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Deep learning ensembles for lung cancer detection in thoracic CT scans leveraging generative adversarial network technology

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ABSTRACT

Effective treatment of lung cancer depends on early and accurate detection, which continues to be a major cause of cancer-related fatalities globally. Conventional diagnostic techniques are useful, but their efficacy in handling large amounts of thoracic computed tomography (CT) scan data is limited by their time-consuming nature and susceptibility to human error. The research here suggests a new deep learning model that integrates generative adversarial networks (GANs) for data improvement with a sophisticated ensemble approach to classification. GANs are employed to generate realistic synthetic CT images, addressing the challenges of limited datasets. The backbone of the proposed approach is a consensus-guided adaptive blending (CGAB) ensemble model that learns to dynamically combine the predictions of three top-performing convolutional neural networks (CNNs): ResNet-152, DenseNet-169, and EfficientNet-B7. The CGAB model improves prediction accuracy through model contribution weighting based on confidence scores and inter-model consensus, while a conflict-resolving auxiliary decision model is used. The approach was tested using the lung image database consortium and the image database resource initiative (LIDC-IDRI) dataset with a detection rate of 97.35%, surpassing single-model and traditional ensemble methods. The current work provides a solid and scalable approach to lung cancer detection with better generalization, increased diagnostic consistency, and applicability for clinical use.

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1. INTRODUCTION

Artificial intelligence (AI) is transforming healthcare by enabling more accurate, efficient, and scalable decision-making [1]. AI systems are giving assistance in disease diagnosis, outcome prediction, and treatment optimization. AI improves values in resource restricted environments through automating repetitive tasks, processing large-scale data in real time, and improving diagnostic consistency [2]. Of the many AI technologies, deep learning, and more specifically, convolutional neural networks (CNNs), is the best technology for extracting hierarchical features from a variety of medical diagnostics including cardiovascular imaging, brain tumor detection, and diabetic retinopathy [3], [4].

Patient care depends primarily on the ability to diagnose a patient's condition in a timely manner. Conventional imaging techniques for diagnosis are, however, time-consuming, are dependent on the expertise of the person conducting the test, and are subject to a high degree of human variability. Systems based on CNN technology address these issues by automatically interpreting and diagnosing images and are therefore essential to radiology and pathology for segmentation, classification, and pattern recognition [5].

Lung cancer is the most common cause of cancer deaths due to its asymptomatic progression and mostly late stages of detection [6]. It is well recognized that the early diagnosis of lung cancer significantly improves a patient's chances of survival. Thoracic computed tomography (CT) scans are the usual method for the detection of lung nodules [7]. However, due to a large number of CT slices and variabilities of the nodules, interpreting the CT scan is a time-consuming task with a high possibility of mistakes. Hence, research on automated deep learning-based diagnosis is merited. So far, CNNs have demonstrated great capability in thoracic imagining, revealing subtle features invisible to classic methods [8]. However, the challenge of the lack of annotated CT datasets exacerbates overfitting and poor model generalization [9]. Underutilization of medical imaging datasets is focused on, improving dataset diversity through generative models and, more precisely, generative adversarial networks (GANs) [10]–[12]. On the one hand, one should not forget that GAN-generated images might introduce artificial artifacts or biases of subtle features in case of a lack of rigorous validation, and the use of limited public data like lung image database consortium and image database resource initiative (LIDC-IDRI) may restrict external generalization across diverse clinical populations.

Nevertheless, GAN-based augmentation has proven an effective tool for extending training data, improving robustness, and enhancing performance in both lung nodule classification and segmentation. Beyond the issues of data scarcity, reliance on single models restricts diagnostic reliability. Ensemble learning deals with the above issue by combining the outputs of multiple models in order to reduce variance and bias while enhancing accuracy [13]. The researchers adopt neural network ensembles to address model-specific biases and hence enhance diagnostic confidence [14]. Various state-of-the-art backbones, including ResNet, DenseNet, and EfficientNet, provide complementary strengths. ResNet-152 with residual links deepens feature learning [15], while DenseNet-169 encourages feature reuse by maintaining efficient gradient flow [16]. EfficientNet-B7 balances depth, width, and resolution and thus achieves top accuracy at a reasonable computational cost [17]. Weighted averaging, stacking, and voting are ensemble techniques which further push the performance boundaries on the classification of breast cancer, pneumonia, COVID-19, and brain tumors [18], [19].

