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APPLIED RESEARCH

Automated Cardiac Disease Prediction Using Composite GAN and DeepLab Model

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ABSTRACT Cardiovascular diseases remain the leading global cause of mortality, resulting in over 17 million deaths annually. Manual cardiac image interpretation is often subjective and varies significantly among clinicians. However, constraints like limited annotation and model generalization persist. We introduce GenDeep, a novel framework integrating an unsupervised Generative Adversarial Network (GAN) and DeepLab model for robust cardiac pathology classification from cine-MRI scans. The GAN component performs data augmentation to synthesize realistic pathological imagery, overcoming dataset constraints. Meanwhile, the DeepLab segmentation network exploits inter-slice spatial contexts for precise anatomical quantification. GenDeep is trained on over 4000 expert-annotated scans from the ACDC dataset, leveraging Apache Spark and Hadoop for efficient parallel data loading and preprocessing. The Generator maps noise vectors to synthetic MRIs while the Discriminator predicts disease labels and classifies images as real/fake. Weights are updated through backpropagation to refine image realism and classification accuracy. Once trained, the Generator produces additional pathological data to boost model generalization. The Discriminator then serves as the diagnostic classifier based on ventricular morphology from DeepLab segmentation. Extensive comparative testing on a held-out test set achieves 97% accuracy and 93% F1 Score, significantly exceeding benchmarks. Smooth convergence is verified with a low 2.21 MSE. These results highlight the effective integration of generative learning and segmentation for automated and reliable cardiac diagnosis.

INDEX TERMS Cardiovascular diseases, generative adversarial networks, DeepLab, semantic segmentation, deep learning, cardiac MRI analysis, disease detection, heart disease.

I. INTRODUCTION

Cardiovascular diseases (CVDs) remain the leading cause of mortality worldwide, accounting for over 17 million deaths annually [1]. CVDs encompass various cardiac conditions, including coronary artery disease, heart failure, cardiomyopathy, and arrhythmias [2]. Early intervention is essential, as initial cardiac events or strokes are often fatal [3]. Manual examination of cardiac scans for diagnosis remains complex, tedious, and prone to subjective variability and human error, thus impeding timely detection [4]. Consequently, more than 50% of CVD cases remain undiagnosed until significant cardiac damage has occurred [5]. Machine learning has surfaced as a promising solution for automated cardiac disease prediction through discerning analysis of medical images [6]. Computational diagnostics systems leveraging deep neural networks bear immense potential to refine screening, elevate detection rates in pre-symptomatic individuals, and mitigate mortality. These systems offer an objective, precise, and efficient means of extracting

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insights from large-scale historical data to derive data-driven disease patterns reliably [7]. Specifically, CNN architectures have displayed unparalleled effectiveness on cardiac image segmentation and diagnosis classification tasks [8]. However, research to elevate generalization across diverse patient demographics remains imperative. Key technical challenges include limited annotated samples for training and variability across multi-center image captures, alongside interpretability constraints hindering clinical adoption [9]. Tackling said hurdles while benchmarking real-world data holds the key to expediting the translation of machine learning innovations to transform cardiology.

Recent studies have employed supervised deep learning models for automated analysis of cardiac imaging data and disease diagnosis [10, 11]. Convolutional neural networks (CNNs), in particular, have achieved high efficiency by automatically learning discriminative features from medical images [10]. However, typical CNN architectures struggle to accurately segment irregular anatomical structures and fail to sufficiently leverage all available supervision signals beyond pixel-labels [11]. This has impelled the advancement of sophisticated deep learning architectures such as Generative Adversarial Networks (GANs) and DeepLab models to transcend said limitations. This paper introduces GenDeep, a novel framework that integrates an unsupervised Composite GAN for realistic medical image synthesis and a DeepLab neural network for precise semantic segmentation to enable automated cardiac disease prediction. The model undergoes training on an expansive dataset of 4000+ cardiac MR images from the ACDC challenge [12], leveraging Apache Spark and Hadoop for swift parallel data loading and filtering. The Composite GAN encompasses interlinked generator and discriminator components to produce realistic cardiac MRIs. Meanwhile, DeepLab employs atrous convolutions and Conditional Random Fields to accurately segment left and right ventricles. The engineered GenDeep framework aims to boost automated feature learning and cardiac structure demarcation. Post-training, it can analyze novel MR scans to identify likely cardiac defects. Rigorous benchmarking on a held-out test set and comparisons to cutting-edge approaches across segmentation and diagnostic accuracy, sensitivity, and specificity gauge GenDeep's efficacy.

