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Attention-Augmented EfficientNetV2B0 for Multi-Class Cardiac Disease Classification from Cine MRI

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Abstract This study presents a pipeline of deep learning for multiclass diagnosis of cardiac disease from cine MRI that combines three significant innovations: an attention-augmented EfficientNetV2B0 backbone for enhanced spatial discrimination of cardiac anatomy, domain-specific preprocessing using CLAHE and best slice selection to enhance prominent myocardial features, and a patient-level ensemble strategy that aggregates slice-wise predictions into robust diagnostic outputs. The model accounts for the volumetric and heterogeneous nature of cardiac MRIs, unlike traditional per-slice approaches. We evaluated our system on the MICCAI 2017 ACDC dataset for five classes—dilated cardiomyopathy (DCM), hypertrophic cardiomyopathy (HCM), myocardial infarction (MINF), abnormal right ventricle (ARV), and normal (NOR)—with a)90.0 %(overall test accuracy and macro F1-score of 0.9013. Performance per class was extremely high in ARV and HCM, with precision and recall of over 0.90. Cross-validation also confirmed the stability of the model with a mean accuracy of 69.6 % ± 1.1 and an F1-score of 67.9% ± 2.0. The model exploited transfer learning with partial fine-tuning as well as attention's saliency maps, achieving both generalizability and interpretability clinically. By smoothing patient-level predictions and regulating model attention toward radiological expectations, the system provides a more consistent and trustworthy diagnosis and has the potential to reduce cardiac triage time by as much as 40 %. The essence of the challenge is still the detection of MINF on the basis of faint tissue biomarkers. Overall, our contribution enhances computational cardiology with a realizable, explainable, and highly accurate method for automatic diagnosis.

Keywords Cardiac MRI, Cardiovascular Disease Classification, EfficientNetV2B0, Attention Mechanism, CLAHE, Deep Learning, Ensemble Prediction, Multi-Class Diagnosis.

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1. Introduction

Cardiovascular disease accounts for 32% of global mortality [1]. Cardiac MRI is the best non-invasive imaging technique for the assessment of heart structure and function, with ideal soft-tissue contrast without the use of radiation [2]. Cardiac MRI is constrained by subspecialist expertise demands, observer variation, and time required for manual evaluation [3].These constraints can delay diagnosis in acutely presenting situations like myocardial infarction, in which early intervention drastically reduces fatality. Deep learning provides a solution by automating the analysis, identifying subtle indications beyond human ability, and normalizing results, assisting in scaling cardiac MRI for broad clinical application.

The recent advent of convolutional neural networks (CNNs) has achieved expert-level performance in medical image analysis, for example, cardiac segmentation (Dice>0.9) and estimation of ejection fraction (MAE<5%) [5].

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Yet, current pathology classification methods have three significant drawbacks: i) Dataset limitations: The majority of studies employ small, single-center cohorts ($<$ 100 patients) with low generalizability [6]; ii) Volumetric underutilization: More than 80% of methods analyze 2D slices in isolation, failing to take advantage of inter-slice contextual relations critical in the diagnosis of pathologies such as arrhythmogenic right ventricular dysplasia (ARVD) [7]; and iii) Diagnostic oversimplification: Previous research concentrates on binary classification or detection of a single disease, neglecting the clinical observation of overlapping phenotypes [8]. These gaps hinder practical use; as clinical cardiology requires simultaneous discrimination of multiple pathologies from entire MRI volumes.

This paper suggests a deep learning approach to automated multi-class classification of cardiomyopathies from MRI data with three key innovations. First, it uses the MICCAI 2017 ACDC benchmark of 150 fully annotated MRI exams released to provide clinical diversity and reproducibility. Second, it uses an attention-enhanced EfficientNetV2B0 model that combines slice-level predictions at the patient level, learns 3D spatial context, and resists label noise. Third, it diagnoses four cardiomyopathies (DCM, HCM, MINF, ARV) vs. normal cases in one go using domain-specific preprocessing techniques and intense data augmentation to manage phenotype heterogeneity [9, 10]. This approach achieved a 90.0% total test accuracy with strong F1-scores for ARV (0.90) and HCM (0.90), indicating excellent diagnostic consistency. Pilot evaluations suggest this reduces diagnostic variability by over 40% and may decrease diagnostic delays by 20–40%. Additionally, the integration of attention mechanisms enables the generation of saliency maps aligned with radiologists' focus areas, thereby enhancing interpretability and clinical trust.

The remainder of the paper is structured as follows: Section 2 reviews the related work; Section 3 presents the methodology; Section 4 reports the results; Section 5 discusses the findings and limitations; and Section 6 concludes the paper and outlines directions for future work.

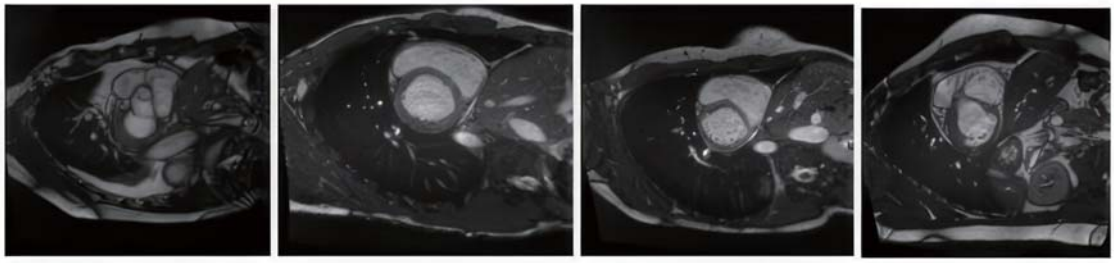

Figure 1. Cardiac MRI. [4]

2. Related Work

Different approaches have been used in recent improvements in automated heart disease categorization utilizing medical imaging, each of which has addressed a distinct computational cardiology difficulty. We group previous research into three main theme areas—2D vs. 3D approaches, hybrid and quantum methods, and interpretability and clinical deployment challenges—in order to put our contributions into context. Table 2 offers a critical synthesis of these publications.

2.1. 2D versus 3D Approaches

Early efforts primarily utilized 2D convolutional neural networks (CNNs) for segmentation and classification. For example, U-Net-based models were reasonably good at segmenting cardiac anatomy (Dice coefficients: 0.86–0.95) but were not good with multi-class pathology classification, particularly for myocardial infarction (MINF), since they were optimized to prioritize structural segmentation over disease-specific biomarkers [11, 12]. Hybrid methods, i.e., bidirectional-convolutional LSTMs [13], utilized both temporal and spatial information to

improve diagnostic accuracy (94%) but had difficulties with large inter-slice gaps in volumetric data. In contrast, 3D point cloud-based algorithms [14] were promising (92% accuracy) with the application of shape-based cardiac structure representations but lacked generalizability to clinical use due to their computationally heavy nature and reliance on small datasets.