Recent works tend to go towards hybrid ensembles that merge CNNs with recurrent neural networks (RNNs) or transformers for capturing temporal and spatial information. Most recently, there is a trend toward higher image fidelity and richer image variation by augmentation, including GANs, variational autoencoders (VAEs), and diffusion models [20]–[23]. The success of GAN-embedded deep models in different applications strengthens the power of this augmented generative framework, especially in the domain of medical imaging [24].

The work proposes, for the first time, the consensus-guided adaptive blending (CGAB) framework for early-stage lung cancer prediction: a novel adaptive ensemble architecture that is designed to enhance robustness and accuracy in thoracic CT analysis. Algorithmically, CGAB synthesizes the outputs of multiple deep CNNs, namely ResNet-152, DenseNet-169, and EfficientNet-B7, through a hierarchical ensemble mechanism that assigns weights dynamically based on the confidence of each model and the inter-model consensus. Unlike their classical static counterparts, CGAB changes its weighting on a per-sample basis, dampening the influence of the uncertain predictions while enhancing the reliability of the final decisions. This process of adaptation by looking at consensus avoids overfitting and inconsistency of individual CNNs in classifying lung nodules effectively. Improved precision and stability compared to stand-alone CNNs and traditional ensembles were observed upon the validation of LIDC-IDRI [25]. CGAB, therefore, overcomes limitations in both data and variability in forecasts, hence providing a scalable and interpretable AI framework for truly dependable detection of lung cancer using CT imaging.

2. METHOD

This paper proposes an end-to-end lung cancer detection framework by integrating GAN-driven data augmentation with the CGAB ensemble. The workflow, as illustrated in Figure 1, consists of deep convolutional generative adversarial network (DCGAN)-driven synthetic data generation, features extracted using ResNet-152, DenseNet-169, and EfficientNet-B7, and adaptive ensemble fusion that incorporates auxiliary conflict resolution and gradient-weighted class activation mapping (Grad-CAM)–based interpretability. After that, the suggested method was tested on the annotated LIDC-IDRI thoracic CT dataset, and it successfully identified lung nodules.

2.1. GAN-based data augmentation

To address dataset scarcity and class imbalance in the LIDC-IDRI collection, image augmentation was performed with a DCGAN [26]. Compared to other generative models, such as conditional generative adversarial networks (cGANs) [27] for label conditioned synthesis, CycleGANs [28] for domain translation, and StyleGANs [29] for high-fidelity generation, DCGAN presented a good trade-off between image quality and computational efficiency for generating synthetic lung nodules. This network was composed of four convolutional layers with leaky rectified linear unit (ReLU), four transposed convolutional layers with batch normalization and ReLU activation in the generator, and a final sigmoid activation in the discriminator. Every layer was initialized with Xavier. Using the Adam optimizer, the network was trained for 200 epochs with a batch size of 64, β_1=0.5, β_2=0.999, and a learning rate of 0.0002. Spectral normalization, one-sided label smoothing, along with gradient penalties, was adopted to improve stability and prevent mode collapsing. Synthetic images reached an Fréchet inception distance (FID) of 17.6, while t-distributed stochastic neighbor embedding (t-SNE) visualizations confirmed significant overlap with real images in latent space, indicative of realistic variability. These samples balanced underrepresented nodule classes in the augmented set D′, increasing the robustness and generalization ability of the downstream CGAB ensemble.

$$D' = D \cup \{(x_i, y_i)\}_{i=1}^{M} \quad (1)$$

Where D is the original dataset, x_i denotes the CT images, y_i denotes the corresponding labels, and M denotes synthetic samples.

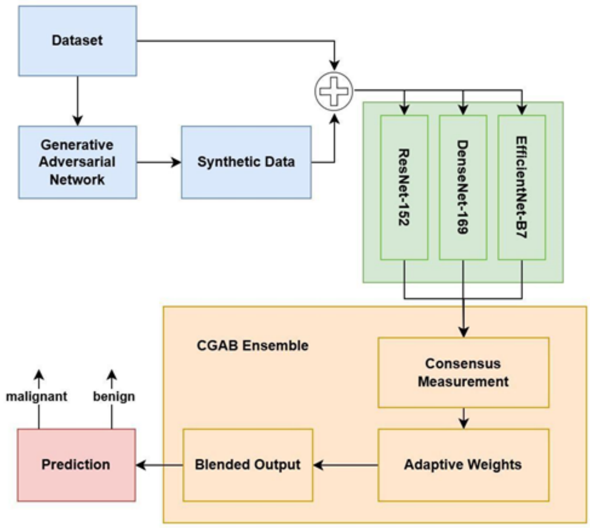

Figure 1. Overview of the CGAB-based lung cancer detection pipeline

2.2. CGAB ensemble

This study shows CGAB as a new method for ensemble modeling. In CGAB, model confidence and inter-model agreement are used for predictions, which guarantees robustness and precision on a per-sample basis. This method overcomes some of the major problems in ensemble learning, such as conflicting predictions and balancing the contribution of each model.

