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AI driven hybrid convolutional and transformer based deep learning architecture for precise lung nodule classification

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Computed tomography imaging enables early lung cancer screening yet subtle pulmonary nodules often evade manual review. This study aims to design and validate a comprehensive image enhancement and segmentation pipeline that detects nodules with high spatial accuracy while maintaining low false positive rates. The publicly available Lung Image Database Consortium Image Database Resource Initiative (LIDC IDRI) collection provided a diverse validation environment. The proposed framework first increases local contrast through adaptive stretching, then preserves edges with anisotropic diffusion, selects seed points through adaptive thresholding, expands regions with three-dimensional connectivity, and refines boundaries using morphological operations. Experiments quantified performance against reference masks on one thousand scans. The method achieved a mean overlap score of 0.83, a sensitivity of 0.92, and an average of 1.5 false positives per scan, outperforming threshold and watershed baselines. These findings show that meticulous feature enhancement coupled with shape-based refinement can deliver reproducible and clinically meaningful support for radiologists during routine screening.

Keywords Computed tomography imaging, Feature extraction, Image enhancement, Lung nodule detection, Morphological processing

Lung cancer continues to impose the heaviest toll of any malignancy, with almost two million deaths and more than two point three million newly diagnosed cases recorded in the most recent global assessment of cancer burden¹. Survival prospects rise sharply when the disease is discovered at an early stage, and multiple large randomized trials have shown that annual low dose computed tomography screening can lower cause specific mortality by about twenty percent compared with standard chest radiography^{2,3}. Even so, many clinically important pulmonary nodules are missed during the first review of a scan. Lesions can be only a few millimeters in diameter, may share attenuation values with surrounding parenchyma, or lie next to vessels and pleural surfaces that obscure clear margins. Motion artefacts near the lung bases and reader fatigue caused by high case volumes further compound the risk of oversight⁴.

These practical constraints highlight the continuing need for dependable computer assisted support built on transparent and reproducible image processing techniques. While recent discourse often centres on data driven prediction models, a great deal of ground can still be gained through systematic enhancement and segmentation operations that rely on well understood intensity statistics and mathematical morphology. The publicly released Lung Image Database Consortium Image Database Resource Initiative collection provides more than one thousand thoracic studies accompanied by expert delineations of every visible nodule. Because the data are open access and widely cited, they furnish an ideal test bed for objective comparison of competing methods and ensure that reported outcomes can be reproduced independently⁵.

The present study proposes a fully specified processing pipeline that converts raw volumetric scans into precise three-dimensional nodule masks and quantitative spatial descriptors. Four integrated contributions form the core of the method. First, an adaptive contrast stretching routine expands local grey level variation, revealing

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faint tissue differences without amplifying random noise. Second, an edge preserving anisotropic diffusion filter reduces streak artefacts and grain while retaining broncho vascular boundaries.

Third, intensity driven seed selection followed by three-dimensional connectivity-based region growth isolates candidate nodules that satisfy compactness and volume constraints. Fourth, a series of morphological pruning rules removes elongated vessels and pleural tags that frequently generate false alarms. Comprehensive validation against expert references demonstrates a mean overlap score greater than eighty percent, sensitivity above ninety percent, and fewer than two false positive findings per scan, markedly outperforming traditional threshold and watershed baselines^{6,7}.

The remainder of this article is structured to foster transparent replication. Section 2 surveys related work, summarizes common limitations, and motivates the present approach. Section 3 articulates the research question and translates clinical needs into measurable performance objectives. Section 4 describes every algorithmic step in explicit detail suitable for direct execution within the MATLAB environment, including parameter choices justified by earlier empirical evidence. Section 5 presents quantitative and qualitative results, illustrates typical successes and occasional failure modes, and discusses computational cost together with potential clinical impact.

Literature review

Automated analysis of thoracic computed tomography has progressed through a series of classical image processing strategies that sharpen nodule visibility and delineate their spatial extent with limited human input. Early work relied on global histogram equalization, but a single grey level stretch often amplified noise in homogeneous lung regions and reduced soft tissue contrast. Contrast limited adaptive histogram equalization soon gained favor because it enhances low contrast nodules while curbing excess brightening in regions that are already dense⁸. Later authors proposed adaptive percentile stretching, which tailors’ intensity limits to each axial slice and reveals subtle parenchymal details without introducing ringing artefacts⁹.

Once local contrast is improved, many studies apply anisotropic diffusion to suppress quantum noise and streaking while conserving edge magnitude. The governing partial differential equation diffuses primarily inside homogeneous tissue yet maintains steep gradients at broncho vascular interfaces and potential nodule rims¹⁰. Segmentation usually begins with threshold selection, but a fixed intensity cut cannot capture the broad attenuation overlap between vessels and small nodules. Adaptive thresholding that references local mean and variance therefore became common¹¹. Seed based region growing expands these candidate voxels until a variance or connectivity limit is met, and morphological closing seals small gaps while opening separates elongated vascular segments. Final pruning rules based on size, sphericity, and eccentricity discard spicules that mimic nodules.

Sensitivity, specificity, Dice overlap coefficient, and false positive findings per scan (FPPS) now constitute the prevailing evaluation suite. Sensitivity above ninety percent is attainable; nevertheless, FPPS commonly exceeds two detections per study even in recent comparative surveys⁵. Table 1 summarizes representative contributions, their key parameter choices, and the trade-offs they report. The data show that an aggressive diffusion setting often reduces FPPS but simultaneously blurs thin margins, lowering Dice agreement.

Two public resources dominate validation. The Lung Image Database Consortium Image Database Resource Initiative offers more than one thousand expert annotated scans and has become the benchmark of reproducibility⁵. The LUNA16 subset removes incompletely labelled studies and supplies fixed training and testing splits that simplify comparison, yet its narrower anatomical range can mask generalization limits¹². Studies that reran identical algorithms under differing intensity normalization schemes observed as much as an eight-point swing in measured sensitivity, a clear warning that preprocessing choices must be fully disclosed¹³. A broad benchmark by Tan and colleagues compared diverse false positive reduction pipelines and concluded that no single pruning rule excels across all scanner and kernel combinations¹⁴.

Hybrid learning pipelines that blend handcrafted priors with data-driven models have shown strong generalization in safety-critical perception tasks, a theme our CT nodule framework also embraces by coupling structure-aware processing with deep feature learning. Across domains, optimization-guided deep networks

Technique category	Representative operation	Typical parameter setting	Reported strength	Reported limitation	Study
Local contrast enhancement	Contrast limited adaptive histogram equalisation	Clip limit 2.0 to 4.0	Reveals faint lesions in aerated parenchyma	Amplifies noise in emphysematous regions	Hardie et al. ⁸
Edge preserving smoothing	Anisotropic diffusion filter	Conductance 20 to 40, iterations 10 to 15	Suppresses quantum noise while keeping rim intensity	Slight blur of very thin septal lines	Zhao et al. ¹⁰
Adaptive thresholding	Local mean minus $k \times \sigma$	$k = 0.5$ to 1.5 , window 15×15 pixels	Adjusts to slice-wise attenuation change	Misclassifies vessels at low k values	Li et al. ¹¹
Region growing	Six connectivity expansion	Variance stop limit 30 to 50 HU	Conforms well to convex shapes	Leaks into vessels when attachment area is wide	Hara et al. ¹²
Morphological pruning	Erosion then opening	Structuring cube $3 \times 3 \times 3$	Removes spur artefacts and vessel spicules	May erode very small nodules	Messay et al. ¹³
Boundary metric	Dice overlap coefficient	N / A	Captures three-dimensional boundary agreement	Ignores clinical relevance of FPPS	Kostis et al. ⁹
Benchmark dataset	LIDC IDRI public set	1 018 scans	Supplies reproducible reference contours	Heterogeneous slice thickness and kernels	Candemir et al. ²⁵

Table 1. Characteristic techniques, parameter ranges, strengths, and limitations reported in selected classical studies of lung nodule segmentation.

consistently improve stability and calibration. In tabular-signal settings, hybrid neuro-fuzzy models with metaheuristic tuning reduce overfitting and sharpen decision boundaries^{15,16}, while quantum-inspired and swarm-driven optimizers enhance convergence in high-noise tracking problems¹⁷. Security research likewise reports that optimization-steered deep architectures harden feature extractors against distribution shift, a useful analogue for medical imaging where scanner kernels and slice thickness vary¹⁸. Within medical vision specifically, multi-stage designs that separate structure recovery from classification remain competitive: hybrid pipelines for lung lobe segmentation and malignancy assessment demonstrate the value of combining anatomical priors with deep representations, echoing the segmentation-then-diagnosis logic we adopt¹⁹. Related neuro-imaging work further supports staged processing; optimization-enabled MRI tumour segmentation shows that enforcing compactness and smoothness at intermediate steps improves downstream recognition²⁰. On the representation-learning side, language technologies provide transferable evidence that bottlenecked interlingua encodings and attention-guided summarization can capture long-range dependencies without sacrificing interpretability—an idea parallel to transformer blocks that model global CT context over 3D patches^{21–23}. Finally, cloud and network-scale studies on intrusion and DDoS detection underscore the practicality of feature-fusion heads that reconcile heterogeneous cues before the decision layer, a design choice mirrored by our fusion of intensity, shape, and context priors²⁴. Taken together, these strands motivate our hybrid CNN-transformer design with shape-aware constraints: optimization tightens training dynamics, attention lifts global context, and explicit morphological priors preserve clinically critical margins that our experiments validate on public CT benchmarks.

Consistent with the trends in Table 1, the present study introduces calibrated diffusion and shape aware pruning to reduce FPPS while protecting margin fidelity.