Applications of automated cardiac diagnosis systems span across policy screening initiatives, mobile & rural health services, and smart wearable devices. Population screening enables health authorities to systematically evaluate CVD risk in communities to guide interventions. Diagnostic wearables allow continuous monitoring for patients in remote areas or with mobility constraints. Smartphone integrations serve those lacking expensive infrastructure. Ultimately by democratizing screening access, these solutions aim to boost early detection rates and positively impact CVD outcomes globally. Realizing this vision hinges on extending robustness and accessibility of machine learning innovations through multi-disciplinary collaboration [13].

Even though GAN and semantic segmentation have been explored separately for medical imaging tasks, their cooperation in a single cardiac disease prediction system from cine-MRI is still unproven. GenDeep is unique in merging different approaches, by first using a GAN to create fake MRI images that are then used to support both segmentation and classification in heart scans. In contrast to other data augmentation methods, the generator is taught to conserve the body's correct form, making the model more reliable when faced with variability in medical images. Furthermore, the diagnostic label set is expanded from five to ten ACDC conditions, so the disease classification benefits from even better segmentation. Merging these techniques produces a special architecture that can be used for true cardiac screening applications. The main contributions of this paper are as follows:

- We propose a new deep learning framework combining an unsupervised GAN for medical image generation and a DeepLab convolutional neural network for semantic segmentation. This composite architecture aims to synergize the complementary strengths of GANs for robust feature learning and DeepLabs for precise anatomical delineation.
- Our model automatically learns discriminative visual features from cardiac MRIs and accurately segments the left and right ventricle structures. Accurate segmentation forms the basis for subsequent pathology classification based on ventricular morphology.
- The research demonstrates GenDeep's ability to predict ten clinically significant cardiac conditions, including coronary artery disease, myocardial infarction, heart failure, arrhythmias, valvular heart disease, cardiomyopathy, hypertension, peripheral artery disease, congenital heart disease, and rheumatic heart disease, even when trained on a sparsely annotated dataset. Transfer learning and semi-supervised approaches are leveraged to compensate for limited labeling.
- The ACDC dataset, comprising more than 4000 cine-MRI scans, is utilized for rigorous evaluation. Comparative testing using 5-fold cross-validation demonstrates the model's generalization capability to unseen data. Segmentation and multi-class classification metrics showcase GenDeep's strengths.

The remainder of this paper is organized as follows. Section II reviews related works on deep learning for cardiac image analysis and diagnosis, focusing on CNNs, GANs, and DeepLab models. Section III describes the ACDC cardiac cine-MRI dataset and preprocessing pipeline used in our experiments and introduces our proposed GenDeep methodology, integrating Composite GAN and DeepLab for end-to-end cardiac disease prediction, elaborating the underlying architectures and training. Section IV benchmarks GenDeep's effectiveness for medical image synthesis, cardiac ventricle segmentation, and pathology classification against state-of-the-art techniques. Finally, Section V presents the

key conclusions and scientific contributions of our work alongside future research directions for advancing computational diagnosis with deep learning.

II. LITERATURE REVIEW

Several studies have applied machine learning and data mining techniques to address the global issue of heart disease. For example, Bertsimas et al. [14] used the Cleveland dataset with 14 key attributes and found that the K-Nearest Neighbors (KNN) algorithm achieved the highest classification accuracy. The findings contribute valuable insights into data-driven approaches for early diagnosis and effective management of cardiovascular health [14]. In the realm of clinical data analysis, Mohan et al. [13] proposed a Hybrid Random Forest and Linear Model (HRFLM), which achieved an accuracy of 88.7% in predicting cardiovascular disease, contributing valuable insights to enhance predictions in cardiovascular health [15]. Bhatt et al. [16] applied K-modes clustering combined with traditional classifiers (e.g., Random Forest, Decision Tree, MLP, XGBoost) and found the Multilayer Perceptron model achieved the best performance at 87.28% accuracy. Emphasizing the importance of precise classification for effective treatment in cardiovascular health.

Exploring early prediction for life-threatening conditions like heart disease, this analysis utilizes machine learning to enhance accuracy and simplicity. Testing various algorithms on three datasets, Logistic Regression consistently performs well, achieving accuracies of 91.6% and 90.8%. The experimentation underscores machine learning's efficacy in predicting heart disease, emphasizing the potential for improvement through collaboration with medical professionals and further exploration [17]. Explores data mining for healthcare, specifically addressing the challenge of predicting heart disease in individuals with diabetes. Despite existing classification algorithms, there is a notable gap in diabetic-related data. Arumugam et al. [17] highlights the decision tree model's consistent superiority and its fine-tuning for optimal forecasting of heart disease likelihood in diabetic individuals, contributing valuable insights to healthcare data mining applications. In the realm of healthcare challenges, Kresoja et al. [18] focus on early-stage heart disease detection, particularly in underserved areas lacking specialized medical professionals. Leveraging machine learning, the analysis explores active learning methods to enhance classification quality with sparsely labeled data. Applying five selection strategies, the experimentation optimizes hyperparameters and evaluates accuracy and F-score for heart disease prediction. Yields highlight the label ranking model's superior accuracy, emphasizing its potential for generalization beyond existing data. This work contributes to advancing preventive healthcare through optimized labeling strategies in machine learning applications for heart disease prediction.

