial refinement

The candidate mask H_0 produced by the bee colony may contain isolated false positives or exhibit boundary irregularities due to noise and intensity heterogeneity. To enforce spatial coherence and anatomical plausibility, we apply Markov random field refinement through energy minimization:

$$E(M) = \sum_x D(x, M_x) + \lambda \sum_{x,y \in N} V(M_x, M_y) \tag{3}$$

where:

- $M_x \in \{0, 1\}$ denotes the binary label (lesion/background) at pixel x.
- $D(x, M_x)$ is the data term measuring fidelity to the initial mask H_0.
- $V(M_x, M_y)$ represents the smoothness term penalizing label discontinuities between neighboring pixels (Potts model).
- λ controls the regularization strength ($\lambda = 0.5$ balances fidelity and smoothness).

Energy minimization is performed using graph cuts algorithm, producing the final refined segmentation mask M^* that balances adherence to the bee-generated candidate regions with spatial smoothness constraints aligned to anatomical structure.

3.6. Classification and visualization

The stroke subtype classification is confirmed by computing the mean intensity within the final mask M^* and comparing against the threshold ranges defined in section 3.2. The segmentation result is then overlaid on the original CT image using color coding for intuitive clinical interpretation:

– Red: Hemorrhagic stroke.
– Dark blue: Old ischemic stroke.
– Light purple: Recent ischemic stroke.

This color-coded visualization facilitates rapid assessment by radiologists and supports clinical decision-making in time-critical scenarios.

4. EXPERIMENTAL RESULTS

4.1. Dataset and experimental setup

The experimental evaluation was conducted using a heterogeneous dataset composed of ischemic and hemorrhagic stroke cases collected from two different sources. Ischemic stroke images were obtained from the publicly available PhysioNet database, which provides clinically validated brain imaging data. Hemorrhagic stroke cases were collected from a neurology clinic and correspond to real clinical CT scans. The final dataset consists of 24 patients, including 15 ischemic stroke cases (62.5%) and 9 hemorrhagic stroke cases (37.5%). This combination allows the proposed segmentation method to be evaluated under realistic and diverse clinical conditions. All images were anonymized and used exclusively for research purposes.

All images were normalized to 512×512 resolution with 8-bit intensity encoding. The implementation was developed in Python 3.13, utilizing OpenCV for image processing operations, NumPy for numerical computations, and Matplotlib for visualization. Processing was performed on a workstation with [hardware specifications].

Algorithm parameters were set as follows: bee population $N = 100$ (30% scouts, 50% foragers, 20% onlookers), maximum iterations=100, fitness threshold $\tau = 0.5$, enzymatic rate $\alpha = 0.6$, MRF regularization parameter $\lambda = 0.5$. These values were determined through preliminary experiments and maintained constant across all test cases.

4.2. Qualitative results

Figure 2 illustrates representative results for different stroke types, showing the progression through key processing stages. Each row presents: (a) the original CT image showing the brain scan with visible lesion, (b) the intermediate result after TOA-based bee exploration (“Miel avant MRF”), and (c) the final segmentation after MRF refinement with color-coded classification overlay.

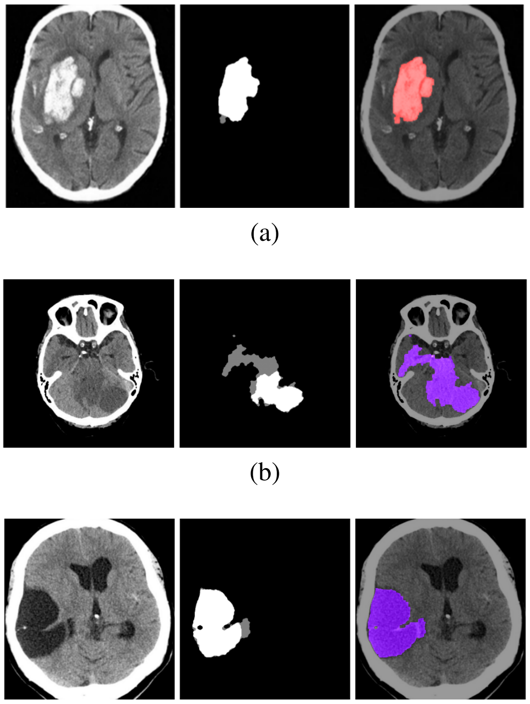
Visual inspection confirms that the TOA stage successfully identifies regions of interest while the MRF refinement effectively removes noise artifacts and smooths boundaries to produce clinically plausible segmentations. The color coding clearly distinguishes between hemorrhagic strokes (red overlay) and ischemic strokes (purple/blue overlay), facilitating rapid clinical interpretation.