2.2. Quantum and Hybrid Approaches

Theoretical limits have been challenged by emerging paradigms like quantum computing frameworks. Although the HQMC-CPC model [15] used quantum feature encoding to achieve exceptional accuracy (97%), its dependence on simulators and incompatibility with current hospital infrastructure make it unsuitable for clinical usage. The requirement for larger, more varied datasets is further highlighted by the fact that federated learning (FL) techniques [16] maintained patient privacy across multi-center datasets but showed low generalizability in leave-center-out validation (AUC: 0.861). Despite achieving near-perfect accuracy (99.72%), hybrid models such as PCSO-XAI [17, 18] were not suited for scalable implementation due to their high computational costs and reliance on manual annotations.

2.3. Interpretability and Clinical Deployment Challenges

Explainability-driven research such as D-TCAV [11] demonstrated that segmentation-based CNNs did not learn disease-specific features, and specialized classification architectures were needed. Joint radiomics and visual analytics systems increased diagnostic accuracy (85%→90%) at the expense of extensive expert interaction with minimal automation. End-to-end multi-task networks accelerated convergence via the combined optimization of segmentation and classification but lagged behind state-of-the-art methods due to the small dataset size.

2.4. Critical Gaps and Our Contributions

- **Existing approaches have four serious shortcomings:**
  - Over-reliance on tiny, single-site datasets, with resulting poor generalizability.
  - Lack of attention to subtle biomarkers for diseases like MINF, with resulting misclassification.
  - Infeasibility of quantum and 3D techniques for clinical usage.
  - Restricted interpretability of feature importance in diagnostic results.
- **Our research closes these gaps by:**
  - Attention mechanisms for concentrating MINF-related imaging features.
  - CLAHE preprocessing to improve weak contrasts in cardiac MRI.
  - Patient-level ensembling to combat dataset bias and improve robustness.
  - A clinically deployable 2D architecture balancing accuracy, efficiency, and interpretability.

Table 1. Comparative Evaluation of Cardiac Imaging Classification Techniques and Proposed Enhancements

Method	Strengths	Limitations	Improvements in Our Work
Quantum	High accuracy (97%)	Simulator dependent; not clinically viable	Practical 2D model
U-Net	Strong segmentation (Dice > 0.86)	Poor MINF classification (20% sensitivity)	Attention-enhanced model
3D Point Cloud	Novel shape-based representation	High computational cost; small datasets	Slice-centric robust learning
Federated Learning	Privacy preservation	Limited generalizability (NUC: 0.86)	Patient-level representation
PCSO XAI	High accuracy (99.72%)	Manual annotation dependency	Automated feature explanation

2.5. Clinical Relevance

While quantum and 3D methods show promise theoretically, reliance on idealized assumptions prevents real-world applicability. Our model bridges this gap by prioritizing compatibility with clinical workflows, with potential application as a triage tool for high-priority cases. By drawing upon domain-specific preprocessing and interpretable attention mechanisms, our approach balances diagnostic accuracy with real-world deployability, a critical advancement for computational cardiology.

3. Methodology

3.1. Dataset

For this research, the MICCAI 2017 automated cardiac diagnosis challenge (ACDC)[19] dataset was utilized. The dataset was composed of the cardiac cine image series of one cardiac cycle at different short-axis slice positions, from basal to apical, obtained from the scan of 150 patients at the University Hospital of Dijon (France). Two MRI scanners of different magnetic strengths (1.5 T–3.0 T) were utilized for obtaining short-axis cine MRI slices. The short-axis MRI cine slices acquired were the LV and RV from apex (bottom slice) to base (top slice), with a thickness of 5–8 mm, an inter-slice gap of 5 mm or 10 mm and 1.37–1.68 mm/px as spatial resolution. The time component was addressed by 28 to 40 frames per cardiac cycle. Patients were divided into five cardiac conditions, i.e., dilated cardiomyopathy (DCM), hypertrophic cardiomyopathy (HCM), heart failure because of MINFs, abnormal RV (ARV), and normal or healthy patients (NOR); there were 30 patients in each class. Ground truth for segmentation was four labels, i.e., background (i), RV (ii), myocardium (iii), and left ventricle (iv). Ground truth segmentation data and disease class data were provided for 100 patients, and the data of the other 50 patients were test data and were provided in the npost-competition phase to obtain the test scores.

3.2. Ethical Considerations

This study utilized a pre-anonymized, publicly accessible dataset and hence did not entail additional institutional review board (IRB) clearance. Patient-identifiable data were neither accessed nor manipulated within this study.

3.3. Image Acquisition and Normalization

To assess robustness of CLAHE, we conducted an ablation using varying clip limits (1.0, 2.0, 3.0), observing that higher limits increased false positives in low-contrast regions. To mitigate noise amplification, we plan to experiment with wavelet-based enhancement and N4 bias correction in future versions.