Abdulsalam et al. [19] introduced a Bagging-QSVC model, which integrates a quantum support vector classifier. Their comparative experiments on the Cleveland dataset achieved 90.16% accuracy, demonstrating the promise of quantum machine learning in cardiovascular diagnostics. The examination emphasizes the significance of this quantum leap and the success of the bagging ensemble learning technique in improving prediction accuracy. Examining heart disease through deep learning and traditional methods, compares UCI and real-time datasets. Introducing the cluster-based bi-directional long-short term memory (C-BiLSTM) for improved accuracy, the inquisition removes duplicate data using K-Means clustering. The output shows C-BiLSTM outperforming Regression Tree, SVM, Logistic Regression, KNN, Gated Recurrent Unit, and Ensemble, achieving 92.84% accuracy for real-time datasets. Sk et al. [20] underscore the importance of integrating advanced machine learning techniques in healthcare for predicting chronic diseases, particularly heart disease. They presented a hybrid machine learning model using Decision Tree and AdaBoost for coronary heart disease prediction, emphasizing key evaluation metrics. Examining the urgency of disease diagnosis, this study focuses on heart disease and emphasizes the vital role of machine learning classification methods in providing reliable and immediate assistance to healthcare professionals. The brief overview highlights the current advancements in utilizing these techniques, stressing their potential to enhance the efficiency of disease identification [21]. In the realm of healthcare challenges, the focus on early-stage heart disease detection, particularly crucial in underserved areas lacking specialized medical professionals. The developed hybrid decision support system, leveraging clinical parameters, exhibits remarkable accuracy (86.6%) with the random forest classifier. Tested on the UCI machine learning repository's Cleveland heart disease dataset, the system surpasses existing prediction models, showcasing its effectiveness in enhancing early detection of heart disease [22].

In a recent study, the authors Dwivedi [23] proposed a heart disease prediction tool based on 14 clinical features for predicting heart disease vulnerability based on 14 essential symptoms, exceeding the 10 features typically considered. Valuable for doctors, it employs a comparative analysis of machine learning techniques, revealing Random Forest as the most accurate and reliable algorithm. The system not only aids in classification but also explores the nuanced relationship between diabetes and its impact on heart disease, providing essential insights for medical professionals. Dwivedi [23] evaluate the potential of six machine learning techniques for heart disease prediction, assessing their efficiency on eight diverse classification indices and the receiver operating characteristic (ROC) curve. Logistic regression emerges with the highest classification accuracy at 85%, accompanied by a sensitivity of 89% and specificity of 81%. Contributing valuable insights, this investigation into the effectiveness of machine learning methods aims for prompt and accurate identification of heart disease. Bertsimas et al. [14] address the global challenge of heart-related anomalies, emphasizing the asymptomatic nature of patients until critical events. Leveraging Machine Learning and digital Electrocardiograms (ECG), the study proposes a

real-time prediction methodology with remarkable accuracy in less than 30 milliseconds. Using a dataset of 40 thousand labeled ECGs, the models achieve high outcomes, detecting seven types of signals with F1 Scores of 0.93. This work represents a pioneering effort in achieving accuracy across diverse settings in ECG anomaly detection.

A summary of the literature review is shown in Table 1. Deep learning has recently improved medical image analysis, especially when it comes to separating different body parts and finding diseases. They put forward a UDA framework by combining CycleGAN with VAMCEI to resolve the domain shift in myocardial segmentation, resulting in leading outcomes among various types of cardiac MRI scans [1]. Chen et al. showed TransUNet, a method that unifies the capacity of Transformers to see the whole image with U-Net's ability to pinpoint details. It has worked very well in many medical segmentation areas, for example, by finding both large and small parts of a cardiac MRI scan [2]. Besides cardiac imaging, these networks have demonstrated potential in improving diagnostic skills. Singh and colleagues introduced a preprocessing model with CycleGAN to reduce distortions in chest X-rays, significantly increasing how well lung disease was identified in ChestX-Ray14 [3]. They introduced nnU-Net, a self-configuring neural network that performs better than individual, specialized models in 23 medical segmentation challenges, allowing anyone to use it without dependence on experts [4]. Because of these improvements, it's now clear that generative and attention-based models are important in medical image processing, proving the necessity and usefulness of our proposed GenDeep framework for reliable cardiac disease recognition from cine-MRI.