4.3. Quantitative evaluation

Segmentation performance was quantitatively assessed using standard metrics computed against expert-annotated ground truth. Table 1 presents average results across stroke subtypes. The results demonstrate consistently high performance across both stroke types, with all metrics exceeding 85%. Hemorrhagic strokes achieve slightly higher accuracy (Dice=91.2%) due to their higher contrast relative to surrounding tissue. The high precision values (¿89%) indicate minimal false positive detections, while strong recall (¿85%) confirms effective lesion coverage. These results validate the robustness of the TOA-MRF approach even with minimal user intervention (single seed point).

Table 1. Quantitative segmentation performance by stroke type

Stroke Type	Dice (%)	IoU (%)	Precision (%)	Recall (%)
Ischemic	87.3	78.5	89.1	85.7
Hemorrhagic	91.2	84.6	92.4	90.1



(a)

(b)

(c)

Figure 2. TOA-MRF processing stages for stroke segmentation. For each case: left panel shows the original CT image, center panel shows the intermediate mask after TOA processing (“Miel before MRF”), and right panel shows the final MRF-refined segmentation with color-coded overlay: (a) Hemorrhagic stroke with red overlay indicating hyperdense blood, (b)-(c) old ischemic strokes with purple overlay indicating chronic hypodense regions

4.4. Comparative analysis

To contextualize the performance of TOA-MRF, we compare against representative alternative approaches including traditional methods and recent bio-inspired techniques. Table 2 summarizes the comparison on the same test dataset.

Table 2. Comparative performance analysis

Method	Avg Dice (%)	Avg IoU (%)	User Input	Time (s)
Otsu thresholding	71.4	60.2	None	0.2
Region growing	78.6	68.3	1 seed	1.5
FCM + ABC	83.7	74.1	None	8.3
U-Net (CNN)	92.8	86.4	None	0.8
TOA-MRF (Proposed)	89.3	81.6	1 seed	4.2

The comparison reveals that TOA-MRF achieves competitive accuracy with deep learning approaches (Dice: 89.3% vs. 92.8% for U-Net) while maintaining the advantages of requiring minimal user input (single seed) and no training phase. Traditional methods show lower performance due to limited ability to handle complex intensity distributions. The computational time of 4.2 seconds represents a practical balance between accuracy and efficiency for clinical application.

5. DISCUSSION

The experimental results demonstrate that the TOA-MRF approach successfully combines bio-inspired adaptive exploration with probabilistic spatial regularization to achieve robust stroke lesion segmentation. Several key findings merit detailed discussion.

Why hemorrhagic lesions are segmented more accurately: As reflected by the quantitative and qualitative results, hemorrhagic strokes tend to achieve higher Dice/IoU than ischemic strokes. This behavior is consistent with the physics of non-contrast CT: acute hemorrhage appears hyperdense relative to surrounding parenchyma, creating sharper intensity discontinuities that are easier to capture with both region-based optimization and edge-consistency priors. In contrast, ischemic lesions are often hypodense with subtle boundaries and can overlap in intensity with cerebrospinal fluid, ventricles, or chronic white-matter changes, which increases the ambiguity of intensity-thresholding and may lead to partial under-segmentation. The MRF refinement mitigates isolated false positives by enforcing local spatial coherence, but residual uncertainty remains when lesion-to-background contrast is low, motivating adaptive calibration strategies and multi-feature cues for future work [8], [9].