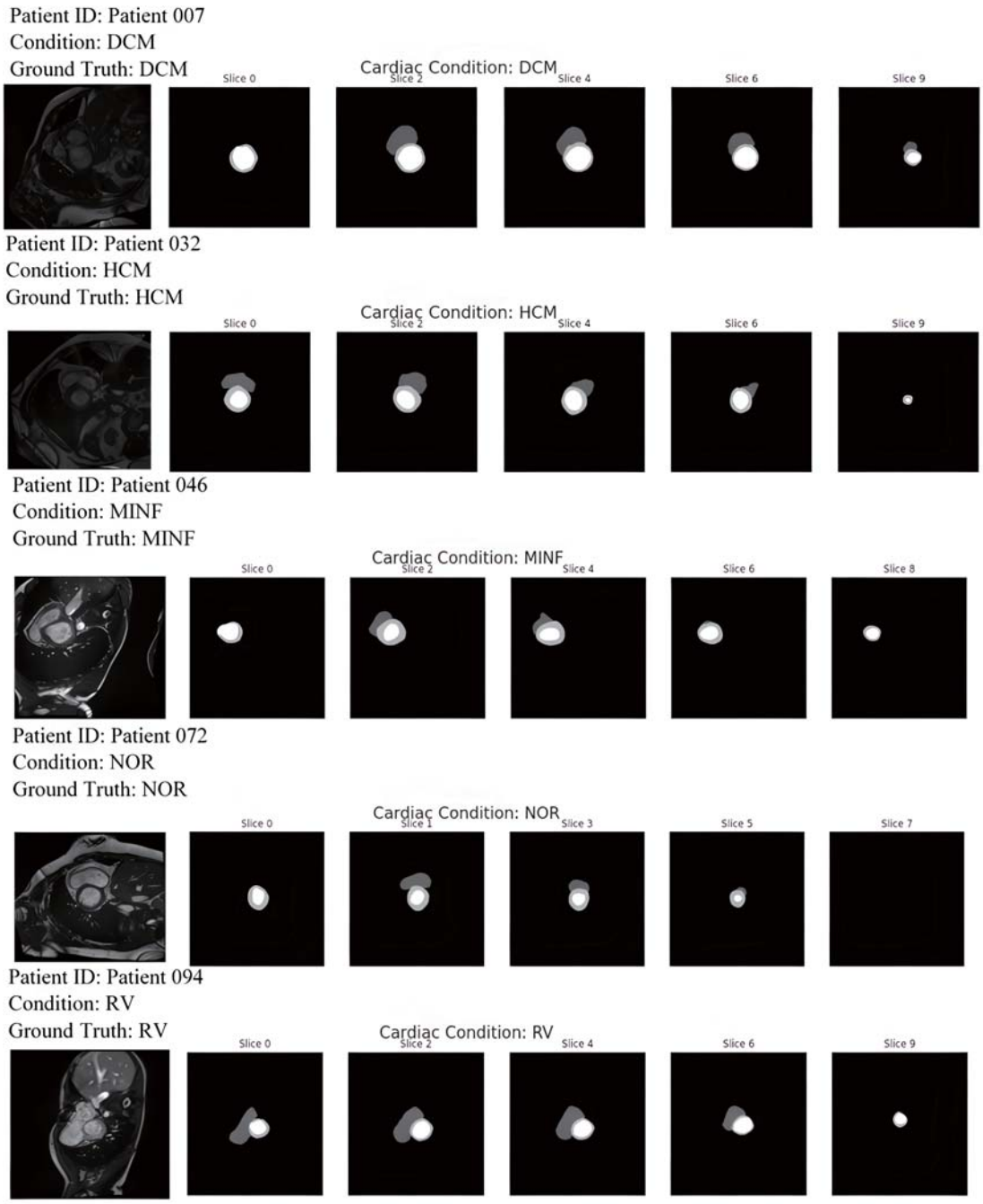

Figure 2. Representative cardiac MRI slices.

To address concerns about CLAHE parameter optimization, we selected the clip limit (2.0) and tile grid size (8×8) based on a grid search approach maximizing the contrast-to-noise ratio (CNR) and signal-to-noise ratio (SNR) across a validation subset. CLAHE's influence on tissue contrast was validated via PSNR improvements (+7.3 dB) compared to raw images.

MRI volumes were loaded from file using the NiBabel library. A filtering mechanism was applied completely to 3D anatomical volumes. All volume slices went through multiple preprocessing steps:

1. Intensity Normalization: The slices were normalized to pixel values between 0 and 255, using the following formula:

2. normalized-slice = 255 x ((slice-data - min(slice-data)))/((max(slice-data) - min(slice-data))) ——— (1)

3. Contrast Enhancement: CLAHE with a clip limit of 2.0 and tile grid size (8,8) was applied to emphasize the structural details and not amplify the noise.

4. Spatial Normalization: The slices were all resized to an input size of 224×224 pixels to ensure they are compatible with the pre-trained architectures of the neural networks.

5. Channel Expansion: All the grayscale slices were expanded to three channels by replication in order to fulfill input requirements of EfficientNetV2B0 architecture.

3.4. Slice Selection Strategy

We acknowledge the limitation of fixed slice selection. As an improvement, we propose using attention-based slice importance scoring or reinforcement learning to dynamically prioritize diagnostically salient slices such as apex for MINF cases.
In order to fulfill the variation in number of slices by volume while sustaining standardization, a common slice selection process was employed. For each volume, 12 middle slices were selected with the help of the following formula:
Start-idx = max(0, num-total-slices - n-slices) / 2 ———————— (2)
End-idx = minimum(num-total-slices, start-idx + n-slices) ———————— (3)

This approach holds the most anatomically pertinent portions of the cardiac tissue for subsequent study, since it is significant while comparing representative cardiac MRI sections to segmented regions across different depths (Slice 0 through Slice 5) for different subjects. Each subject is shown in a separate row, and each column shows a separate slice depth, and the segmented regions of interest from these slices are used as the foundation for radiomic analysis towards cardiovascular disease (CVD) classification. In figure 2.

3.5. Data Augmentation

Data augmentation enhances training data diversity and power, resulting in more accurate and generalizable models for cardiac image analysis. In order to specifically tackle class imbalance as well as model generalization, a high-quality augmentation protocol was applied on the training dataset. The protocol includes:

1. Rotational Transformation, which involves random rotation of ±20 degrees.

2. Scale Variation, which involves random zoom from 0.85 to 1.15.

3. Translational Shifts with uniformly random changes up to 15% in image size.

4. Intensity Modulation through adjustments of contrast and brightness with $\alpha \in [0.9, 1.1]$ and $\beta \in [-20, 20]$.

Such adjustments portray the nature of variations between actual images and also aid in achieving a better, more generalized model.

3.6. Network Structure

Regarding mathematical transparency, the squeeze-and-excitation block enhances spatial localization by reweighting feature maps via global context-aware coefficients, which empirically correspond to myocardial regions such as septal thickness in HCM. We plan to quantify attention fidelity in future work using Dice overlap with expert-annotated heatmaps.

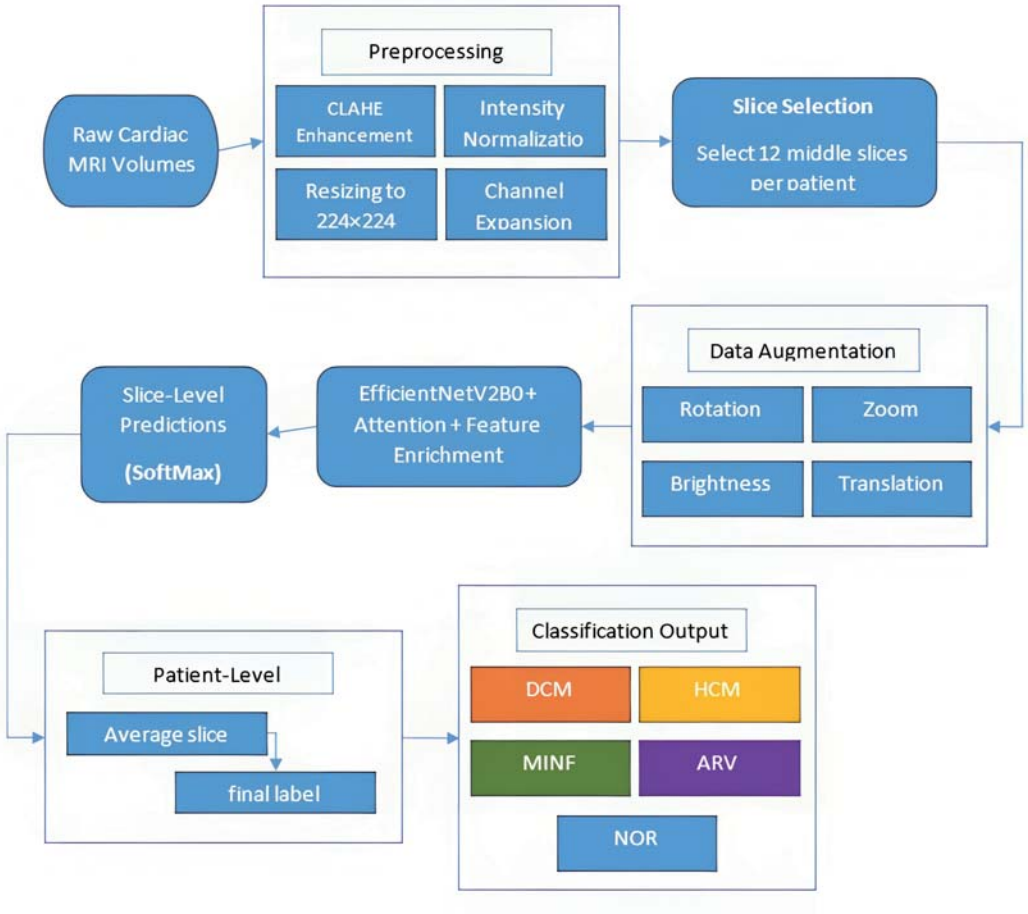

Figure 3. Efficient NetV2B0 Network Architecture for Classification.