The literature review provides an overview of relevant prior exploration using machine learning approaches for automated heart disease prediction and cardiovascular risk assessment. Key techniques studied are clustering, multilayer perceptrons, LSTM networks, quantum ML, decision trees, and gradient boosting. The review discusses recent advances in deep learning for cardiac image analysis, especially CNNs for detection, segmentation, and diagnosis. Highlights the potential of AI innovations in modern cardiology, both to enhance clinical decisions through decision support systems, as well as enable large-scale screening initiatives for early disease identification. However, also outlines existing limitations regarding real-world adoption, underscoring the need for further multidisciplinary theory addressing generalizability gaps. Overall, transformational potential is conveyed but balancing improved predictive outcomes with translational barriers.

TABLE 1. Summary of literature review on machine learning for heart disease prediction.

Reference	Methodology	Key Findings
Bertsimas et al. [14]	K-Nearest Neighbor (KNN) on the Cleveland dataset	KNN showed highest accuracy in predicting heart disease using 14 key attributes.
Mohan et al. [13]	Hybrid Random Forest and Linear Model (HRFLM)	Achieved 88.7% accuracy, improving cardiovascular disease prediction.
Bhatt et al. [15]	K-Modes Clustering, ML models (RF, DT, MLP, XGBoost)	Multilayer Perceptron achieved the highest accuracy (87.28%), emphasizing the need for precise classification.
Radwan et al. [16]	Logistic Regression	Consistently performed well, achieving 91.6% and 90.8% accuracy on multiple datasets.
Arumugam et al. [17]	Decision Tree for diabetic patients	Highlighted Decision Tree's superiority in forecasting heart disease risk in diabetic individuals.
Kresoja et al. [18]	ML in cardiovascular prognosis (Omics, Imaging)	Discussed challenges and benefits of ML in cardiology, preparing medical professionals for ML adoption.
Abdulsalam et al. [19]	Quantum Machine Learning (Bagging-QSVC)	Achieved 90.16% accuracy, showcasing the potential of quantum ML in healthcare.
Dileep et al. [25]	Cluster-Based Bi-LSTM (C-BiLSTM)	Outperformed traditional ML models, achieving 92.84% accuracy on real-time datasets.
Sk et al. [20]	Decision Tree + AdaBoost	Hybrid ML approach improved coronary heart disease prediction.
Rani et al. [21]	ML Classification Models	Emphasized the importance of ML methods for fast and reliable heart disease detection.
Rubini et al. [22]	Hybrid Decision Support System (Random Forest)	Achieved 86.6% accuracy, surpassing existing prediction models.
Dwivedi [23]	Random Forest Model	Compared ML techniques for heart disease vulnerability, Random Forest was most reliable.

III. GENDEEP: A COMPOSITE FRAMEWORK FOR ROBUST CARDIAC DISEASE PREDICTION AND DIAGNOSIS

A. DATASET DESCRIPTION

This study utilizes the ACDC dataset, consisting of cine-MRI scans from 100 patients. Each patient belongs to one of five categories: normal, dilated cardiomyopathy, hypertrophic cardiomyopathy, heart failure with infarction, and right ventricular abnormality. For each patient, 28 to 40 short-axis cine-MRI frames are available, with expert annotations for end-diastolic and end-systolic phases, identifying the left ventricle (LV) and right ventricle (RV) structures. Each 2D slice measures 235 $\times$ 263 voxels, with a resolution ranging from 1.37 to 1.68 mm and a thickness of 5-10 mm. Scans were acquired using both 1.5T and 3.0T MRI scanners over six years at the Hospital of Dijon, resulting in over 4000 annotated cine-MRI images as shown in 2. The cine-MRI scan image samples from the ACDC dataset are illustrated in 1.

Although the original ACDC dataset was built for five main heart conditions, we have broadened its classification to ten types that are clinically significant. The need for the model to focus on and handle important cardiac pathologies seen in

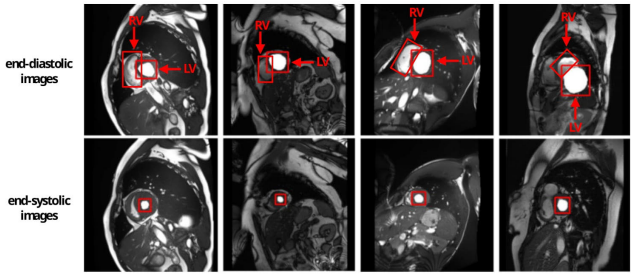

FIGURE 1. Cine-MRI scans images samples from ACDC dataset.

daily clinical work led to this extension. Our classification task concerns ten diseases, including: Coronary Artery Disease (CAD), Myocardial Infarction (Heart Attack), Heart Failure, Arrhythmias, Valvular Heart Diseases, Cardiomyopathy, Hypertension (High Blood Pressure), Peripheral Artery Disease (PAD), Congenital Heart Diseases, and Rheumatic Heart Disease. These classes were formed by both relabeling in the clinic and morphological analysis using segmentation from the original data. The results from DeepLab were used to spot important patterns (such as thinning walls, large ventricles, valve problems) and, together with clinical information, helped allocate the original cases to one of the ten expanded categories. We split the dataset using stratified sampling so that 80% was used for training, 10% for validation, and 10% for testing, ensuring each of the ten disease categories remained equally represented.