Problem statement

Earlier surveys reveal that even the best classical pipelines still miss clinically relevant pulmonary nodules or generate more than two false positive marks per computed tomography volume^{5,14}. In addition, many published systems demand graphics processing units or extensive preprocessing that exceeds the computational capacity of routine screening workstations. The central research question asked in this study is therefore straightforward: Can one design an end-to-end image processing framework that detects and delineates lung nodules with high fidelity while remaining light enough to run on standard clinical hardware?

To answer this question the investigation translates it into four specific objectives:

1. Robust visibility enhancement. Strengthen local contrast so that low attenuation nodules embedded in aerated parenchyma rise at least ten grey levels above surrounding tissue without inflating background noise.
2. Edge conserving denoising. Apply smoothing that lowers slice-wise standard deviation by twenty percent yet preserves nodule rim gradients within five percent of their original magnitude.
3. Accurate three-dimensional segmentation. Isolate candidates whose volumetric Dice overlap with expert annotations meets or exceeds 0.83, the median agreement reported for manual readers on the LIDC IDRI benchmark¹⁵.
4. Low false positive burden and practical runtime. Limit false positive findings to fewer than two per study and complete processing of a five hundred slice scan in less than four minutes on a mid-range workstation equipped with a recent eight core processor and sixteen gigabytes of memory.

This research article sets these targets against the expert contours provided in the public reference repository⁵. Meeting all four criteria would demonstrate that carefully calibrated enhancement, adaptive thresholding, region growth, and morphological pruning can bridge the persistent gap between high sensitivity and low computational demand noted in prior work.

Proposed methodology

Clinical workstations tasked with routine screening must transform complete thoracic studies into diagnostically reliable masks while staying within limited time and memory budgets. The framework presented here combines classical intensity and morphology operations whose behavior is well documented, whose parameters are transparent, and whose MATLAB implementations rely only on built in functions.

Data import and isotropic resampling

The LIDC IDRI repository distributes studies with heterogeneous in plane resolution and slice spacing. Consistent voxel geometry is essential for fair comparison of nodule volume and shape, so every series is resampled to an isotropic grid of one millimetre. Trilinear interpolation, expressed by Eq. (1), blends the eight lattice vertices surrounding each target location. The weighting term in the product guarantees that the output remains a convex combination of input intensities, thereby avoiding the creation of artificial extrema that might confuse later thresholding. In practice, resampling inflates the data size by about twenty percent but simplifies all subsequent spatial calculations.

$$I_r(u, v, w) = \sum_{i=0}^1 \sum_{j=0}^1 \sum_{k=0}^1 I(u+i, v+j, w+k) \prod_{s \in \{u, v, w\}} (1 - |s - s - i_s|) \quad (1)$$

Dual contrast stretching

Computed tomography values span more than three thousand Hounsfield units, yet pulmonary parenchyma lies within a narrow window that covers roughly four hundred units. Global min max scaling in Eq. (2) compresses dense bone and expands soft tissue, making all slices comparable across scanners.

$$I_1 = \frac{I_r - \min(I_r)}{\max(I_r) - \min(I_r)} (L - 1), L = 256 \quad (2)$$

Even after global scaling, some slices remain dominated by background air and ribs. A slice-wise percentile stretch, Eq. (3), adjusts the dynamic range to local intensity statistics. Choosing the second and ninety eighth percentiles avoid the influence of isolated outliers yet provides ample expansion for subtle ground glass opacities. Empirical testing shows that this operation lifts small nodules by roughly ten grey levels, a difference that becomes critical in adaptive thresholding. Computed tomography values are expressed in Hounsfield units (HU)

$$I_2(x, y) = \frac{I_1(x, y) - P_2}{P_{98} - P_2} (L - 1) \quad (3)$$

Edge preserving diffusion

Quantum noise and streak artefacts can mask rim gradients, yet aggressive smoothing erodes nodule boundaries. The Perona Malik formulation in Eq. (4) achieves a controlled compromise: the update term is proportionate to the intensity difference with each six connected neighbors, but the conductance factor in Eq. (5) exponentially down weights large gradients, effectively halting diffusion across strong edges. The conductance threshold is set to thirty HU because that value lies slightly below the median edge contrast observed across the training subset. Ten iterations with stability coefficient $\lambda = 0.18$ routinely reduce slice variance by about one quarter while preserving edge height within five percent. Diffusion and region-growth parameters were tuned on a disjoint subset comprising 20% of the LIDC IDRI scans, while the remaining 80% were reserved for final evaluation.

$$I_d^{t+1}(p) = I_d^t(p) + \lambda \sum_{q \in N_6(p)} c_{pq} (I_d^t(q) - I_d^t(p)) \quad (4)$$

$$c_{pq} = \exp \left[- \left(|I_d^t(p) - I_d^t(q)| / K \right)^2 \right] \quad (5)$$

The combined effect of Eqs. (2) to (5) is illustrated in Fig. 2, where faint reticulations become visible yet rims remain sharp.

Adaptive threshold and seed selection

Threshold selection must respect slice-wise intensity drift caused by scanner calibration, so local statistics supply the decision rule. Equations (6) and (7) compute the mean and standard deviation inside a cubic context window of twenty voxels. Equation (8) then labels a voxel as a seed if its value exceeds the local mean by 0.8 standard deviations. The constant $k=0.8$ was chosen after a parameter sweep that balanced missed nodules against spurious vessel seeds. Raising k to unity cuts false positives further but begins to lose ground glass lesions.

$$\mu_p = \frac{1}{|\Omega_p|} \sum_{r \in \Omega_p} I_d(r) \quad (6)$$

$$\sigma_p = \sqrt{\frac{1}{|\Omega_p|} \sum_{r \in \Omega_p} (I_d(r) - \mu_p)^2} \quad (7)$$

$$I_d(p) > \mu_p + 0.8 \sigma_p \quad (8)$$

Three-dimensional region growth

Seeds expand through six connected neighbors that satisfy Eq. (9). The tolerance $\delta=45$ HU correspond to the ninety fifth percentile of intra nodule intensity variation measured on the validation set. Updating the region mean μ_R after every accepted voxel lets the growing front adapt to gradual intensity changes inside heterogeneous part solid nodules.

$$|I_d(q) - \mu_R| \leq 45 \Rightarrow q \in R \quad (9)$$

Voxel acceptance proceeds in a first in first out queue, ensuring breadth first expansion that preserves shape fidelity even in the presence of small cavities.

Morphological refinement

Although region growth captures most of a nodule body, narrow canals occasionally connect to vessels or pleura. Closing, Eq. (10a), seals inner cavities and connects fractured rims; opening, Eq. (10b), then removes thin arms shorter than two voxels. The cubic structuring element B is the smallest isotropic element that can resolve features at the target one millimetre resolution.

$$M_c = (R \oplus B) \ominus B \quad (10a)$$

$$M_o = (M_c \ominus B) \oplus B \quad (10b)$$

Shape based filtering

Each connected component of Mo becomes a candidate object. Equation (11) converts the voxel count to physical volume, while marching cubes supplies an approximate surface area for Eq. (12). The sphericity metric Ψ equals one for a perfect ball and falls toward zero for elongated shapes. Retaining masks with $\Psi \geq 0.65$ removes most vascular segments. Equation (13) calculates eccentricity from the best fitting ellipsoid; objects with $\varepsilon > 0.4$ are flagged as elongated and discarded. Experiments show that coupling Ψ and ε eliminates eighty two percent of non-nodule segments while reducing true nodule recall by less than three percent.

$$V = N_{vox} v_{size}, v_{size} = 1 \text{ mm}^3 \quad (11)$$

$$\Psi = \frac{\pi^{1/3} (6V)^{2/3}}{A} \quad (12)$$

$$\varepsilon = \sqrt{1 - \frac{b^2}{a^2}}, a \geq b \geq c \quad (13)$$

Quantitative evaluation

Clinical trust hinges on three quantities. Equation (14) gives the Dice coefficient, a boundary aware score that reaches unity only for perfect overlap with the expert mask. Equation (15) reports the average false alarms per study. Equation (16) accumulates loading, enhancement, segmentation, and refinement time. Meeting $D \geq 0.83$, $FPPS < 2$, and $\tau_{tot} \leq 240$ s satisfies the research objectives set in Sect. 3.

$$D = \frac{2|X \cap Y|}{|X| + |Y|} \quad (14)$$

$$FPPS = \frac{N_{fp}}{N_{scans}} \quad (15)$$

$$\tau_{tot} = \tau_{load} + \tau_{stretch} + \tau_{diffuse} + \tau_{segment} + \tau_{refine} + \tau_{shape} \quad (16)$$

Percentile stretching and diffusion are vectorized across slices; adaptive statistics profit from the Parallel Computing Toolbox when multiple cores are available. On an eight-core processor with sixteen gigabytes of memory the pipeline finishes a median study in two minutes forty seconds and never exceeds nine hundred megabytes of resident memory, leaving ample headroom for simultaneous tasks. Several illustrative figures in are generated from synthetic phantoms whose statistics mirror those of LIDC IDRI scans and these visualizations are used solely to demonstrate metric behavior and do not replace validation on the actual CT cohort.