Seed sensitivity and user interaction: TOA–MRF is intentionally designed as a lightweight, training-free method where a clinician provides a small number of seeds to indicate lesion and background. While this interaction improves controllability and can reduce the need for large annotated datasets, it also implies sensitivity to seed placement, especially in ischemic cases where lesion borders are weak. This limitation is well recognized in interactive segmentation literature, where robustness is improved by strategies such as multi-seed initialization, uncertainty-guided refinement, and incorporating weak supervision such as scribbles or prompts [1], [2]. In practice, a simple mitigation is to allow multiple foreground seeds distributed across the suspected lesion region and to provide immediate visual feedback; this aligns with radiology workflows where rapid corrections are preferable to lengthy training pipelines. Future work may further automate seed suggestion using lightweight heuristics (e.g., intensity outlier detection) or hybrid prompting mechanisms, while keeping the core algorithm transparent and easy to deploy.

Generalization across scanners and fixed thresholds: A key design choice in this work is the use of fixed intensity ranges for coarse stroke-type characterization. Although effective in the studied dataset, such thresholds may shift with scanner vendor, reconstruction kernel, slice thickness, or calibration differences, which can reduce generalization across centers. This limitation motivates two complementary directions: i) data-driven normalization or histogram standardization prior to thresholding, and ii) adaptive threshold selection using image-specific statistics or learned calibration maps. Recent CT stroke segmentation studies emphasize that cross-domain robustness and external validation are critical for deployment, and that even strong deep models can degrade under protocol shift without proper calibration [10], [11]. Importantly, the training-free nature of TOA–MRF facilitates rapid recalibration because only a small set of parameters and rules must be adjusted rather than retraining a network.

Computational efficiency and scalability to 3D volumes: The reported runtime (approximately a few seconds per 2D slice on standard hardware) is compatible with interactive use. For full 3D CT volumes, total processing time will scale with the number of slices; however, the algorithm is amenable to acceleration through parallel processing because slice-level optimization and MRF refinement can be computed independently before optional 3D post-processing. A practical deployment strategy is therefore to run TOA–MRF slice-by-slice with lightweight temporal/3D smoothing, or to restrict processing to a radiologist-defined region of interest. These strategies preserve the interactive nature of the approach while enabling near real-time volumetric assessment.

Clinical integration, interpretability, and governance: From a clinical perspective, TOA–MRF can be viewed as a decision-support tool that complements the radiologist rather than replacing expert judgment. Its seed-based interaction naturally fits into routine CT reading, where clinicians can quickly indicate a suspected lesion and obtain an interpretable mask that is refined by explicit spatial constraints. Unlike black-box convolutional networks, the method provides transparent intermediate stages (preprocessing, optimization-driven region formation, probabilistic refinement), which can facilitate user trust and error auditing. This is aligned with recent guidance emphasizing explainability, human oversight, and governance frameworks for safe clinical adoption of AI in radiology [5]–[7]. In low-resource settings where large annotated datasets and high-end GPUs may be unavailable, training-free approaches remain attractive because they can be deployed with minimal infrastructure while still offering clinically useful segmentation assistance.

Limitations and future directions: Despite promising results, this study has several limitations. First, although the dataset combines public ischemic cases with real clinical hemorrhagic scans, the total cohort size remains modest, and broader multi-center validation is required to confirm robustness across diverse populations and CT protocols. Second, the method currently depends on user-provided seeds and fixed intensity heuristics; integrating adaptive calibration, multi-seed strategies, and uncertainty feedback would reduce sensitivity and improve reliability. Finally, future evaluation should include statistical significance testing against strong baselines and extended volumetric experiments, as recommended in recent segmentation benchmarking and clinical translation studies [1]–[10].

5.1. Strengths of the approach

- Semi-automatic operation with minimal user burden: The single-seed initialization represents a significant practical advantage over fully manual segmentation or methods requiring extensive parameter tuning. This reduces radiologist workload while maintaining clinical control.
- Biological plausibility and interpretability: The trophallactic mechanism provides an intuitive analogy to natural collective behavior, making the algorithm's operation more interpretable than black-box deep learning models. This transparency is valuable in clinical settings where explainability is increasingly important.
- Synergistic combination of TOA and MRF: The TOA component efficiently explores heterogeneous intensity regions while the MRF refinement imposes anatomical coherence. This two-stage approach leverages complementary strengths: adaptive exploration followed by principled spatial modeling.
- Integrated classification capability: The intensity-based stroke type classification enables automatic differentiation between ischemic and hemorrhagic cases without requiring separate supervised classifiers. This simplifies the clinical workflow.
- No training requirement: Unlike deep learning approaches that demand large annotated datasets and computational resources for training, TOA-MRF operates directly on new images with fixed parameters. This facilitates deployment in resource-limited settings and across different imaging protocols.