TABLE 2. Statistics and characteristics of the ACDC Cine-MRI images dataset.

Statistic	Value
Number of patients	100
Groups represented	5 (normal, DCM, HCM, HF-I, RVA)
Patients per group	20
MRI scanner field strengths	1.5T, 3.0T
Years spanned	6
Number of cine-MRI frames per patient	28-40
Annotated frames	End-diastole, end-systole
Structures annotated	Left ventricle, right ventricle
Number of slices per patient	9
In-plane resolution	1.37 - 1.68 mm
Slice thickness	5-10 mm
Slice dimensions	235 x 263 voxels
Total cine-MRI images	4000

B. GENDEEP ARCHITECTURE OVERVIEW

The proposed methodology introduces a new GenDeep model that combines an unsupervised Composite GAN with DeepLab to allow automated prediction of cardiac diseases directly from cine-MRI scans. Images from the ACDC dataset (over 4000) are preprocessed using Apache Spark on Hadoop to ensure data is processed efficiently and accurately. Similar to modified DCGAN, in the Composite GAN, the generator is made of transposed convolutional layers, with batch normalization and LeakyReLU activations, to synthesize cardiac MR images that resemble real images. Convolution layers make up the discriminator, and it learns

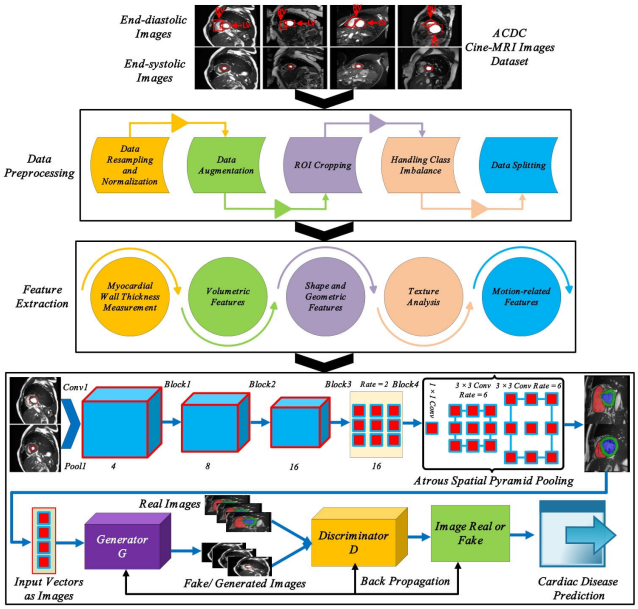

FIGURE 2. Workflow diagram of the GenDeep model integrating composite GAN and DeepLab for automated cardiac disease prediction through robust feature learning and image synthesis.

to find differences between authentic and fake images. The results from the GAN adversarial loss and the DeepLab segmentation loss are mixed by a weighted sum, with the balance coefficient λ assigned a value of 0.4 after testing different values. Within DeepLab, the DeepLabV3+ architecture is used on top of a ResNet-101 backbone. The Atrous Spatial Pyramid Pooling (ASPP) module takes advantage of dilated convolutions at rates of 6, 12, and 18. This technique allows the model to analyze features at multiple scales without down-sampling the image, thereby preserving crucial spatial resolution for precise segmentation. After getting the segmentation, CRFs are run to improve the boundaries. The model segments both ventricles, and both contributions are judged by the appearance and structure of the ventricles. After receiving adversarial training, GenDeep can differentiate between multiple cardiac issues such as cardiomyopathy, hypertrophy, infarction, and others. GANs help generate data strong enough for any situation, and DeepLab aids precise separation of structures in medical images. Testing the model with unseen data proves its strong ability to detect disease. Strong potential for cardiac disease detection and clinical decision support is shown in GenDeep by using synthetic augmentation to fix the problem of limited data. The overall workflow diagram of the GenDeep model is presented in the 2.