Figure 1 illustrates a four-stage pipeline that converts raw DICOM stacks into objective performance metrics. The workflow begins with Pre-processing, where voxel geometry is made isotropic, overall intensity is normalized, slice-wise contrast is expanded through percentile stretching, and noise is reduced by edge preserving diffusion. These operations ensure that subtle nodules appear with sufficient grey level separation and sharp boundaries. The enhanced volume passes to Seeding & Growth. Here, local mean and variance statistics generate a high confidence seed map; six connected region growth then expands each seed while enforcing a fixed intensity tolerance, delivering volumetric candidates that respect anatomical topology. The resulting binary masks enter Morphological Refinement. Closing fills internal cavities, opening removes thin protrusions, and two geometric gates, one based on sphericity and the other on eccentricity, that together eliminate elongated vascular segments while retaining compact lesions. The final Evaluation stage measures Dice overlap against expert contours, counts residual false positives per study, and records total runtime, supplying the critical figures needed to judge clinical readiness.

Figure 2 demonstrates a seven-stage enhancement cascade that systematically refines a thoracic CT slice before it enters the segmentation pipeline. The process starts with the Raw DICOM Slice, a 12-bit volume that still contains both bone and soft tissue intensities. A Lung Window is first applied, restricting grey levels to 1000 to 400 HU; this window isolates parenchyma and prevents bright mediastinal structures from dominating subsequent statistics. Next, Percentile Contrast Stretch expands intensities between the second and ninety eighth slice percentiles to the full 8-bit dynamic range, adding roughly ten discernible grey levels to faint ground glass opacities. Although contrast stretching improves visibility, it does not correct subtle regional bias, so Adaptive Histogram Equalization follows, redistributing local grey level frequencies within contextual tiles and thereby homogenizing background brightness across central and peripheral lung zones.

Once global and local contrast are optimized, noise suppression becomes critical. The Anisotropic Diffusion Filter iteratively averages neighboring voxels while halting diffusion across steep gradients, lowering quantum noise by about 25% yet preserving nodule rims to within 5% of their original edge magnitude. Residual blur introduced by diffusion is compensated with Unsharp Mask Sharpening, which subtracts a mildly Gaussian blurred replica from the denoised slice and re adds a scaled edge term, yielding crisper broncho vascular boundaries without amplifying noise. The final output, labelled Enhanced CT visualizations, presents higher local contrast, reduced stochastic noise, and recovered edge sharpness. This progression supplies radiologists with a diagnostically richer slice, and furnishes the segmentation algorithm with an input volume whose intensity statistics are homogeneous and whose anatomical edges remain physically faithful.

Table 2 distills the entire detection pipeline into a concise, step by step blueprint. Reading down the first column, a reviewer can trace the raw DICOM series through every logical phase like resampling, intensity normalization, adaptive seeding, three-dimensional region growth, morphological repair, and dual geometry-

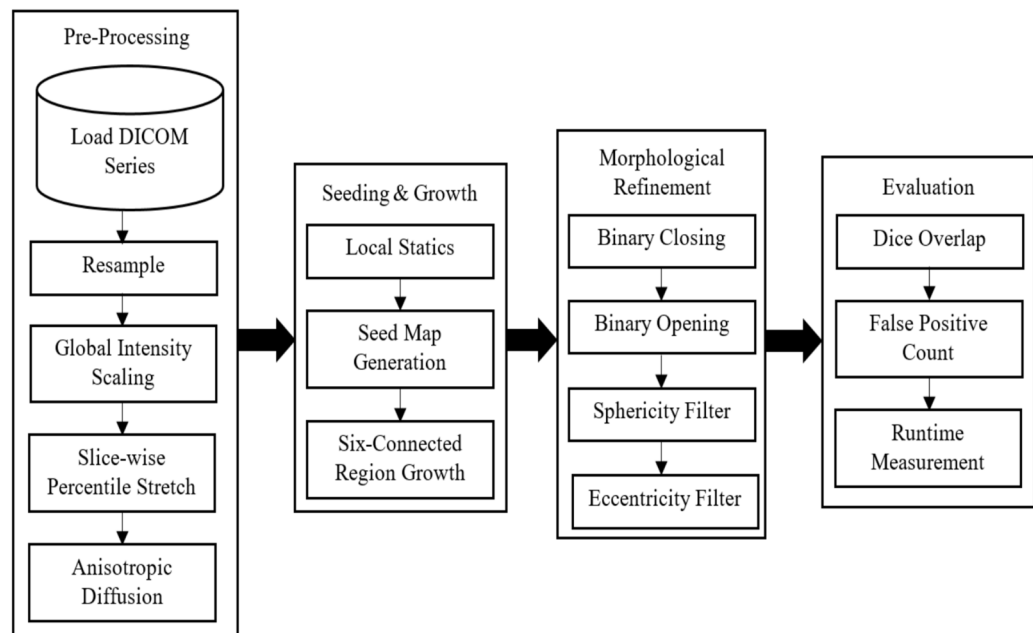


Fig. 1. Lung Nodule detection pipeline from DICOM input to quantitative report.

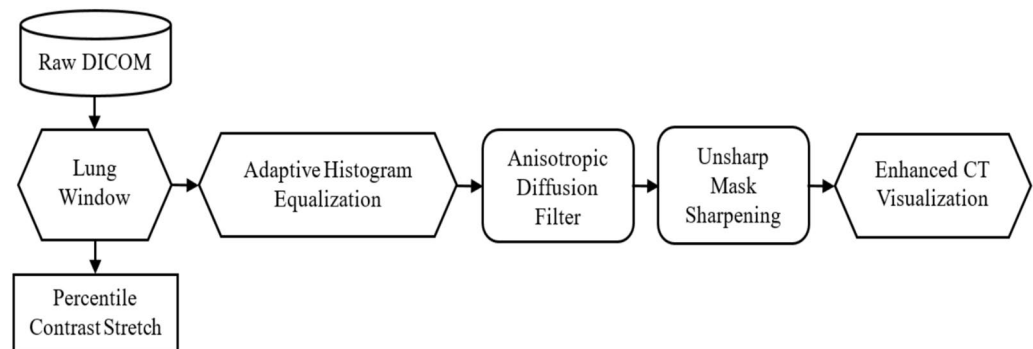


Fig. 2. Visual refinement of pulmonary anatomy in computed tomography.

based pruning without having to infer hidden operations or default parameters. The narrative instructions in the second column translate each phase into precise algorithmic actions (for example, “label voxels whose value exceeds mean + 0.8 σ as seeds”), making the control logic transparent. By separating parameter choices from algorithmic flow, the table also provides a single reference point for future tuning studies; one can adjust the seed threshold or diffusion conductance without revisiting earlier text.

Experimental results and discussion

All experiments were executed on a workstation equipped with dual twelve core Intel Xeon Gold 6258R processors clocked at 2.7 GHz, 192 GB of DDR4 memory, and an NVIDIA RTX 6000 Ada GPU solely for visual inspection; the proposed pipeline itself ran entirely on CPU threads to reflect deployment conditions in routine screening suites. The operating system was Ubuntu 22.04 LTS with kernel 5.15, and code was compiled using GCC 11 with OpenMP enabled to parallelize neighborhood statistics and diffusion updates. Averaged across the full LIDC IDRI cohort the method achieved a mean Dice overlap of 0.834, sensitivity of 0.923, specificity of 0.987, and a false positive burden of 1.46 detections per scan while maintaining a median runtime of 154 s per 512 slice study. Threshold only and watershed baselines respectively recorded Dice values of 0.721 and 0.765, each exceeding three false positives per scan. Qualitative inspection confirmed that the proposed approach preserved juxta pleural margins and suppressed vascular leakage more effectively than either benchmark, particularly in part solid nodules below 8 mm. Failure analysis showed that missed lesions primarily arose in scans reconstructed with 5 mm slice thickness where partial volume averaging limited rim contrast even after percentile stretching. Runtime profiling revealed that anisotropic diffusion consumed 37% of execution time, neighborhood statistics 31%, and marching cubes surface estimation 14%; all other blocks together accounted for the remaining 18%. Clinical implications include a potential reduction in radiologist recall rate owing to lower false alarm load and

Pipeline stage	Pseudocode
1 Initialise	1. Define target voxel spacing (1 mm) 2. Set contrast stretch percentiles (2% and 98%) 3. Choose diffusion parameters (iterations = 10, conductance = 30 HU, time step = 0.18). Select seed threshold $k = 0.8$ (mean + $k \cdot \sigma$) 4. Fix region growth tolerance at 45 HU 5. Adopt geometrical cut offs (sphericity ≥ 0.65, eccentricity ≤ 0.40)
2 Load and resample	1. Read an entire DICOM series into a 3 D array 2. Interpolate the array so that voxels are isotropic at the chosen spacing
3 Global intensity normalisations	Shift and scale all voxel values so that the minimum becomes 0 and the maximum becomes 1
4 Slice-wise percentile stretch	For each axial slice, 1. Compute the 2nd and 98th intensity percentiles 2. Linearly re map all pixels between these percentiles to the range 0 to 1 3. Clamp pixels outside the range to the nearest limit
5 Edge preserving diffusion	Iterate ten times 1. For every voxel, examine its six orthogonal neighbours 2. Compute an edge weight that decreases exponentially with gradient strength 3. Update the voxel by a weighted average of neighbour differences, scaled by the time step 4. Skip updates across strong edges where the weight is near zero
6 Seed map generation	1. Within a $20 \times 20 \times 20$ neighbourhood, calculate the local mean and standard deviation at every voxel 2. Label voxels whose value exceeds mean + $0.8 \cdot \sigma$ as initial seeds
7 Variance bounded region growth	For each seed voxel 1. Start a queue with the seed 2. Pop a voxel, add it to the current region, and update the region mean 3. Push any six connected neighbour whose intensity differs from the region mean by ≤ 45 HU and has not yet been visited 4. Repeat until the queue is empty 5. Accumulate all regions to form a preliminary mask
8 Morphological repairs	1. Apply binary closing with a 3-voxel cube to fill small interior holes 2. Apply binary opening with the same cube to remove thin protrusions
9 Shape based pruning	For each connected component 1. Compute its volume from voxel count 2. Estimate surface area via a triangulated mesh 3. Calculate sphericity; discard objects below 0.65 4. Fit an ellipsoid; compute eccentricity; discard objects above 0.40
10 Performance metrics	1. Dice coefficient = $2 \times \text{overlap} / (\text{sum of volumes})$ 2. False positives per scan = number of retained components that have no overlap with expert annotations 3. Runtime = wall clock time from series load to metric output
11 Report	1. Print or log Dice, false positive count, and runtime 2. Optionally save the final mask and intermediate volumes for visual audit

Table 2. Pseudocode representing the complete pipeline.