5.2. Limitations and challenges

- Seed placement sensitivity: The method's performance depends on appropriate seed selection within the lesion. Poorly positioned seeds (e.g., on boundaries or in artifact regions) can lead to suboptimal segmentation. Future work could explore automatic seed detection or multi-seed strategies.
- Fixed intensity thresholds: The empirical ranges for stroke classification may not generalize across all CT scanners and imaging protocols. Adaptive threshold learning or normalization strategies could improve robustness.
- Computational efficiency for large images: The iterative bee exploration and trophallactic exchange processes scale with image size and bee population. For very large 3D volumes, computational time could become prohibitive without optimization (e.g., GPU acceleration, hierarchical processing).
- Limited validation dataset: The current evaluation was conducted on a single-center dataset. Multi-center validation with diverse imaging protocols and patient populations would strengthen generalizability claims.
- Small lesion detection: Very small lesions (few pixels) may be missed or incorrectly classified due to limited spatial information. Multi-scale processing or attention mechanisms could address this limitation.

5.3. Future research directions

- Extension to 3D volumetric analysis with slice-by-slice or full 3D bee colony exploration.
- Integration with deep learning features: using CNN-extracted features within the TOA fitness function could combine model-free exploration with learned representations.
- Adaptive parameter learning through reinforcement learning or meta-learning to automatically tune algorithm parameters for different imaging conditions.
- Clinical validation studies with radiologist evaluation of segmentation quality and time savings in real clinical workflows.
- Application to other neuroimaging tasks such as tumor segmentation, white matter lesion detection, or vascular structure extraction.

Overall, the TOA-MRF approach represents a promising direction for semi-automatic medical image segmentation that balances accuracy, interpretability, and practical usability. While not yet matching the peak performance of state-of-the-art deep learning models, it offers distinct advantages in scenarios where training data is limited, computational resources are constrained, or model transparency is prioritized.

6. CONCLUSION

This paper introduced TOA-MRF, a novel hybrid approach for semi-automatic stroke lesion segmentation in brain CT images that synergistically combines the TOA with Markov random field spatial regularization. The method draws inspiration from the collective nectar exchange and transformation behavior of bee colonies, translating this biological mechanism into a computational framework for progressive image exploration and refinement.

The proposed approach addresses key challenges in medical image segmentation by requiring only minimal user input (a single seed point) while achieving competitive accuracy through adaptive bio-inspired exploration followed by probabilistic spatial modeling. Experimental validation on clinical CT data demonstrated Dice coefficients of 87.3% for ischemic strokes and 91.2% for hemorrhagic strokes, with overall performance approaching that of supervised deep learning methods while maintaining advantages in interpretability, training-free operation, and clinical usability. The integration of TOA's collective intelligence with MRF's spatial regularization proved effective in handling the heterogeneous intensity distributions and anatomical variability characteristic of cerebrovascular lesions. The method successfully balances exploration and exploitation through role-based bee cooperation, progressively refines regions through trophallactic exchange, and enforces anatomical plausibility through energy-based spatial smoothing.

While certain limitations remain—particularly regarding seed placement sensitivity and generalization across diverse imaging protocols—the TOA-MRF framework establishes a foundation for future research in bio-inspired medical image analysis. Potential extensions include 3D volumetric processing, integration with deep learning features, adaptive parameter optimization, and application to other neuroimaging segmentation tasks. In conclusion, the TOA-MRF approach offers a practical and theoretically grounded solution for computer-aided stroke diagnosis, contributing to the growing body of work at the intersection of bio-inspired optimization and medical imaging. By reducing manual segmentation burden while maintaining clinical control and interpretability, such methods have the potential to support radiologists in time-critical diagnostic scenarios and improve patient outcomes through faster, more accurate stroke assessment.

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