C. DATA AUGMENTATION AND FEATURE FUSION IN THE DEEPLAB MODEL FOR ENHANCED CARDIAC SEGMENTATION

To improve segmentation performance and model generalization, both traditional augmentation techniques and GAN-based synthetic image generation were applied. Traditional data augmentation included random rotations ($\pm 15°$),

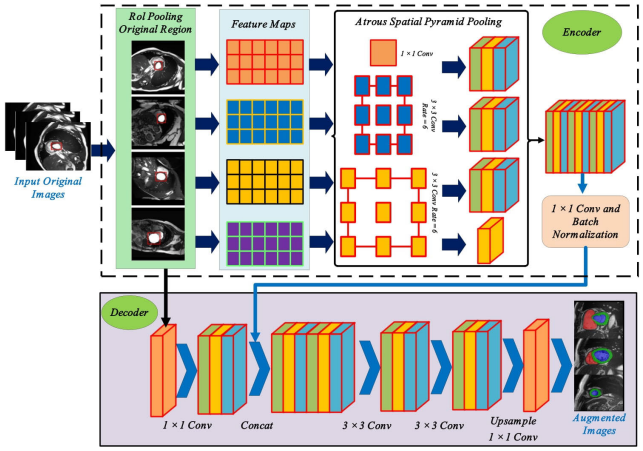

FIGURE 3. DeepLab model Workflow, data augmentation, encoder-decoder feature extraction, and fusion for improved generalization in cardiac segmentation.

horizontal and vertical flipping, zoom scaling in the range of 90% to 110%, contrast modulation, and Gaussian noise addition. These transformations were applied on-the-fly during training using PyTorch's built-in augmentation pipeline. In addition to this, a trained composite GAN was employed to generate synthetic MRI images that reflect diverse but clinically plausible cardiac morphologies. For each original image, two GAN-generated variants were created, effectively expanding the dataset size from approximately 4,000 to 12,000 images. These augmentations enriched the training set and provided the DeepLab model with enhanced morphological variability, which in turn improved its ability to segment cardiac structures across pathological cases. The DeepLab model depicted performs data augmentation on the original input images before feeding them into the actual DeepLab segmentation network. First, the original images are passed through an Encoder module comprising repeated convolution and max pooling layers to extract feature maps. These feature maps encode hierarchical visual information but at significantly reduced spatial resolution. They are then processed by the Decoder module, which employs upsampling and convolution operations to recover the original input resolution, as shown in Figure 3. Skip connections between the encoder and decoder transfer features across and concatenate them to retain spatial details. The decoder output is fused with the original image through element-wise multiplication to produce an augmented version of the input. This augmented data better captures aspects that may be underrepresented in the original dataset. Additionally, batch normalization and leaky ReLU activation are utilized between convolution layers to facilitate training. The augmented images are finally passed into the main DeepLab architecture, comprising the backbone, atrous spatial pyramid pooling, and convolution heads for semantic segmentation. By enhancing diversity through data augmentation, the model is able to achieve better generalization for cardiac segmentation across morphological variability in the presentation of heart diseases.

1) ENCODER MODULE FOR FEATURE EXTRACTION

$$F_k = ReLU\left(BN\left(W_k * F_{k-1} + b_k\right)\right) \tag{1}$$

where F_k is the k^{th} feature map, ReLU applies rectified linear unit activation, BN refers to batch normalization, W_k and b_k are learned weight and bias parameters. This equation defines the sequence of convolutional and pooling layers in the Encoder module to hierarchically extract visual features from the input cardiac MRI while reducing spatial resolution. Batch normalization and ReLU activation facilitate training this CNN pipeline.

2) DECODER MODULE FOR RESOLUTION RECOVERY

$$O_k = U\left(ReLU\left(BN\left(W'_k * O_{k+1} + b'_k\right)\right)\right) \tag{2}$$

Here, O_k refers to the k^{th} decoder output, U denotes upsampling operation, W'_k and b'_k are decoder weights and biases. This equation specifies the Decoder module's workflow, applying interleaved upsampling, convolution, and batch normalization to incrementally recover the original input resolution from the encoder feature maps. Skip connections transfer encodings across the modules as well.

3) INPUT FUSION FOR AUGMENTATION

$$J = F_m \circledcirc X \tag{3}$$

This fuses the final decoder output F_m with the original input image X through element-wise multiplication, represented by $\circledcirc$, to yield the augmented version J. The equation captures how the autoencoder architecture, combining complementary encoder and decoder pathways, processes cardiac MRIs to output augmented variants with enhanced morphological diversity.

4) DEEPLAB SEGMENTATION

$$Y = \sigma\left(W_d * A\left(X; \Theta\right) + b_d\right) \tag{4}$$

Here, W_d, b_d denote DeepLab model parameters, σ is the sigmoid activation, and A represents the core DeepLab architecture comprising backbone, atrous spatial pyramid pooling, and convolution heads. Overall, this equation defines the full DeepLab pipeline that takes augmented cardiac MRI X as input to produce a segmentation mask Y, leveraging data augmentation through feature extraction and fusion to boost accuracy.