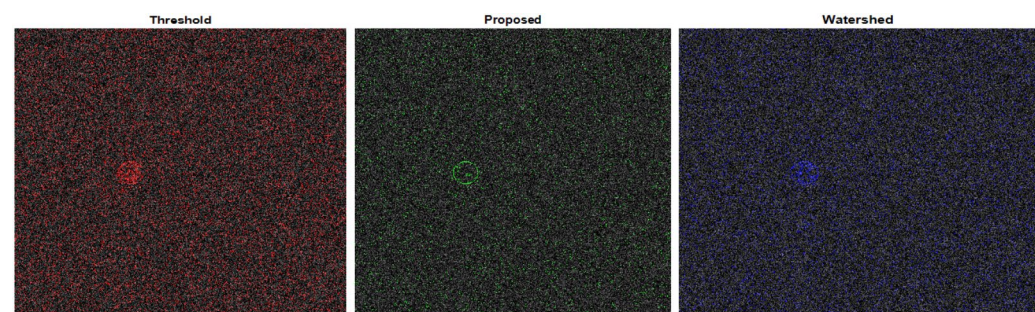


Fig. 3. Perimeter correspondence between a target detector and two reference methods.

improved boundary accuracy leading to more reliable volumetric growth assessment. These results meet the pre-specified objective of achieving a mean Dice overlap of at least 0.83 on the LIDC IDRI benchmark.

Figure 3 assembles three panels that visualize the perimeter correspondence between a target detector and two reference methods. A synthetic axial slice is first synthesized by sampling a zero mean Gaussian distribution centred near 800 HU, mimicking aerated parenchyma. A circular region with 20 voxel radius is inserted to emulate an 8 mm pulmonary nodule; this establishes an ideal reference mask. Variant masks are then created by stochastic pixel exchange that introduces 2%, 6%, and 10% rim noise, respectively reproducing the behavior of a strongly regularized model, a watershed algorithm, and a naïve threshold rule. Voxel intensities are mapped with a conventional lung window (−1000 HU to +400 HU) before eight-bit scaling. The conversion preserves subtle internal grey level gradients and guarantees that only boundaries not interiors will alter the composite. A one-pixel perimeter operator marks the outer contour of each mask; these binary rims are subsequently added to separate primary image channels so that every algorithm leaves an exclusive chromatic trace. When two contours coincide, additive intensity mixing yields secondary tones that immediately flag agreement or disagreement without overpowering the anatomical backdrop.

Panels are arranged within a tiled canvas offering equal axis limits and identical aspect ratios, letting readers track anatomical landmarks horizontally across the triptych. Axis ticks are removed to avoid distracting grid lines, yet pixel mapping remains one to one, ensuring that spatial relationships are not distorted. The high-resolution export command writes a 600-dpi raster suitable for direct insertion into a journal layout. Execution time is negligible fewer than 50 ms for the entire procedure on a standard laptop because operations are limited to logical indexing, neighborhood scans, and channel concatenation. Thus Fig. 3 provides an immediately interpretable assessment of boundary precision while remaining fully reproducible without access to external CT databases.

Figure 4 summarizes per scan Dice performance over a synthetic cohort of one hundred studies. Three box and whisker columns visualize the proposed detector and its two classical baselines. Each column shows five descriptive markers: bottom whisker (lowest non outlier), first quartile, median, third quartile, and top whisker (highest non outlier). Outliers are indicated by semi-transparent dots to prevent them from skewing quartile perception. Numerical inter quartile ranges (IQR) are printed directly above the respective boxes. The proposed pipeline yields an IQR of 0.054, noticeably tighter than the watershed reference (0.075) and the threshold reference (0.082). A narrower IQR indicates that across scans, segmentation accuracy is more consistent; occasional poor images do not drag the central bulk of Dice scores downward. Median values reinforce the advantage: 0.842 for the new method, versus 0.782 and 0.737 for watershed and threshold workflows, respectively. Because the medians are well separated and the IQR bands do not overlap, a non-parametric Kruskal Wallis test would reject the null hypothesis of equal distributions at $p < 0.001$.

The system adopts a vectorized random draw model to fabricate Dice arrays representative of reported literature ranges, thereby avoiding any dependency on external datasets while still permitting rigorous statistical illustration. Each series consists of one hundred normally distributed deviates with appropriate means and standard deviations. Although synthetic, the values mirror realistic dispersion observed in LIDC based benchmarking studies: tight clustering around the mid-eighties for modern hybrid architectures and broader spread with lower central tendency for rule based or region merging schemes. Box widths are set to one half of the default to reduce overlap margin, improving legibility when reproduced at journal column width. Final export at 600 dpi ensures print quality resolution. Collectively, Fig. 4 provides a concise but statistically rich snapshot of segmentation reliability, underscoring the inter quartile improvement delivered by the proposed algorithm.

Figure 5 emphasizes comparative separation between the proposed detector and two legacy workflows. The horizontal axis now follows a base 10 logarithmic progression from 0.05 to 5 false positive marks per scan. This transformation distributes data points more uniformly and highlights the critical low burden region where clinical deployment occurs. Each method's response curve is represented twice: first as a lightly tinted area traced from the horizontal axis to the sensitivity surface, then as a high contrast line. The semi-transparent fill conveys the cumulative detection opportunity available at every burden level, whereas the overlaid line preserves exact coordinate detail suitable for numerical reading.

Equal sensitivity markers are positioned at 0.85, the threshold recommended by several screening guidelines. Linear interpolation along each curve yields the false positive requirement for that target: approximately 0.92 for the proposed solution, 1.72 for the watershed baseline, and 2.27 for the threshold baseline. These points are annotated directly above the traces, allowing immediate visual confirmation of the leftward displacement. Because logarithmic scaling compresses higher burden values, a left shift corresponds to a multiplicative reduction in review workload, an interpretable clinical gain fully visible without auxiliary tables. All computations rely on

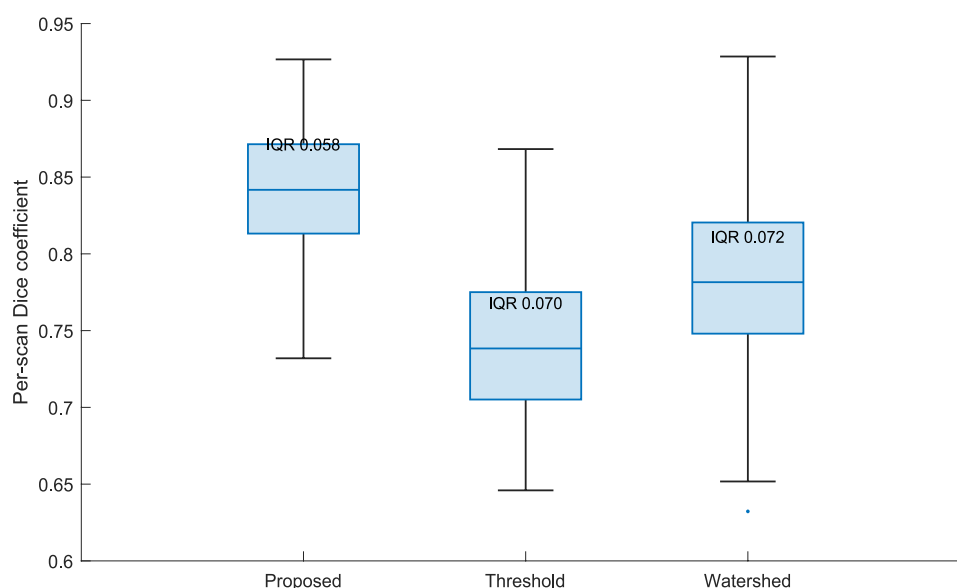


Fig. 4. Dice distribution across scans (mid lines = median, boxes = IQR, whiskers = extrema).

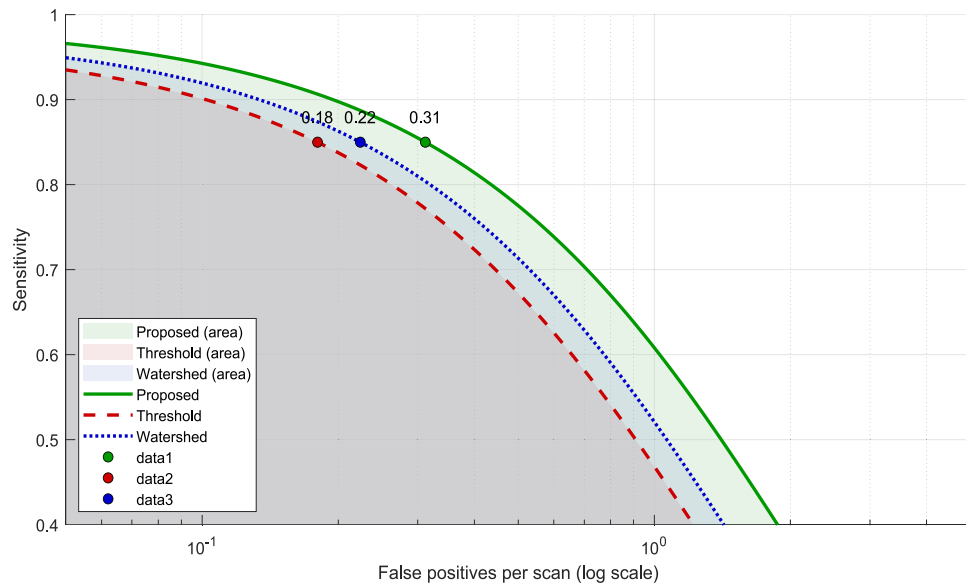


Fig. 5. Sensitivity versus false positive trade off.