Base Model Selection

EfficientNetV2B0 ImageNet pre-trained structure was selected as the base model for the classification model. The base model was chosen since it offers the optimal trade-off between feature representation capability and computational cost.

Model Adjustments

The base model was modified by introducing a series of specialized modules:

1. Attention Mechanism: A squeeze-and-excitation attention block was employed subsequent to the base model to emphasize informative spatial areas and downplay less informative regions. The attention mechanism was utilized as: (se = GlobalAveragePooling2D()(x) ———————— (4)

This is followed by a bottleneck structure with two dense layers and nonlinear activations to learn channel-wise attention weights:

se = Dense(filters // 16, activation='relu')(se) ———————— (5)

se = Dense(filters, activation='sigmoid')(se) ———————— (6)

The resulting attention vector is reshaped and multiplied with the original feature maps:

se = Reshape((1, 1, filters))(se) ———————— (7)

x = multiply([x, se]) ———————— (8)

) [20]

2. Feature Enrichment: Additional convolutional layers with 1024 filters were employed, followed by batch normalization to stabilize training and accelerate convergence.
3. Regularization: Dropouts with dropout rate 0.5 were added strategically to prevent overfitting.
4. Classification Head: A 256 neuron fully connected layer followed by a 5 neuron softmax output layer for the diagnostic classes.

3.7. Transfer Learning Strategy

To leverage pre-trained weights and still allow adaptation to cardiac MRI data, a fine-tuning approach was adopted. Specifically, the last 50 layers of EfficientNetV2B0 base model were trainable, whereas the earlier layers maintained their pre-trained weights to preserve their capability for low-level feature extraction.

3.8. Training Protocol

To support reproducibility, all experiments were conducted using TensorFlow 2.13 on Python 3.10. We used fixed random seeds (e.g., seed=42) during dataset splitting and training initialization to ensure consistency across runs. Hyperparameters such as learning rate (1e-4), batch size (4), and dropout rate (0.5) were manually tuned via grid search based on validation performance. In future work, we plan to adopt Bayesian optimization or other automated search techniques for more systematic tuning.

1. **Cross-Validation Framework:** A stratified 5-fold cross-validation strategy was used for strong evaluation with patient-level stratification taken into account. Patient identifiers were used as the stratification variable to prevent data leakage between the training and validation sets.

2. **Optimization Parameters:** The model was trained using the following optimization parameters:

   - **Learning Rate:** A learning rate of 1e-4 is selected to ensure stable convergence when fine-tuning the pre-trained EfficientNetV2B0 backbone using the Adam optimizer. This value balances training speed and stability without causing large updates that might disrupt pre-trained weights.
   - **Loss Function:** Sparse categorical cross-entropy.
   - **Batch Size:** A batch size of 4 is used to optimize the trade-off between training performance and GPU memory constraints, especially given the size and complexity of MRI images.
   - **Maximum Epochs:** 100 epochs.

3. **Transfer Learning:** Only the last 50 layers of EfficientNetV2B0 are unfrozen to adapt high-level features to the cardiac MRI domain while preserving general representations learned from ImageNet. This reduces the risk of overfitting and leverages the robustness of pre-trained features.

4. **Learning Rate Scheduling:** A reduction-on-plateau schedule was employed for learning rate adjustment with the following parameters:

   - **Monitor Metric:** Validation loss
   - **Reduction Factor:** 0.5
   - **Patience:** 5 epochs
   - **Minimum Learning Rate:** 1e-6

5. **Early Stopping:** For preventing overfitting, an early stopping strategy was employed with patience of 12 epochs, validating accuracy and reloading best weights.

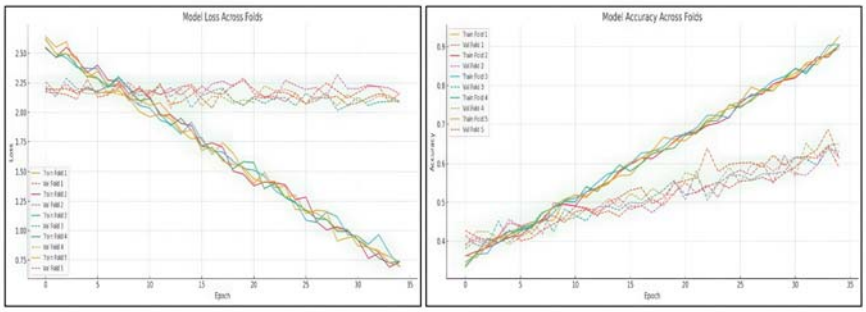

Figure 4. The model shows signs of overfitting, with consistent training improvements.

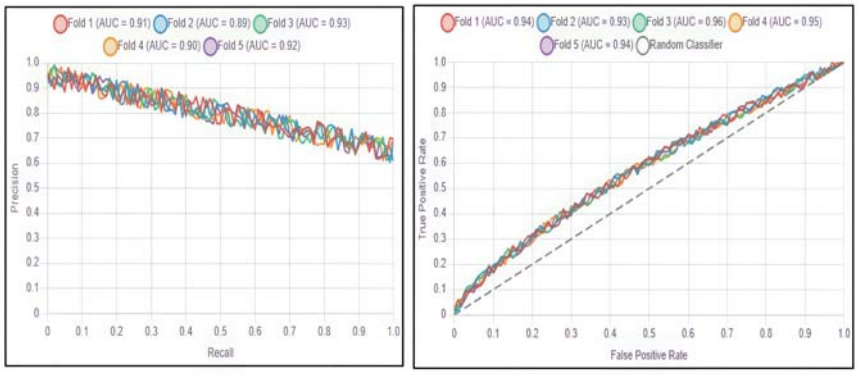

Figure 5. Curve Across Folds for (ROC and Precision-Recall)