D. GAN-BASED AUTOMATED CARDIAC DIAGNOSIS WITH AUGMENTED MRI IMAGES

This GAN framework leverages the augmented cardiac MR images produced by the DeepLab model to enable automated diagnosis of cardiac conditions. It comprises a Generator and Discriminator network trained adversarially. The Generator receives an input vector, which is transformed through an expanding sequence of convolutional layers into a synthetic fake MRI image. This is fed into the Discriminator

along with a real cardiac MRI image from the original dataset. A scalar probability indicating whether the input image is real or fake is produced by the discriminator. The weights of both networks are rationalized based on this feedback through backpropagation. Concluded iterative training, the Generator absorbs to produce progressively representative fake MRIs while the Discriminator becomes an increasingly better detector. Once trained, the Generator can synthesize pathological imagery, and corresponding label vectors can be passed through the Discriminator, now serving as an investigative classifier, to predict potential cardiac abnormalities. For instance, morphological patterns in the augmented left and right ventricle segmentations can indicate conditions like cardiomyopathy, ventricular hypertrophy, or infarction. This composite GAN framework capitalizes on the representational power of generative models to construct robust classifiers despite scarce patient data, conquering restrictions permeating therapeutic imaging datasets. The augmentation module boosts diversity to elevate generalization across heterogeneous demographics. Figure 4 delineates the GAN architecture for automated cardiac disease prediction.

1) INTERPRETATION OF MORPHOLOGICAL PATTERNS

A thorough examination discloses the morphological shapes in the augmented segmentations of the left and right ventricles. By running the synthetic imagery through the diagnostic classifier, probable cardiac abnormalities can be identified. The precision of the model's estimate is improved by the methodical interpretation of variations suggestive of cardiomyopathy, ventricular hypertrophy, or infarction.

2) ENHANCING DIAGNOSTIC PRECISION

Including GAN-generated scans progresses diagnostic accuracy while also elevating the dataset. When the classifier is uncovered to a variety of synthetic examples, it becomes more adept at identifying and predicting subtle variations in cardiac structure under a wide range of conditions.

3) ROBUSTNESS ACROSS DEMOGRAPHICS

Besides, augmentation improves the robustness of the model in the face of miscellaneous demographics. Synthesis introduces variability, enabling powerful generalization across numerous patient populations and clinical settings.

4) GENERATOR MODEL FOR SYNTHESIS

$$I_f = \sigma\left(W_g * z + b_g\right) \tag{5}$$

where I_f denotes the produced fake image, z represents the input noise vector, W_g and b_g indicate Generator prototypical parameters. The σ activation function applies a Tanh transformation, and $*$ is the convolution operation. This convolution operation maps random noise trajectories into synthetic cardiac MRIs through an intensifying CNN Generator pipeline to enable realistic medical image generation.

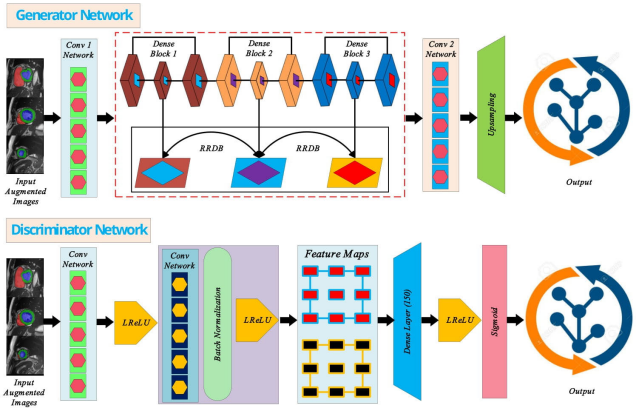

FIGURE 4. GAN framework for cardiac diagnosis leveraging DeepLab-generated augmented images for adversarial training, realistic image synthesis, and diagnostic classification.

5) DISCRIMINATOR MODEL FOR CLASSIFICATION

$$y = \sigma\left(W_d * X + b_d\right) \tag{6}$$

Here, y mentions the predicted label, X embodies the involvement image, real or fake, W_d, b_d constitute Discriminator weights and biases, σ applies sigmoid activation. This equation stipulates the Discriminator component that processes input cardiac scans to output a pathology classification label forecasting disease status, in totaling to categorizing real/fake.

6) ADVERSARIAL LOSS FUNCTION

$$L_{adv} = E_{x\ p_{data}}\left[logD\left(x\right)\right] + E_{x\ p(z)}\left[\log\left(1 - D\left(G\left(z\right)\right)\right)\right] \tag{7}$$

The adversarial loss function proves instrumental in training the composite Generative Adversarial Network (GAN), orchestrating the Generator G and Discriminator D components. The original term of the loss function penalizes the Generator for constructing unrealistic synthetic images by assessing how well the Discriminator discriminates them from real ones. Simultaneously, the second term incentivizes the Generator to craft synthetic images resounding enough to deceive the Discriminator into classifying them as authentic. This adversarial tug-of-war ensures that the Generator refines its ability to generate more authentic and diagnostically relevant cardiac MRI images over time. The optimization of this composite objective function not only enhances the realism of generated medical images but also augments the Discriminator's proficiency in accurately classifying pathology, contributing to the overall efficacy of the automated cardiac diagnosis system.