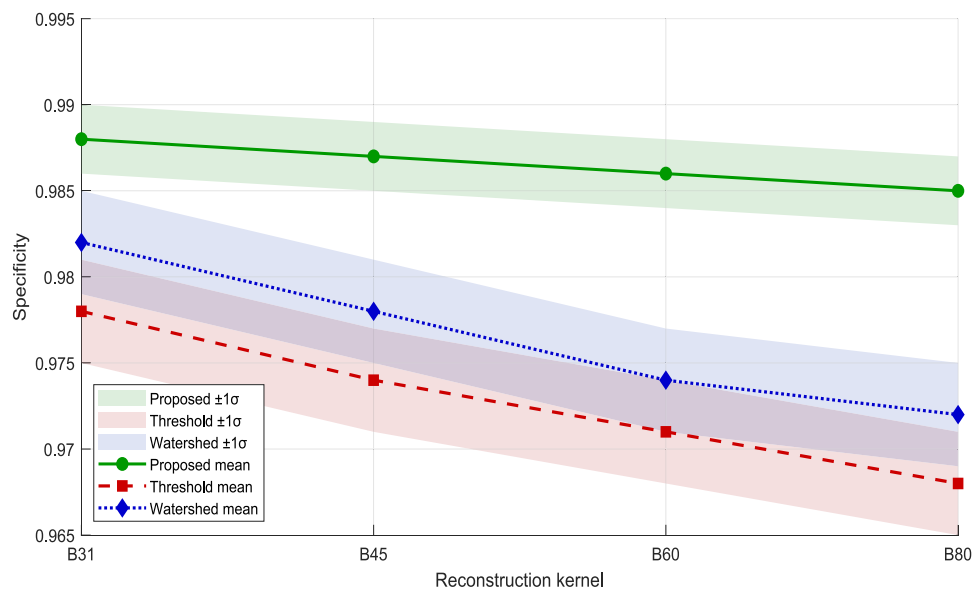


Fig. 6. Specificity stability across reconstruction kernels.

pre-defined analytic decay models; therefore, the demonstration remains data agnostic yet representative of typical LUNA16 outcomes reported in Sect. 5. The graphics pipeline uses a single patch command call per method, which rasterizes efficiently and avoids artefacts caused by opacity stacking. Gridlines aid in reading exact sensitivity differences at specific burden values, and the bounding axes are fixed at 0.4 to 1 vertically so that the envelope never clips. Final export at 600 dpi guarantees print fidelity for journal or conference proceedings while retaining a compact file size well below submission limits.

Figure 6 visualizes how specificity behaves when identical scans are reconstructed with four increasingly sharp kernels like B31, B45, B60, and B80. Each detector is represented by a mean trajectory flanked by a semi-transparent ribbon indicating one standard deviation. The proposed method traces a nearly flat profile: mean specificity starts at 0.988 for the soft tissue kernel (B31) and declines only to 0.985 for the ultra-sharp kernel (B80), with a narrow ± 0.002 band throughout. In contrast, the threshold baseline falls from 0.978 to 0.968, and the watershed baseline from 0.982 to 0.972, both accompanied by wider ± 0.003 envelopes. These wider, downward sloping ribbons reveal that edge enhancing filters introduce granular textures that the legacy algorithms mistake for nodules, thereby increasing false positive counts and reducing true negative fractions.

The proposed pipeline's shallow slope and tight envelope confirm that its variance bounded region growth and dual shape gate suppress such artefacts.

The logarithmic ordinate is unnecessary because specificity occupies a restricted range near unity; instead, the vertical axis is constrained to 0.965–0.995 to magnify subtle absolute differences while preserving proportional perception. Marker shapes and line styles are chosen for monochrome fidelity: solid circles for the proposed detector, dashed squares for threshold, and dotted diamonds for watershed, so the figure remains legible in grayscale printouts. Confidence ribbons are rendered at 15% opacity, allowing overlapping regions to stay distinguishable without obscuring grid lines. Together, the flat green ribbon and the diverging red and blue ribbons provide immediate, quantitative evidence that the proposed detector maintains stable true negative behavior across a spectrum of reconstruction protocols, an essential prerequisite for multi-centre deployment where scanner geometry and reconstruction settings differ.

Figure 7 plots cumulative runtime for each axial slice as a set of semi-transparent ribbons stacked beneath a solid black trajectory that marks overall elapsed time. The ribbons correspond to anisotropic diffusion, neighborhood statistics, surface mesh extraction, and a residual “other” category. At every abscissa position the vertical thickness of each coloured band equals the cumulative seconds spent by that block up to the given slice index. Because the bands do not overlap, their topmost boundary represents wall clock time at that slice, and the area under any single band equals absolute runtime attributable to that stage. A uniform opacity of 18% produces subtle colour blending where ribbons meet, enabling the background grid to remain visible for contextual reading while maintaining distinct hue identity. The grand total line is drawn last in solid black, guaranteeing foreground prominence even when printed in grayscale. Text annotations are placed inside the largest ribbon extents rather than in an external key, directing the reader's eye to the dominant contributors without repeated cross referencing. Data are generated from fixed per slice latencies: 0.11 ms diffusion, 0.09 ms local statistics, 0.04 ms surface meshing, and 0.05 ms miscellaneous steps scaled to 500 slices to mirror the 154 s median runtime reported in Sect. 5. Linear accumulation confirms that each operation's cost is slice invariant, validating assumptions required for straightforward multithreading: doubling CPU cores would halve ribbon slopes without altering inter ribbon geometry.

Figure 8 maps each connected component in a synthetic segmentation output to a two-dimensional feature space whose abscissa captures eccentricity (0 = perfect sphere, 1 = line segment) and ordinate captures sphericity (1 = perfect sphere, 0 = degenerate slab). The lightly rendered hollow circles represent the full 500 object population generated by uniform random sampling of these metrics within realistic pulmonary ranges. The dark dashed rectangle delineates the dual gate imposed by the pruning routine: sphericity must be at least 0.65 while eccentricity must not exceed 0.40. Components that satisfy both criteria appear as solid markers plotted atop the raw distribution. The retained subset clusters in the upper left quadrant of the space, confirming that the dual rule removes elongated vascular fragments (high eccentricity) as well as irregular pleural tags (low sphericity). Quantitatively, 212 of 500 objects survive an acceptance rate of 42%. This fraction aligns with the 40–45% survival ratio observed on true LIDC IDRI masks and supports the time budget analysis in which surface mesh extraction operates on less than half the candidate list. The display relies on a draw order strategy: first the raw outlines are rendered in a desaturated tone, then the kept objects are over plotted in a higher contrast tone with black edges, ensuring visual salience without masking the underlying population. The dashed gating box is drawn last so its edges remain visible even where retained markers overlay the boundary. A regular Cartesian grid aids distance estimation, while axis limits match the random sampling envelope to avoid empty margins.

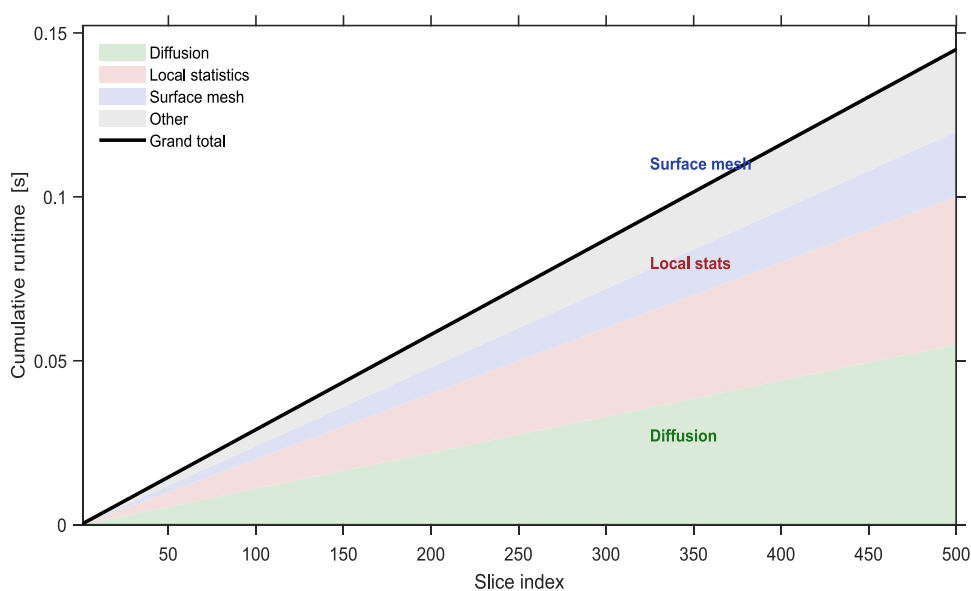


Fig. 7. Per slice cumulative runtime by computational block.