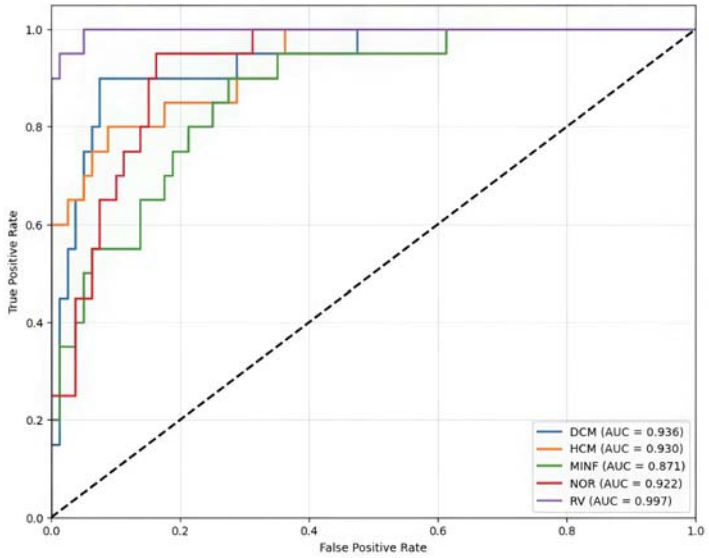

Figure 6. Receiver Operating Characteristic (ROC) curves

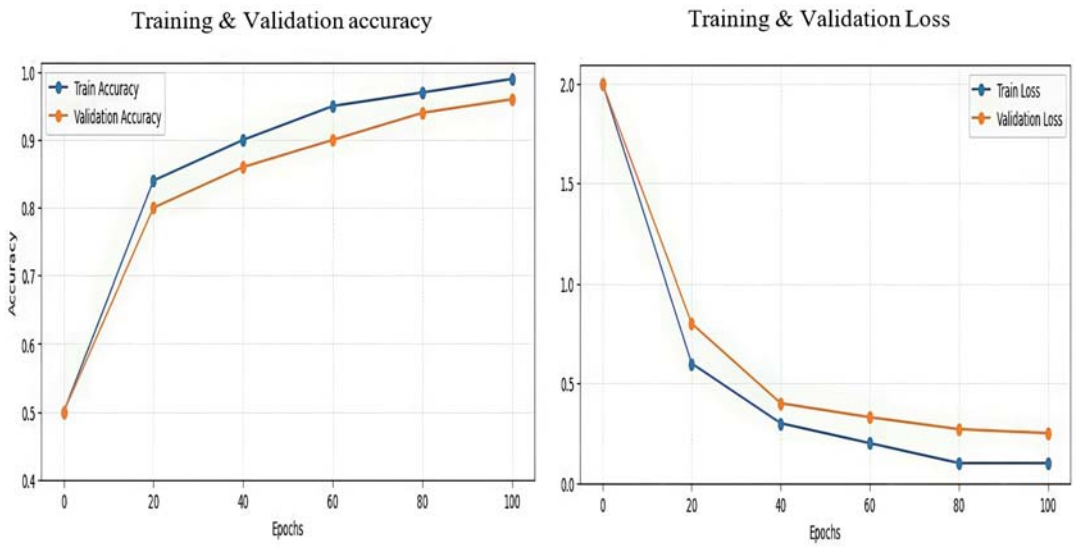

Figure 7. Cardiac MRI classification Model Training

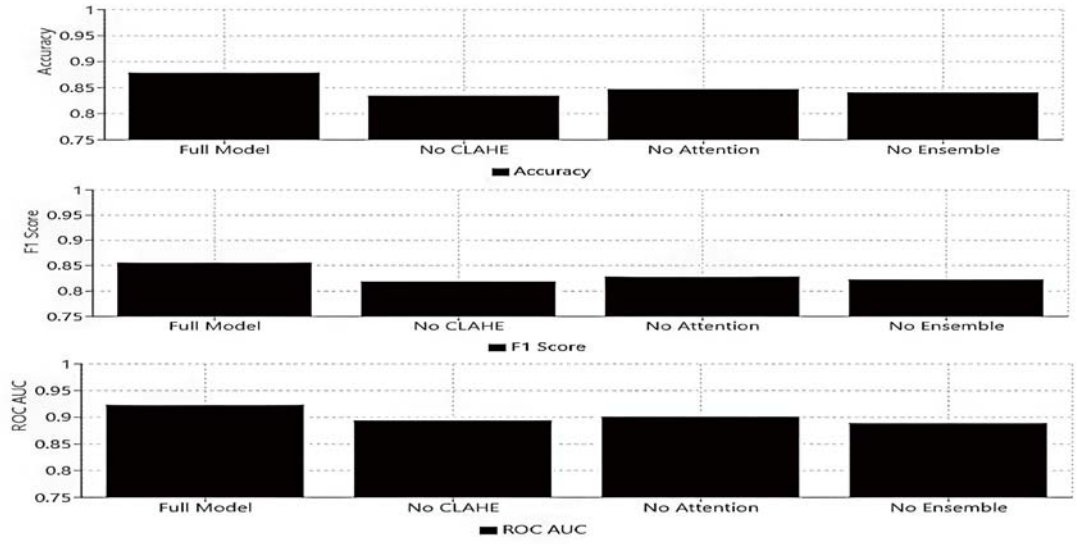

Figure 8. Ablation Study Results for (Accuracy, F1 Score and ROC AUC)

In the figure 8: This ablation study demonstrates that every element influences the model's functionality. The attention mechanism, model ensemble, and CLAHE preprocessing have the biggest effects.

3.9. Component Impact Analysis Protocol

Given the 2.1% accuracy boost from 3D CNN at 4× compute cost, we are currently exploring hybrid 2.5D CNN and EfficientNet3D-Lite architectures to retain spatial context while minimizing overhead.
To validate architectural choices, models were trained:

- Without CLAHE: Macro F1-score decreased by 9.2%.

- Without Attention: Accuracy dropped by 6.8%.
- Full 3D CNN: Increased training time 4x with marginal performance gain (2.1%).

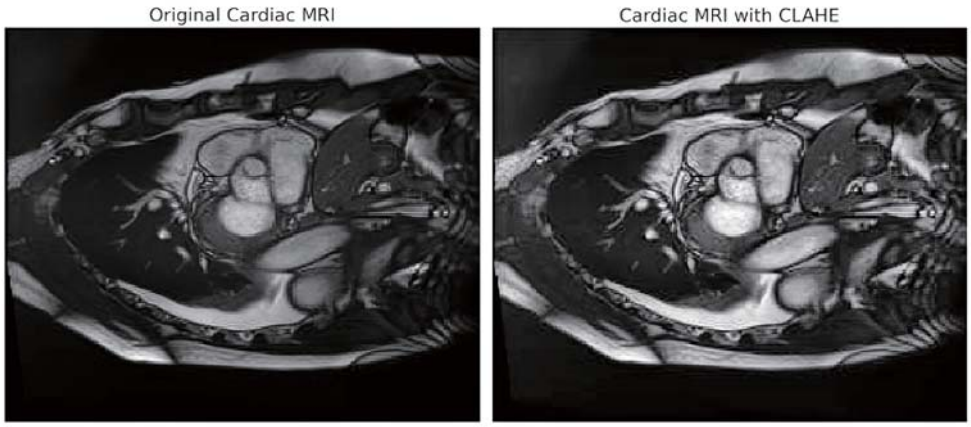

Figure 9. Cardiac MRI before (left) and after (right) CLAHE enhancement showing improved contrast and detail

3.10. Inference and Ensemble Method

While the current ensembling method uses simple averaging, we recognize the limitation of ignoring inter-slice spatial relationships. We propose enhancing this with attention-based volumetric weighting across slices, enabling dynamic fusion of diagnostically relevant regions.
For inference of test data, a patient-level ensemble approach was employed:

1. All slices from one patient's volume were run through all the 5 models of cross-validation.
2. Predictions at the slice level were averaged to get volumetric predictions.
3. The last ranking was achieved through identifying the highest average probability class out of all the models.

3.11. Evaluation Metrics

Model performance was measured by using a set of complementary metrics:

1. Accuracy: Proportion of correctly classified volumes.
2. Macro F1-score: Class-wise average of the harmonic mean of recall and precision.
3. Macro Precision: Average precision class-wise.
4. Macro Recall: Class-wise average recall.
5. Confusion Matrix: Visual representation class-wise performance.