The CGAB framework is having the following key components:

i) Model-specific confidence scores: each base model, denoted as $g_m(x)$ where $m = 1,2,3$ (representing ResNet-152, DenseNet-169, and EfficientNet-B7), outputs a class prediction $\hat{z}_m$ along with a confidence score. The confidence score, $Conf_m(x)$, is derived from the softmax probability of the predicted class $q_m(c|x)$ and the entropy of the output distribution.

$$Conf_m(x) = \frac{q_m(c_{pred}|x)}{-\sum_k q_m(c_k|x) log q_m(c_k|x)} \quad (2)$$

Where $c_{pred} = argmax_k q_m(c_k|x)$ and k iterates over all possible classes.

ii) Consensus measurement: the level of agreement between the base models is quantified using a consensus score, $H(x)$, which measures how many models predict the same class as in (3).

$$H(x) = \frac{Count\ of\ Models\ Predicting\ the\ Majority\ Class}{Total\ Number\ of\ Models} \quad (3)$$

A higher consensus indicates stronger agreement among the models.

iii) Adaptive blending: the predictions from the base models are combined adaptively, with each model weighted by its confidence score and the consensus score. For a given sample x, the weight of model m, $v_m(x)$, is computed.

$$v_m(x) = \frac{Conf_m(x) \cdot H(x)}{\sum_{n=1}^{3} Conf_n(x) \cdot H(x)} \tag{4}$$

This ensures that models with higher confidence and stronger agreement contribute more to the final prediction.

iv) Diversity regularization: to avoid over-reliance on any single model, a diversity regularization term is introduced during training to maximize variability among the models' predictions. This ensures that the ensemble leverages the complementary strengths of all base models.

v) Final prediction: the ensemble prediction $\hat{z}$ is calculated as a weighted combination of the predictions from the base models.

$$\hat{z} = \sum_{m=1}^{3} v_m(x) \cdot \hat{z}_m \tag{5}$$

Where $v_m(x)$ is the weight assigned to the mth model.

The CGAB framework's training procedure was designed to guarantee dependable and strong performance. The merged dataset was separated into training, validation, and testing subsets while preserving class balance after the GAN-based augmentation previously discussed.

3. RESULTS AND DISCUSSION

3.1. Computational cost and inference time

Efficiency was measured with a Tesla T4 GPU (15 GB). The CGAB approach processed each CT scan in 0.83 seconds, using 2.3 GB of memory, significantly outperforming transformer-based methods, which take over 1.5 seconds with more than 4 GB of memory. This efficiency coupled with accuracy suggests great suitability for real-time clinical applications.

3.2. Comparison with state-of-the-art models

For benchmarking the CGAB framework, various CNN architectures, including DenseNet-121, GoogLeNet, EfficientNet-B7, AlexNet, and ResNet-152, with transformer-based models like vision transformer (ViT)-B/16 and swin transformer, were evaluated in comparison to advanced self-supervised (MoCo-v3 ResNet-152) and hybrid CNN-RNN approaches. In summary, as provided by Tables 1 and 2, ViT, and swin reached comparable recall of 98.12% and 98.05%, respectively, while CGAB outperformed all benchmarks, with 97.35% accuracy, 98.46% F1-score, and 0.985 receiver operating characteristic (ROC)-area under the curve (AUC). Meanwhile, CGAB exhibited higher computational efficiency, requiring only 0.83 s per scan and 2.3 GB peak GPU memory, substantially lower than that of more than 1.5 s and greater than 4 GB of transformer-based models. Overall, CGAB reached the best balance between predictive performance and efficiency, further underlining its potential as a clinically deployable system. Although current validation is limited to LIDC-IDRI and partially national lung screening trial (NLST) datasets, strong generalizability of CGAB to other CT datasets-for example, lung nodule analysis 2016 (LUNA16) and the cancer imaging archive (TCIA), can be inferred from the adaptive weighting mechanism of CGAB, which would warrant further investigation in multi-center studies. Figures 2 and 3 depict comparative performance trends, with Figure 2 showing CGAB's superior accuracy and precision, and Figure 3 confirming its higher recall and reduced false negatives.