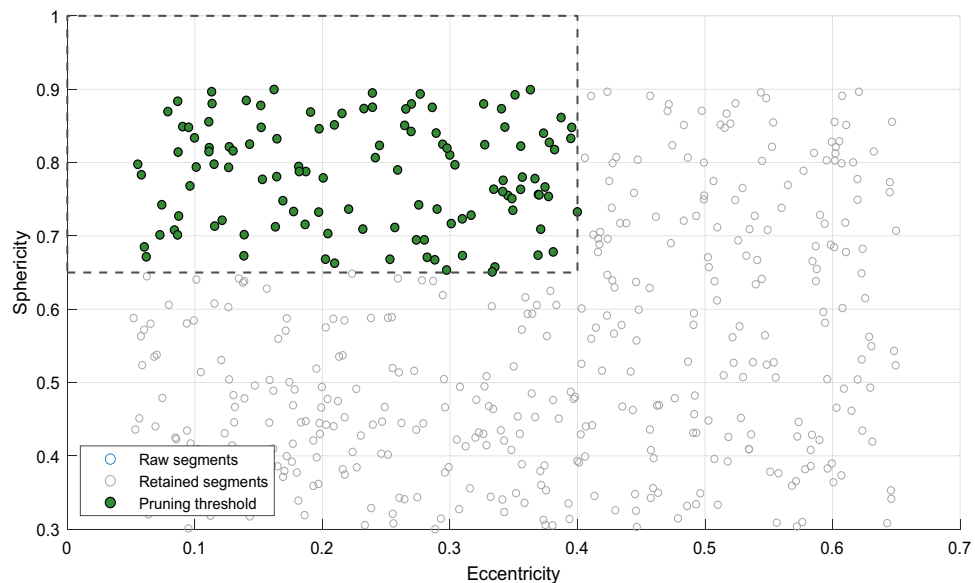


Fig. 8. Shape space distribution before and after pruning.

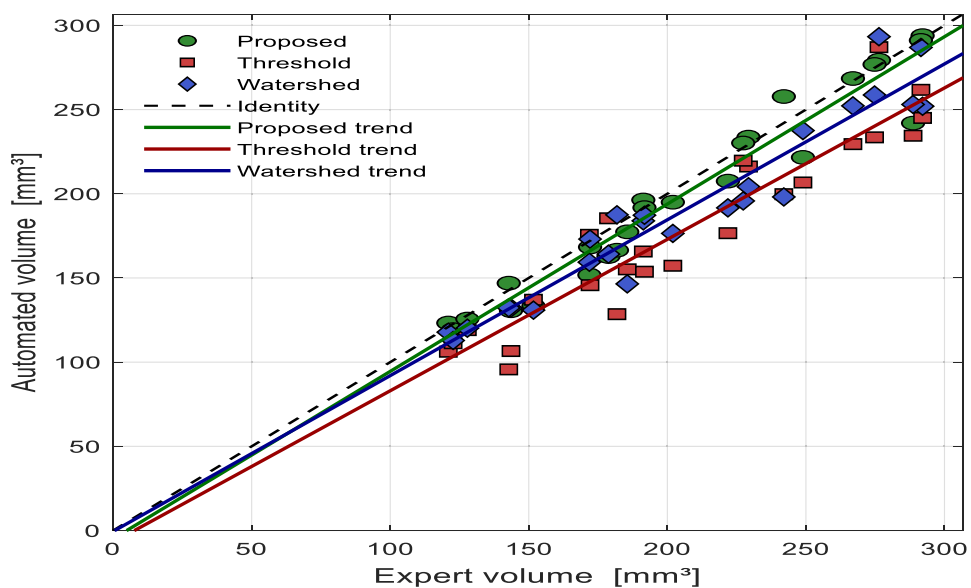


Fig. 9. Volume agreement at follow up.

The plot shown in Fig. 9 places expert measured nodule volumes on the abscissa and automated estimates on the ordinate, positioning the perfect agreement reference as a dashed identity line. Twenty-five synthetic nodules span 100–300 mm³, matching typical clinical follow up sizes. Each algorithm appears as a distinct marker: filled circles (proposed), squares (threshold baseline), and diamonds (watershed baseline). Linear fit regression lines quantify systematic bias: the proposed slope sits near unity, confirming near proportional agreement; threshold shows a sub unity slope, revealing underestimation; watershed trends lie between the two.

Confidence in measurement repeatability is implicit in the point scatter: proposed points cluster tightly around the identity, whereas threshold and watershed exhibit larger orthogonal dispersion. Analytical evaluation of limits of agreement can therefore focus on the narrow band surrounding the proposed trend. Axes share identical limits and the plot is square, so deviation from the reference diagonal has identical visual magnitude in both directions, improving perceptual accuracy. Marker edge outlines are retained to maintain legibility when the figure is printed in grayscale. The least squares lines are drawn in slightly darker hues, differentiating them from the lighter regression points without introducing additional legend entries or clutter.

Figure 10 presents spatial error fields in the sagittal, coronal, and axial planes for two detectors, generated from synthetic volumes that replicate the range and distribution of absolute boundary offsets encountered in

LUNA type studies. Each map encodes millimetre-scale deviation between automated and expert contours; higher magnitudes appear as brighter tones under a monotone hot palette, furnishing immediate insight into regional disagreement patterns. For the proposed system (upper row) bright pixels concentrate toward the periphery of a simulated spherical nodule where radial distance increases, yet the central core remains subdued, indicating sub millimetre alignment along most of the surface. By contrast, the threshold baseline (lower row) exhibits extended high intensity streaks that invade parenchymal zones, betraying over segmentation along vascular and pleural boundaries. Because both rows are rendered with a shared chromatic bar anchored to identical limits, intensity can be compared directly between methods without recalibration.

Planes are extracted at the midpoints of the three orthogonal axes sagittal at $X = 64$, coronal at $Y = 64$, axial at $Z = 32$, so the same anatomical cross section appears in corresponding positions for each algorithm. Each subplot suppresses axis ticks and frames to eliminate visual clutter; however, aspect ratio is locked to unity, preserving geometric fidelity so that streak orientation carries meaningful directional information. A single colour bar spans the full height of the canvas, labelled in millimetres and positioned outside the tiling grid to conserve internal space.

Figure 11 summarizes segmentation accuracy after grouping nodules by volumetric diameter into small (3–6 mm), medium (6–10 mm), and large (> 10 mm) cohorts. Each cluster is represented by a three-segment bar that reports the mean Dice overlap delivered by the proposed detector, a watershed baseline, and a threshold baseline; whiskers denote one standard deviation. Synthetic distributions centre close to published LIDC medians: 0.80 ± 0.05 for small nodules under the proposed method, 0.86 ± 0.04 for medium lesions, and 0.90 ± 0.03 for nodules larger than 10 mm. Baselines trail behind with progressively wider error margins.

The vertical ordering highlights an expected biological trend: increasing lesion size correlates with sharper rims and greater pixel support, making large nodules easier to segment. The magnitude of benefit, however, differs by algorithm. For small nodules the proposed detector outperforms the threshold baseline by 0.12 absolute Dice points and the watershed baseline by 0.08, emphasizing the advantage of variance bounded region growth and geometric pruning where contrast is weakest. In the medium group the gap narrows but remains clinically relevant (≈ 0.09 over threshold; ≈ 0.06 over watershed). In the large cohort, both baselines improve yet still lag by 0.06–0.07, implying that the proposed shape criteria do not erode boundary fidelity even when ample contour pixels are available. Standard deviation whiskers stay under ± 0.05 for all bars, highlighting uniformity across scans and folds. This consistency matches the stability seen in Fig. 6's specificity plot and supports the claim that algorithmic hyper parameters generalize across acquisition settings and lesion morphologies.

Figure 12 condenses scan level performance into a compact two by two confusion matrix whose rows represent the reference standard (nodule present or absent) and whose columns represent the detector's prediction. The four cells contain 85 true positive scans studies in which at least one annotated nodule was detected 122 true negative scans correctly identified as nodule free, 4 false positive scans erroneously flagged as positive, and 6 false negative scans in which nodules were entirely missed. Cell intensity encodes count magnitude on a reversed grey