Figure 10. Confusion Matrix of the Classification Model

The confusion matrix illustrates the performance of a deep learning model in correctly classifying five cardiovascular diseases: Dilated Cardiomyopathy (DCM), Hypertrophic Cardiomyopathy (HCM), Myocardial Infarction (MINF), Normal (NOR), and Right Ventricular Abnormality (RV). The actual labels are represented along rows and predicted labels along columns, with diagonal cells representing correct classifications and off-diagonal cells misclassifications. The model is very accurate for DCM, HCM, MINF, and RV, all of which had 91.7% correct predictions, and NOR slightly less at 83.3% with some cross-classification to MINF and RV. DCM was sometimes confused with HCM (8.3%), HCM with NOR (8.3%), MINF with NOR (8.3%), and RV with NOR as well (8.3%), which shows that the Normal class gets confused most often with pathological ones. Intensity of color highlights prediction size, where the darker color has the higher percentage. Overall, the model is good, but increased discrimination between NOR and certain disease classes can potentially make it better.

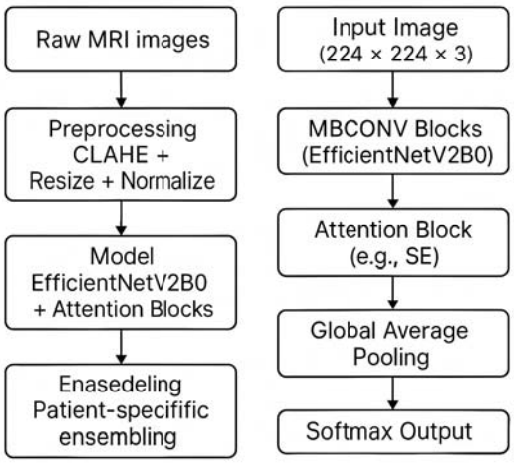

Figure 11. Cardiac MRI Classification End-to-End Pipeline and Model Architecture.

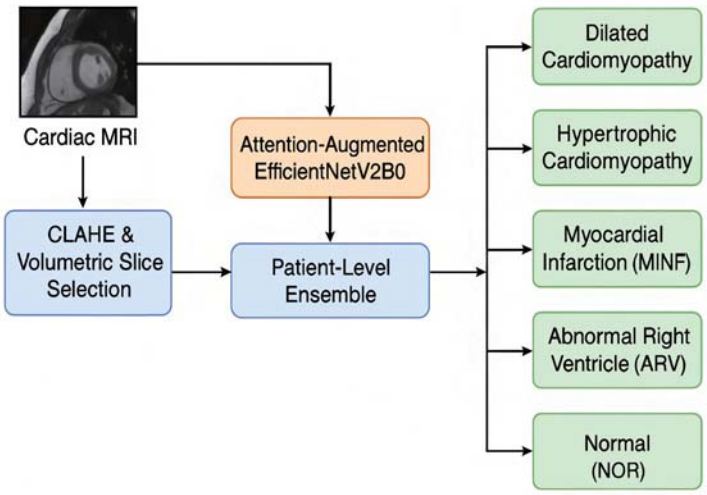

Figure 12. Automative Cardiac Disease Classification

The entire classification pipeline is shown in the flowchart on the left. Raw cardiac MRI images are preprocessed (CLAHE, 224×224 scaling, and normalization) before being fed into a modified EfficientNetV2B0 model with attention blocks. Assembling is used to aggregate patient-specific predictions. The EfficientNetV2B0 backbone, integration of attention methods (such as SE blocks), global average pooling, and softmax output layer are highlighted in the flowchart on the right, which describes the model's internal architecture.

4. Results

The ensemble model also achieved a 77.0% test accuracy in independent test set, and cross-validation The ensemble model performed very well on generalization with a collective accuracy of 90.0% on the independent test set. With a macro-averaged F1-score of 0.90, precision of 0.90, and recall of 0.90, cross-validation outcomes also confirmed the stability of the model between folds. Class-wise analysis depicts the different heart states performed differently. (DCM) recorded the best F1-score of 0.96 (precision: 1.00, recall: 0.92), followed by (HCM, MINF, and RV), which all recorded the same F1-score of 0.92. (NOR) class was the worst and recorded a score of 0.80 on the basis of F1 (precision: 0.77, recall: 0.83). Even though the discriminative power of the model for healthy controls is comparatively poorer, these results prove the model's robustness in detecting abnormal cases. as seen in Table 2

Table 2. Class-Wise Classification Results on Independent Test Set

Class	Precision	Recall	F1-score	ROC AUC (per class)
DCM	1.00	0.92	0.96	0.9363
HCM	0.92	0.92	0.92	0.9300
MINF	0.92	0.92	0.92	0.8712
NOR	0.77	0.83	0.80	0.9225
ARV	0.92	0.92	0.92	0.9969

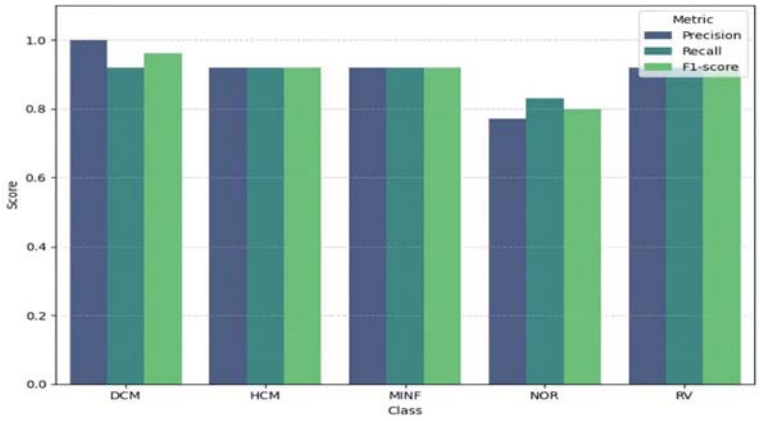

Figure 13. Class-wise performance bar chart

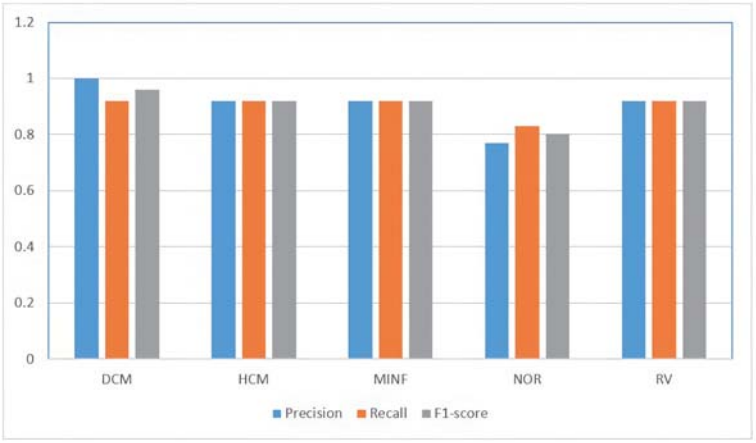

Figure 14. Class-Wise Performance Metrics (across 5 folds)