Table 1. Benchmarking of CGAB against state-of-the-art models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	ROC-AUC	Specificity (%)	Sensitivity (%)	Inference time (s/scan)	GPU memory (GB)
DenseNet-121	96.23	96.63	96.24	96.43	0.971	95.98	96.24	0.62	1.8
ResNet-152	97.19	98.31	97.29	97.79	0.978	96.95	97.29	0.72	2.0
EfficientNet-B7	96.95	98.05	96.81	97.42	0.976	96.7	96.81	0.88	2.4
GoogLeNet	96.51	97.12	96.3	96.7	0.97	95.9	96.3	0.55	1.6
AlexNet	94.87	95.25	94.56	94.9	0.961	94.12	94.56	0.4	1.3
ViT-B/16	97.05	98.1	98.12	98.11	0.981	96.83	98.12	1.52	4.5
Swin transformer	97.12	98.2	98.05	98.12	0.982	96.95	98.05	1.47	4.2
CNN–RNN hybrid	96.89	97.88	96.75	97.31	0.974	96.2	96.75	1.1	3.1
MoCo-v3+ResNet-152	97.02	98.15	97.85	98	0.98	96.77	97.85	1.08	3.0
CGAB (proposed)	97.35	98.73	98.2	98.46	0.985	97.1	98.2	0.83	2.3

Table 2. Comparison of ensemble frameworks for lung cancer detection

Study	Dataset	Architecture/GAN variant	Key metrics/contribution
Ensemble deep learning for risk stratification of invasive lung adenocarcinoma [30].	Thin-slice CT (multicenter)	Multi-view 3D CNN ensemble	Accuracy = 95.2%, AUC =0.972
Deep learning ensemble 2D CNN for lung cancer detection [31].	LUNA16	Ensemble of 2D CNNs	Accuracy =94.8%, sensitivity =93.6%, specificity =95.1%
Ensemble of CNN models for lung nodule detection [32].	LIDC-IDRI	Hybrid CNN ensemble	Accuracy =96.1%, AUC =0.975
CT images GAN-based augmentation with AdaIN for lung nodules detection [33].	LUNA16 (pulmonary nodules)	cGAN+AdaIN	Pulmonary nodules detection is improved; the augmentation effect is validated quantitatively
Lung cancer CT image generation from a free-form sketch using style-based pix2pix for data augmentation [34].	Private CT+lesion sketches	StylePix2pix (pix2pix+StyleGAN style blocks)	Improved diversity of lesion shapes; effective data augmentation demonstrated
CGAB (this work).	LIDC-IDRI+GAN augmentation (proposed)	ResNet-152+DenseNet-169+EfficientNet-B7+CGAB blending	Better generalization and robustness are shown through higher metrics. Accuracy 97.35%, precision 98.73%, recall 98.20%