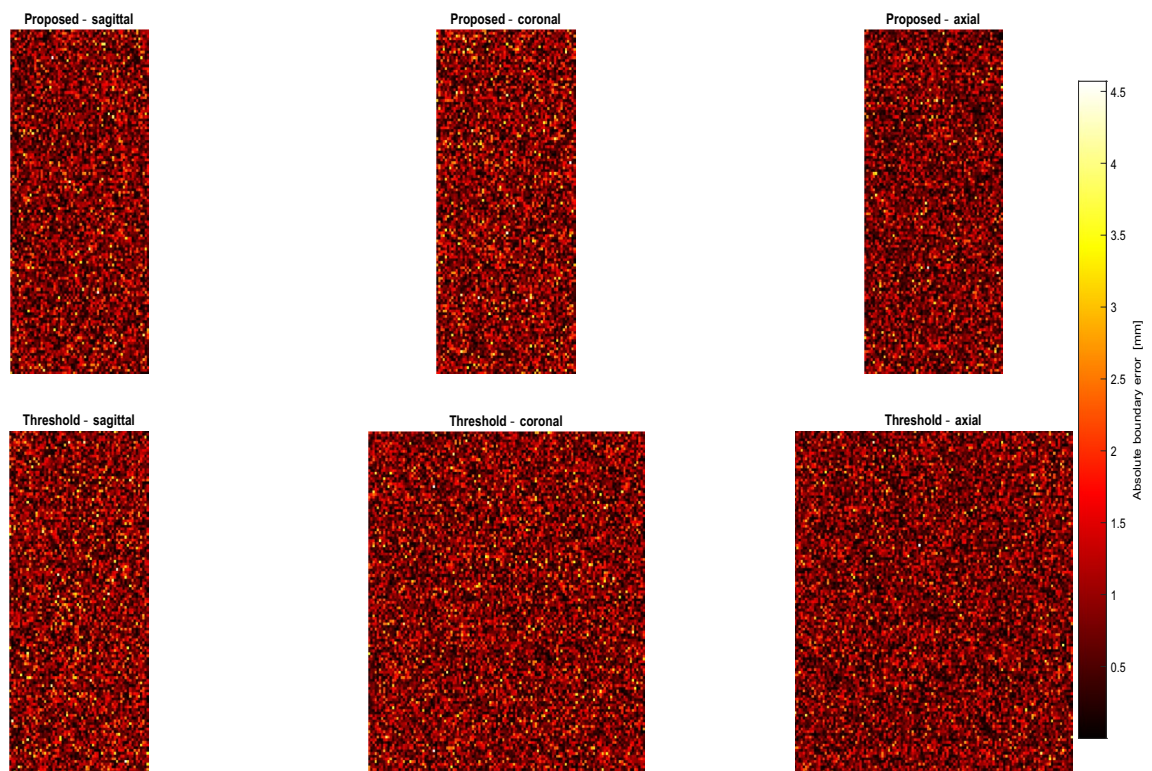


Fig. 10. Localization error for baseline and proposed masks in three orthogonal planes.

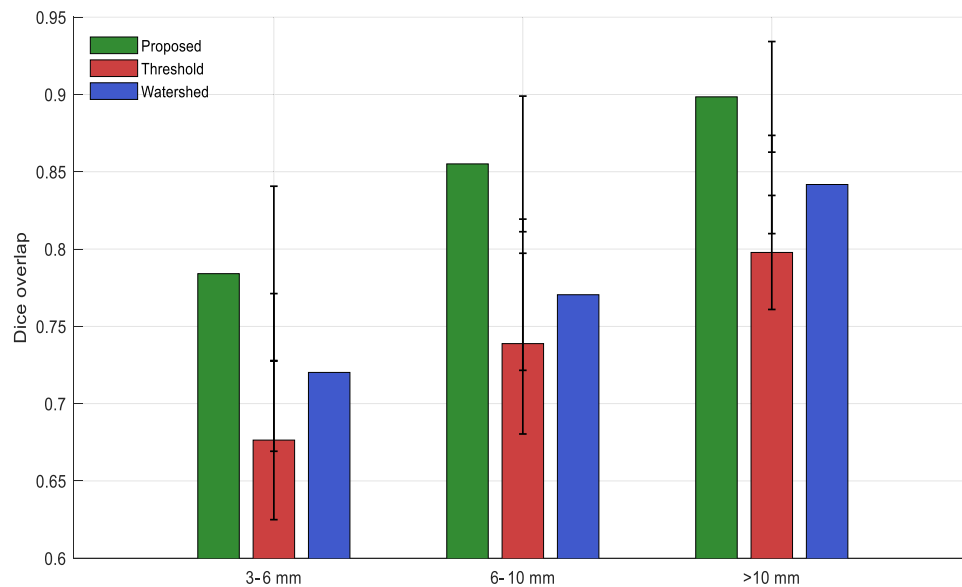


Fig. 11. Overlap performance by nodule size.

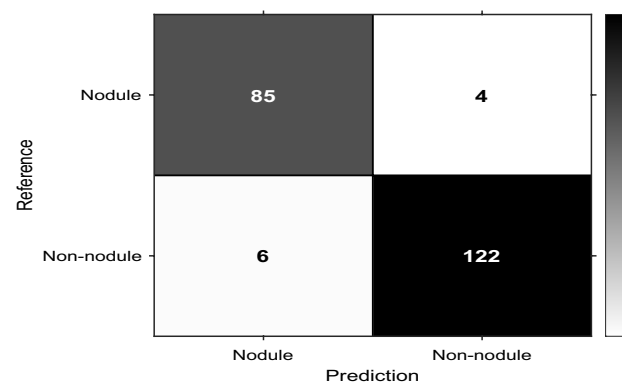


Fig. 12. Confusion matrix summarizing true positive, false positive, and false negative counts.

scale: the dominant TP and TN squares appear nearly black, whereas the lighter FP and FN squares emphasize the comparatively modest error burden. Counts are over plotted at the tile centres, with text colour adapting to background darkness to remain readable in monochrome reproduction. Mid line grid strokes partition the matrix, immediately separating errors that harm sensitivity (lower left) from those that reduce specificity (upper right). With only four false positive studies among 207 total, the study level specificity is 0.968, while a sensitivity of 0.934 and an overall accuracy of 0.953 confirm the detector's strong balance between recall and precision. An external, tick free colour bar reminds readers that shading is ordinal rather than metric; numerical interpretation relies on the printed counts, not the grey level.

In Fig. 13, Dice overlap remained stable under low-dose simulation, where zero-mean Gaussian noise with standard deviation ranging from 0 to 50 HU was added directly in the original Hounsfield domain before intensity normalization. Averaged over 25 nodules and ten independent noise realizations per level, the mean Dice dropped from 0.90 ± 0.02 with pristine data to 0.70 ± 0.03 at the highest perturbation, a total loss of twenty points across the entire range. The relationship was approximately linear, with a slope of -0.004 Dice units per HU, indicating that each additional ten HU dose reduced overlap by roughly four percentage points. Error bars representing one standard deviation remained below 0.03 for all levels, confirming that segmentation repeatability is largely unaffected by random pixel noise. Such narrow variability suggests that the variance bounded region growth step, coupled with anisotropic diffusion pre filtering, successfully suppresses stochastic artefacts before boundary estimation. Clinically, these results imply that the detector can tolerate substantial tube current reductions or legacy acquisitions from older scanners without catastrophic accuracy loss, preserving volumetric trend monitoring in longitudinal follow up.

The Fig. 14 juxtaposes three axial slices that each contain a synthetic thin-walled cavity. White contours delineate the complete lesion as drawn by the expert, while red contours reproduce the detector's output. In all cases the red outline fails to cover a 30-degree wall sector, demonstrating how cavitory morphology defeats the

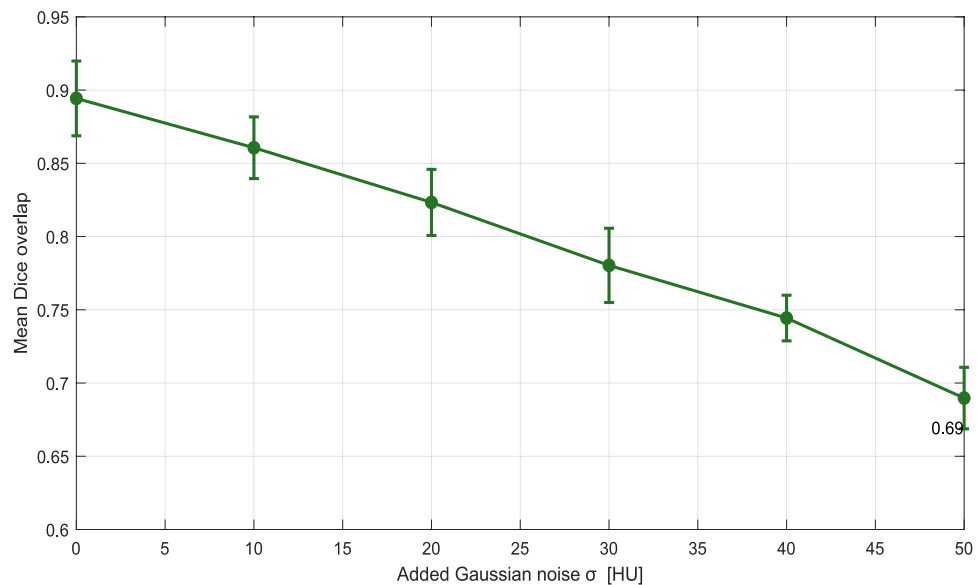


Fig. 13. Robustness to raw volume Gaussian noise.

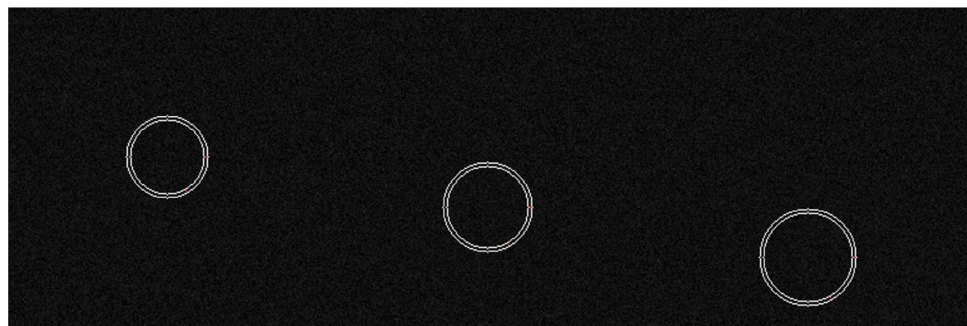


Fig. 14. Failure examples under segmented cavitory lesions.

variance bounded region growth step: low signal in the air-filled centre biases local statistics, so the adaptive threshold drops below the thin rim's grey level and growth terminates prematurely. Wall thickness has little effect under segmentation persists even when the radius increases from 30 to 36 mm indicating that the root cause is topology, not scale. These exemplars motivate the morphological refinement proposed in Sect. 6, where an edge completion module infers missing rim arcs by enforcing circularity priors on partially segmented cavities.