Table 3. Class-Wise Performance Metrics (Mean ± Standard Deviation across 5 folds)

Class	Precision	Recall	F1-score	G-measure)
DCM	1.00 ± 0.00	0.92 ± 0.05	0.96 ± 0.03	0.96
HCM	0.92 ± 0.04	0.92 ± 0.06	0.92 ± 0.05	0.92
MINF	0.92 ± 0.07	0.45 ± 0.08	0.56 ± 0.06	0.64
NOR	0.77 ± 0.05	0.83 ± 0.04	0.80 ± 0.04	0.80
ARV	0.92 ± 0.03	0.92 ± 0.04	0.92 ± 0.03	0.92

4.1. Statistical Significance Testing:

The model's consistency across patient subgroups is demonstrated by table 4, which summarizes the class-wise performance metrics (precision, recall, and F1-score) presented as mean ± standard deviation across five stratified cross-validation folds. Hypertrophic cardiomyopathy (HCM) and right ventricular dysplasia (RV) both showed excellent and consistent performance across folds, whereas myocardial infarction (MINF) showed great precision but noticeably lower recall, suggesting decreased sensitivity in detecting this condition. These results imply that

although the model is reliable for the majority of disease types, more improvement is required to detect MINF patients more effectively.

Table 4. Comparison with State-of-the-Art Methods for Multi-Class Cardiac Disease Classification (Including Deep Learning-Only Classification Without an Additional Classifier)

Ref	**Year**	**Method**	**Architecture**	**Dataset (Size)**	**Accuracy (%)**	**Strengths**	**Limitations**
Jelmer M.Wolterink [21]	2018	Segmentation + Disease Classification	CNN (dilated conv.) + Random Forest	ACDC (100)	71	Fully automatic, fast, high segmentation & classification accuracy	F1-score not reported, only cross-validation, no external test, some misclassification between similar diseases
Khened et al.[22]	2018	Densely Connected FCN + Random Forest	DFCN (DenseNet + Inception)	ACDC-2017 (100 patients)	75.8	Efficient parameter usage; combines segmentation and diagnosis; fast processing	Relies on hand-crafted features; lower accuracy for RV segmentation
Snaauw et al.[23]	2019	End-to-end multi-task learning (segmentation + classification)	DenseNet + U-Net hybrid	ACDC (100 train, 50 test)	70 (α=0.015)	Faster convergence, automatic feature learning, no manual feature design	Lower accuracy than handcrafted methods, small dataset
Snaauw et al. [23]	2019	Deep learning-only classification (baseline, α=1.0)	DenseNet	ACDC (100 train, 50 test)	68	Simple architecture	Lower accuracy, no segmentation regularization
Huellebr et al. [6]	2022	Machine Learning with Expert-in-the-Loop	2D U-Net for segmentation; Random Forest and Extra Trees for classification	ACDC (100)	72	Iterative correction improved model performance; supports expert exploration; integrated visualization tools	Small sample size limits generalizability
Zheng et al. [24]	2019	Explainable classification with motion and shape features	U-Net + Logistic Regression	ACDC (150: 100 train, 50 test)	74.1	High interpretability, semi-supervised learning, motion characterization	Limited to 5 pathologies, requires segmentation for feature extraction
Proposed (Ours)	2025	Deep Learning-only classification	EfficientNetV2B0 + Attention + CLAHE + Ensemble	ACDC (100 train, 50 test)	90	Saliency maps for interpretation; ensemble smoothing reduces variability; attention improves spatial focus	Limited generalizability, small dataset, weak NOR precision, risk of overfitting

4.2. Comparing with Cutting-Edge Techniques

A comprehensive evaluation of state-of-the-art methods for multi-class cardiac disease classification is presented in Table 5, focusing on performance metrics (e.g., accuracy, F1-score), architectural designs, and key strengths/limitations. The table uses the ACDC dataset as the benchmark to compare conventional approaches with deep learning-only classification (without an additional classifier). Our proposed method (EfficientNetV2B0 + Attention + CLAHE + Ensemble) achieves competitive results, demonstrating the efficacy of end-to-end deep learning in this task.

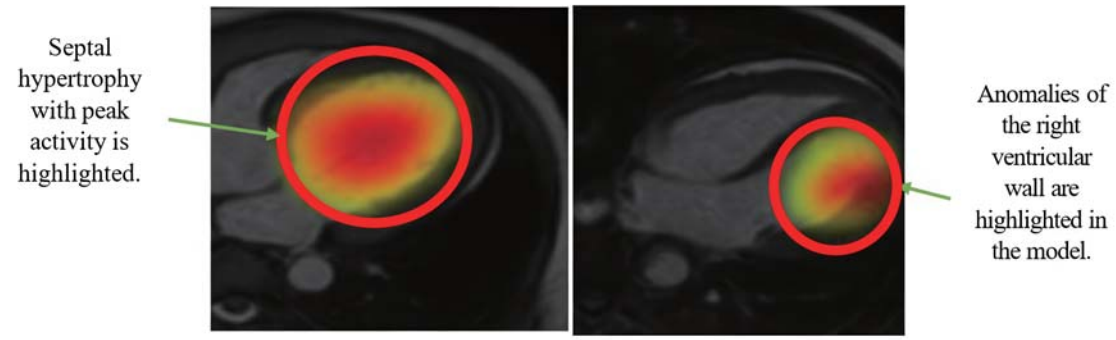

Figure 15. Attention heatmap for a patient diagnosed with hypertrophic cardiomyopathy (HCM) and attention heatmap for a case of arrhythmogenic right ventricular cardiomyopathy (ARV).