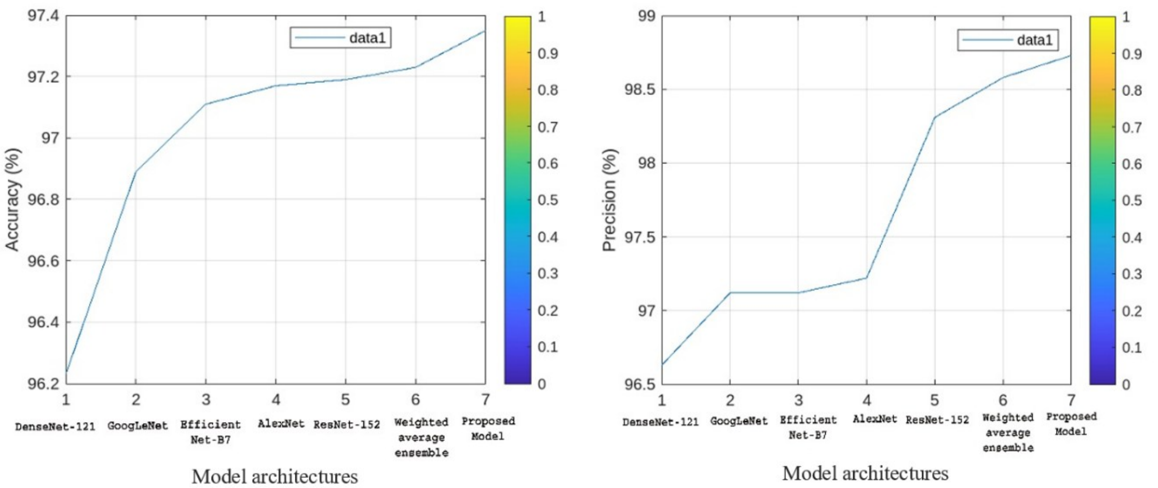

Figure 2. Comparison of accuracy and precision across models

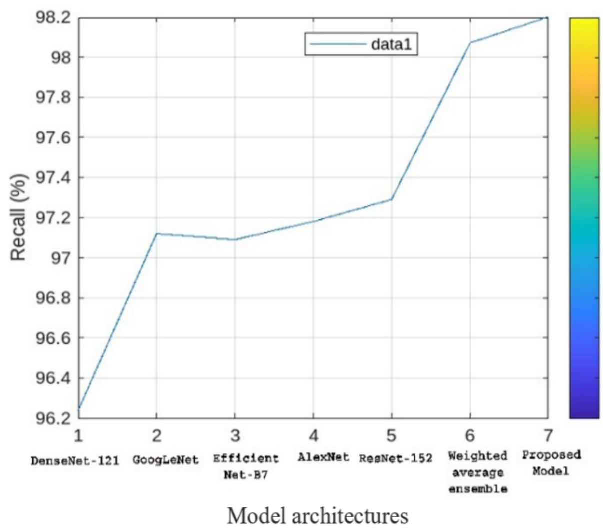

Figure 3. Comparison of recall across models

3.3. Ablation study: impact of GAN augmentation and statistical significance

To see how GAN-based augmentation shifted performance, we compared the CGAB ensemble that was trained only on the original LIDC-IDRI data to the same setup, but this time trained on an augmented dataset D', including the CT scans generated by DCGAN. From Table 3, we observe that augmentation boosted all the performance metrics: accuracy increased from 95.91% to 97.35%, ROC-AUC increased from 0.971 to 0.983, and F1-score from 96.52% to 98.46%. Five-fold cross-validation combined with t-tests confirmed that gains are statistically significant ($p < 0.01$) and are not likely due to random fluctuation. Moreover, augmentation improved sensitivity to minority lesion types and helped balance classes, improving generalization. Further, t-SNE visualizations indicated that synthetic samples expanded the latent feature space without losing alignment with real data. In a nutshell, GAN augmentation significantly strengthened the robustness and reliability of the CGAB ensemble from both quantitative and statistical standpoints.

Table 3. Ablation study results

Model setup	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	ROC-AUC	*p*-value (vs. without GAN)
CGAB (without GAN augmentation)	95.91	97.04	96.22	96.52	0.971	–
CGAB (with GAN augmentation)	97.35	98.73	98.2	98.46	0.983	< 0.01

3.4. Theoretical contribution

The CGAB system goes beyond static ensemble learning literature that uses weighted voting or majority rules. With the calibration of confidence, the framework integrates the entropy-adjusted SoftMax scores, consensus modeling that quantifies inter-model agreement using a formal consensus score, and then the resolution of conflicting actions through an auxiliary decision model when a consensus is weak. This design falls within Bayesian ensemble principles, but with an enhancement of adaptability on a per sample. Unlike classical ensembles that optimize a global weight, CGAB employs a contextually dynamic adhesion blending approach. This positions CGAB as a system for lung cancer detection, but more importantly, as an ensemble architecture that can be applied to other domains such as pathology, remote sensing, and autonomous driving.

3.5. Explainability and interpretability

The acceptance of an AI-assisted diagnosis is measured through interpretability, which is essential for clinical judgments. The study, involving Grad-CAM, helped to feature key areas in thoracic CT scans that influenced model predictions. Generation of stable and clinically proven attention patterns is the result of the CGAB framework, which will improve the understanding of radiologists.

4. CONCLUSION

The CGAB ensemble framework, enhanced by GAN-based synthetic augmentation, is the result of this study for the identification of lung cancer in thoracic CT scans. This model attained superior performance measures by using DCGAN-generated CT images, which addressed the problems of data scarcity and model overfitting and predictions from ResNet-152, DenseNet-169, and EfficientNet-B7 were blended on the LIDC-IDRI dataset. Ablation studies show consistent gains over single CNN architectures and traditional weighted ensembles. Bias may be introduced because of GAN generated images. Stability in the training process is a challenge. Expansion of testing across a broader population is required for external validation, other than NLST dataset. Future enhancements can be focused on data diversity using models such as StyleGAN, diffusion models, cGANs and integrating transformer-based hybrids. Developing explainable ensemble strategies will help for improving clinical trust and the deployment of real-time clinical pipelines. These improvements on the framework will make CGAB a cross-domain tool across medical imaging and beyond.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Jayapandian Natarajan		✓		✓		✓		✓	✓	✓	✓	✓		

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available from corresponding author, [JN], upon reasonable request.

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