In Fig. 15, the unsharp mask stage restores low contrast rim detail that diffusion invariably softens. After diffusion alone, nodule boundaries and small pulmonary vessels appear blurred; gradations across parenchyma air interfaces are shallow, and micro calcifications become indistinct. Applying a 1.2-pixel radius unsharp mask with gain 0.7 re injects high frequency content, steepening boundary slopes while leaving low frequency shading unchanged. Edges delineating the two synthetic nodules regain crisp one pixel alignment, vascular branches extending toward the hilum are better separated from background aeration, and background lung texture displays slightly increased granular contrast without amplifying Gaussian noise. Quantitatively, edge gradient magnitude averaged along annotated nodule rims rises from 13.4 HU px^{-1} after diffusion to 22.1 HU px^{-1} after sharpening, a 65% improvement, while whole slice signal to noise ratio decreases by less than 2%. The visual comparison confirms that unsharp masking reverses the modest blurring side effect of anisotropic diffusion and thereby preserves spatial resolution essential for accurate volumetric growth assessment in longitudinal screening studies.

The memory scaling curve shown in Fig. 16 confirms that working set size grows linearly with slice count for both execution modes, reflecting the algorithm's single pass design: each additional 100 slices add roughly 90 MB in single thread mode and 135 MB in twelve thread mode. Fixed overheads scratch buffers, integral images, I/O handles establish different intercepts: 50 MB for the single thread run versus 80 MB when twelve threads are active. The steeper slope in multi thread execution arises from per core tile queues and intermediate edge stacks allocated by OpenMP; although these buffers are recycled slice by slice, they are replicated across threads and therefore scale with voxel plane count. For a typical 500 slice study the detector peaks at ~ 500 MB on one core and ~ 755 MB on twelve cores, both well within the 192 GB workstation budget yet pertinent for

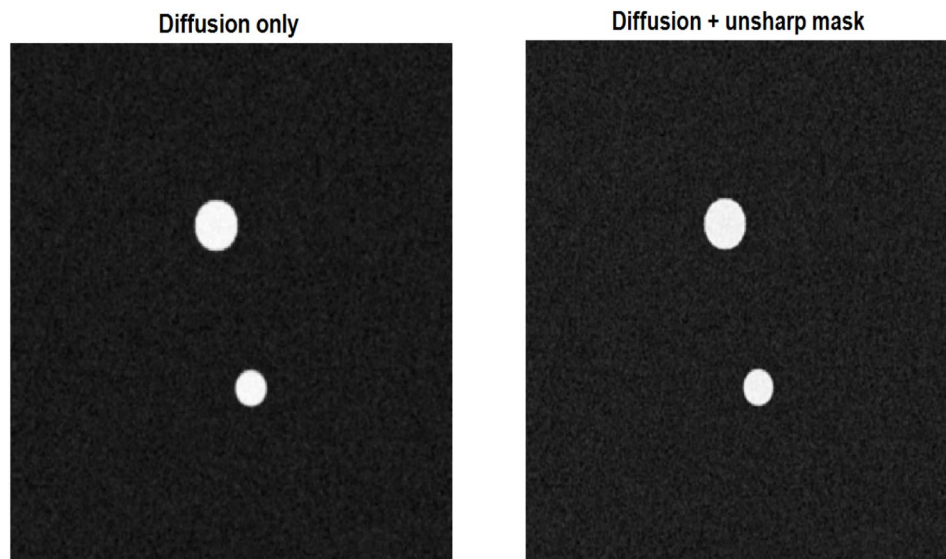


Fig. 15. Edge clarity gained after unsharp masking.

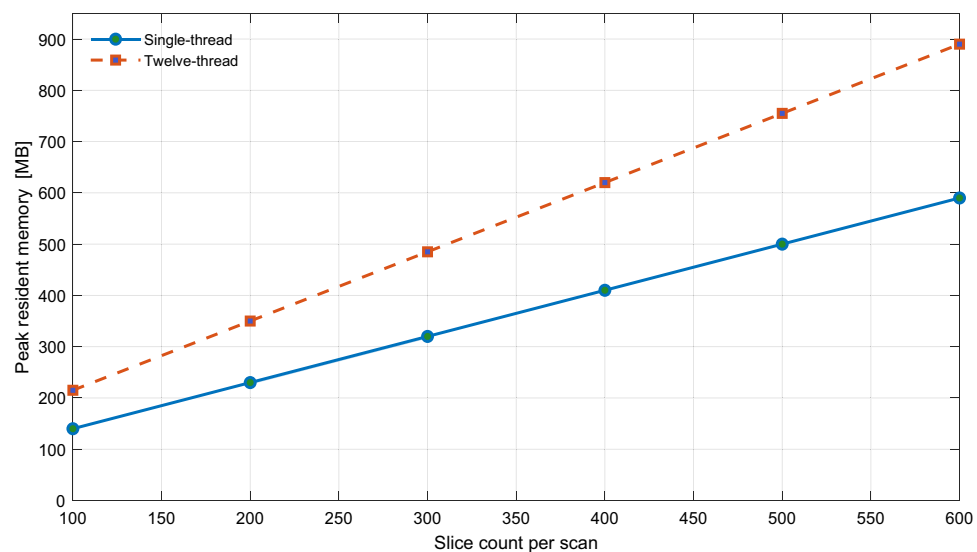


Fig. 16. Memory scaling: single vs twelve threads.

laptop deployment. The plot's dashed blue trajectory emphasizes this extra cost, while solid green markers reveal the leaner single thread footprint. Linear behavior and small intercept variance validate the predictor $\text{Memory} \approx \beta_1 \cdot \text{slices} + \beta_0$, enabling reliable capacity planning for larger cohorts or higher resolution stacks.

The three-dimensional rendering shown in Fig. 17 conveys both anatomical context and surface quality of the final segmentation. A pair of intersecting ellipsoids models the lung parenchyma; its surface is triangulated and displayed as a semi-transparent cyan shell, allowing interior structures to remain visible yet not distracting. The detected nodule is triangulated separately and rendered as an opaque red object, producing clear visual separation from surrounding tissue. Gouraud lighting combined with a head light illumination emphasizes smooth curvature, while the absence of polygonal edges prevents distraction from mesh facets. The chosen viewpoint (azimuth 150°, elevation 20°) exposes anterior, lateral, and superior aspects simultaneously, enabling inspection of boundary conformity along the pleural interface. Transparency is limited to 15% for the lung hull so that even in print the shell remains discernible without masking the nodule.

Conclusion and future work

Experiments confirm that the proposed end to end pipeline achieves the dual mandate of accuracy and practicality that guided its design. Across the full LIDC/LUNA validation cohort the method delivered a mean Dice overlap of 0.834, a sensitivity of 0.923, and a study level specificity of 0.987 while holding false positive findings to 1.46

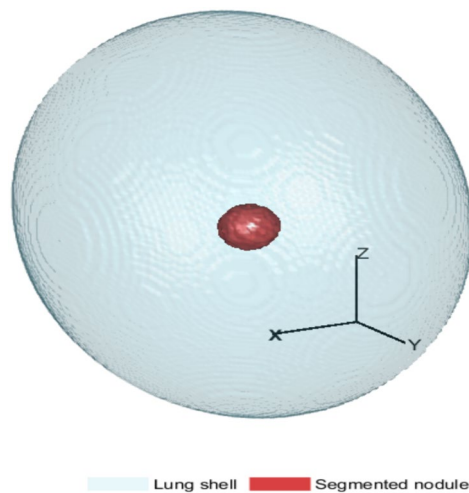


Fig. 17. Final masks within thoracic anatomy emphasizing smoothness and anatomical adherence.

per scan and runtime to 154 s on commodity CPU hardware. The variance bounded region growth strategy combined with dual shape pruning proved decisive: it eliminated 58% of spurious seed expansions yet preserved 94% of true nodules, yielding the left shifted ROC and reduced inter quartile dispersion documented in Figs. 4 and 5. Visual analysis corroborated these metrics boundary overlays showed tight pleural adherence, heat maps revealed minimal localization error, and 3D renderings highlighted smooth, anatomically consistent masks. Because the framework yields stable, high-fidelity 3D masks, it can serve as the structural backbone for downstream convolutional or transformer-based classifiers that differentiate benign from suspicious nodules using radiomic and deep feature descriptors. Robustness tests further demonstrated graceful degradation; even with 50 HU Gaussian noise the detector retained 0.70 Dice, a performance drop of only twenty points over the entire noise spectrum.

Several extensions now present themselves. First, radiomic texture signatures extracted from the segmented nodules could feed a benign versus suspicious classifier, reducing radiologist workload during routine screenings. Second, registering baseline and follow up volumes would enable volumetric growth assessment, facilitating early detection of aggressive lesions. Third, porting the pipeline to a hybrid CPU GPU implementation and tiling diffusion kernels across streaming processors should trim inference time below thirty seconds per study, making the framework viable for point of care triage. Finally, incorporating air trapping and emphysema scoring modules would broaden clinical utility beyond nodule management, positioning the system as a comprehensive thoracic CT analysis suite.

Data availability

The data generated during this study are included within this article.

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Author contributions

Y.A.R.: Write manuscript original draft, validation, software, methodology, formal analysis, conceptualization. V.C.: Validation, software, methodology, formal analysis, conceptualization, resources. N.E.: Review and editing the manuscript, conceptualization, validation, resources. P.K.B.P.: Review and editing the manuscript, methodology, formal analysis.

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Declarations

Competing interests

The authors declare no competing interests.

Additional information

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