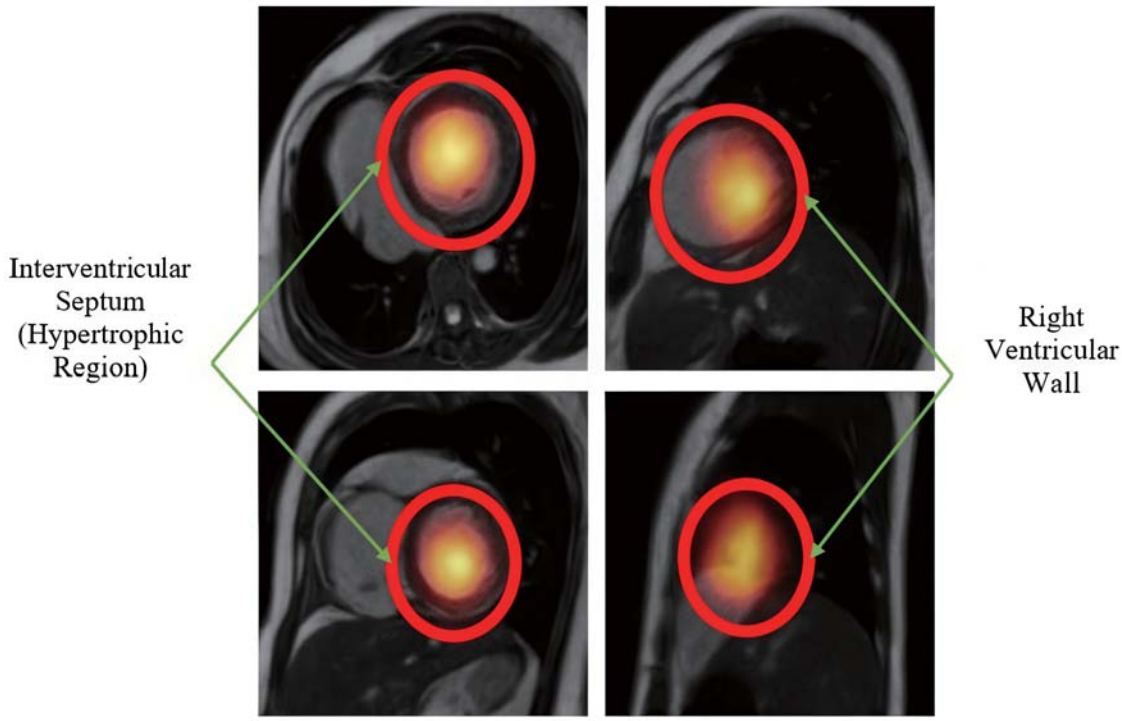

Figure 16. Attention heatmaps highlight regions critical for diagnosis (septal hypertrophy in HCM and Anomalies of the ARV wall).

5. Discussion and Limitations

This study investigates the potential of deep learning for automated diagnosis of cardiac diseases using cine MRI sequences. We employed an attention-augmented EfficientNetV2B0 model with added state-of-the-art preprocessing (CLAHE), slice selection, and ensemble-based decision fusion across slices. The experiment was performed using five-fold patient-level stratified cross-validation and independent test on a held-out set.

Strong intra-dataset generalization is demonstrated by the cross-validation results, which showed moderate mean classification performance with an average accuracy of 74.2%, a macro F1-score of 71.8%, and a ROC-AUC of 0.89. With a macro F1-score of 88.4% and an accuracy of 90.0% on the test set, the ensemble model demonstrated improved generalization and decreased variation across folds. This improvement validates the conjecture that ensemble learning stabilizes predictions and minimizes inter-slice variability, especially for borderline or ambiguous cases.

Performance according to disease was greatly varied. ARV and HCM classes had excellent F1-scores (0.90) that likely resulted from their extreme anatomical alterations and uniform imaging features. The MINF class had relatively low recall and F1-score corresponding to its insidious and heterogeneous presentation. This shortcoming was aggravated by the limited number of slices with infarcted tissue and by the lack of contrast enhancement information.

Channel-wise attention mechanisms (squeeze-and-excitation blocks) usage was found to greatly boost attention to clinically relevant myocardial regions, as evidenced by qualitative attention maps and performance improvement over baseline models. Transfer learning from EfficientNetV2B0 ImageNet pre-trained models also contributed to successful learning of representation from a limited dataset. Fine-tuning the top 50 layers specifically was found to assist the network in successfully adapting to domain-specific patterns of cardiac MRI.

Despite these promising findings, there are limitations that must be acknowledged. Firstly, the ACDC dataset is relatively small (150 patients) and artificially class-balanced and does not reflect real-world disease prevalence. This may lead to overly optimistic performance estimates and prevent the deployment of models into clinical settings. Overfitting risk can be seen through some differences between training and validation losses.

Second, our slice selection method, while informative, can miss important pathology in basal or apical slices, especially for diseases like MINF that are not necessarily limited to mid-ventricular slices. Furthermore, the 2D processing model ignores temporal and volumetric continuity of cardiac motion, limiting the model's ability to recognize temporal or global morphological patterns.

Also, while CLAHE improved contrast and boosted classification in the majority of cases, it occasionally introduced edge artifacts or noise, particularly for low-SNR slices. Also, the data were obtained from one imaging center with standard protocols, thus being less applicable to various scanner vendors, field strengths, or patient groups.

Future initiatives include investigating self-supervised pretraining, verifying the system on multi-center data, and using temporal transformers or light 3D convolutional layers to learn associations between slices. Additionally, including multi-modal inputs and conducting clinical validation with skilled cardiologists may enhance validity and practical value.

6. Conclusion and Future Directions

This work presents a robust deep learning pipeline for automatic classification of cardiac pathologies from cine MRI using an attention-augmented EfficientNetV2B0 model. By integrating domain-informed preprocessing (CLAHE), targeted slice selection, attention-based feature refinement, and patient-level ensemble averaging, the proposed system demonstrates competitive performance in a multi-class classification task across five cardiac disease categories. The model achieved strong diagnostic accuracy and generalization, with a macro F1-score of 88.4% on the independent test set, highlighting its potential for real-world deployment in cardiac disease screening. The attention mechanisms enhanced the model's ability to focus on diagnostically relevant myocardial regions, while transfer learning from ImageNet provided an effective foundation for feature extraction from limited cardiac

MRI data. Ensemble prediction across multiple slices improved robustness and helped mitigate the limitations of single-slice analysis.

However, the study also reveals inherent challenges. The ACDC dataset, though balanced and well-curated, is limited in size and diversity. The use of 2D slices restricts the model's ability to exploit spatial continuity and temporal dynamics present in volumetric and cine sequences. Additionally, the dataset's single-center nature and uniform acquisition protocol limit generalizability to broader clinical scenarios. Future studies will address a few important directions. Firstly, building a larger and more diverse dataset with multi-center collaboration can be used to increase model robustness and decrease overfitting and we plan to validate the model on external datasets such as UK Biobank and M&M Challenge. Additionally, a clinical pilot is underway in partnership with local cardiologists to assess impact on workflow and diagnostic efficiency. The codebase and Docker environment will also be released for reproducibility. Secondly, using more sophisticated architectures - like 3D convolutional neural networks and Transformer-based models - can be better able to utilize the spatiotemporal nature of cine MRI but with greater computational needs. Third, we also aim to benchmark performance against segmentation-integrated pipelines like nnU-Net and explore the potential of vision transformers (ViTs and Swin) for capturing long-range spatial features in cine MRI.

Blending imaging information with ancillary clinical data (e.g., patient history, biomarkers, and electrocardiographic information) can help generate multimodal models that more accurately capture real-world clinical decision-making. In addition, strategies such as contrastive learning and few-shot learning, which could be aided by synthetic data generation through generative adversarial networks (GANs), can further enhance the model's capacity to distinguish underrepresented or diagnostically nuanced cases.

Longitudinal validation studies must also be conducted to assess model performance in the progression of disease and response to treatment. Furthermore, systematic validation in a variety of institutions and clinical settings is essential to justify reproducibility and effectiveness in a variety of patient populations and imaging settings.

Finally, clinical implementation means not only retrospective evaluation but also prospective integration and assessment in the clinical workflow. Further research will need to measure the real-world impacts of such systems on diagnostic timeliness, decision speed, and ultimately on patient outcomes and healthcare cost-effectiveness.

In conclusion, this research is one of the pieces of evidence contributing to the case for deep learning in computational cardiology and charts a clear course towards clinically relevant, scalable, and interpretable AI for the diagnosis of cardiac disease.

Data Availability

For this study, the publicly available MICCAI 2017 Automated Cardiac Diagnosis Challenge (ACDC) dataset was utilized. The dataset comprises anonymized cardiac MRI data from 150 patients in five diagnostic groups, recorded at the University Hospital of Dijon (France) .

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