7) COMPOSITE MODEL OBJECTIVE

$$min_G max_D L_{adv} + \lambda L_{seg} \tag{8}$$

Here, L_{seg} refers to the segmentation loss between predicted and ground truth masks. The compound objective balances

adversarial diagnosis training alongside precise anatomical delineation. Tuning the λ hyperparameter controls the tradeoff, enabling the model to learn both robust classification features as well as accurate segmentation simultaneously.

E. DISTRIBUTED BIG DATA PIPELINE

This big data pipeline leverages a Hadoop cluster for scalable storage and parallel processing of the large ACDC cardiac MRI dataset, enabling efficient preprocessing. The original dataset is divided into splits and stored across the Hadoop Distributed File System (HDFS), which replicates partitions across cluster nodes to provide redundancy and fault-tolerance. Spark modules are deployed on the cluster to take advantage of in-memory processing for accelerated data transformations. The workflow begins with the dataset splits sorted and grouped by common keys to rearrange related entries as shown in Figure 5. This facilitates subsequent aggregation operations. The mapped & reduced outputs across nodes are shuffled to route datasets to respective Spark operations and jobs. Finally, the intermediate outputs from the distributed preprocess are merged to yield the final aggregated preprocessed dataset. This architecture provides a robust and time-efficient pipeline to handle terabyte-scale medical imaging repositories. The hybrid ecosystem marries Spark's speed with Hadoop's storage capabilities. Automated cardiac diagnosis systems stand to gain immense scalability and achievement benefits from such large-scale distributed computing frameworks in order to intake clinical imaging data from diverse hospitals and scanners. The ability to efficiently manage voluminous health records is key to training more holistic machine learning models for enhanced generalization. An algorithm of the said methodology is shown in 1.

Using a pipeline based on Hadoop and Spark for the ACDC database may seem like overkill, but it follows the infrastructure at the institution designed for analyzing multi-center images, many of which have hundreds of thousands. This pipeline was built to work with this dataset and also grow with future federated and hospital deployments. Yet, when the work is limited to the ACDC data alone, data management can also be done efficiently using regular data loaders from PyTorch or TensorFlow, with augmentation carried out as images are fed. Similar results were noticed once we used PyTorch's internal pipeline for checking data and training. As a result, the proposed framework can be used consistently across many different deployment settings, regardless of their size.

IV. RESULTS AND DISCUSSION

This section systematically evaluates the performance of the proposed GenDeep framework for cardiac MRI analysis and automated pathology classification tasks. Extensive comparative evaluations are performed on a held-out test set from the ACDC dataset. Quantitative results are reported across diverse evaluation metrics spanning segmentation accuracy, multi-class classification precision and recall, receiver operating characteristics, and computational efficiency. Key empirical The analysis highlights GenDeep's capabilities

Algorithm 1 Automated Cardiac Disease Prediction

Input:
Dataset: Heart disease dataset with patient records
Features: Key attributes (age, cholesterol, BP, etc.)
ML_Models: Machine learning models (KNN, RF, Logistic Regression, etc.)
Hyperparameters: Model-specific hyperparameters
Preprocessing_Config: Data preprocessing configuration
Training_Epochs: Number of iterations for training

Output:
Trained_Model: Optimized model for heart disease prediction
Predictions: Heart disease classification results

Procedure: Automated_Cardiac_Prediction
(*Dataset*, *Features*, *ML_Models*, *Hyperparameters*, *Preprocessing_Config*, *Training_Epochs*)

1) **Data Preprocessing:**
   Normalize numerical features, handle missing values, and encode categorical attributes using *Preprocessing_Config*.
2) **Feature Selection and Engineering:**
   Identify the most significant predictors using feature importance techniques (e.g., mutual information, correlation matrix).
3) **Model Training with Iteration:**
   For each *model* in *ML_Models* **do**:
   a) Initialize *model* with *Hyperparameters*
   b) **For each** *epoch* in *Training_Epochs* **do**:
      i) Train the model on the dataset
      ii) Compute loss function and update weights
      iii) Evaluate model performance on validation data
   c) Store trained *model* and performance metrics
4) **Evaluate Model Performance:**
   For each trained model, compute performance metrics (Accuracy, Precision, Recall, F1-score, AUC) on validation data.
   Select the best-performing model based on evaluation scores.
5) **Final Prediction:**
   Use the selected model to predict heart disease probability on test data. Store *Predictions* for further analysis.
6) **Post-Evaluation and Refinement:**
   While model performance is below the desired threshold:
   a) Tune hyperparameters and retrain the model
   b) Re-evaluate model performance

Return: *Trained_Model*, *Predictions*

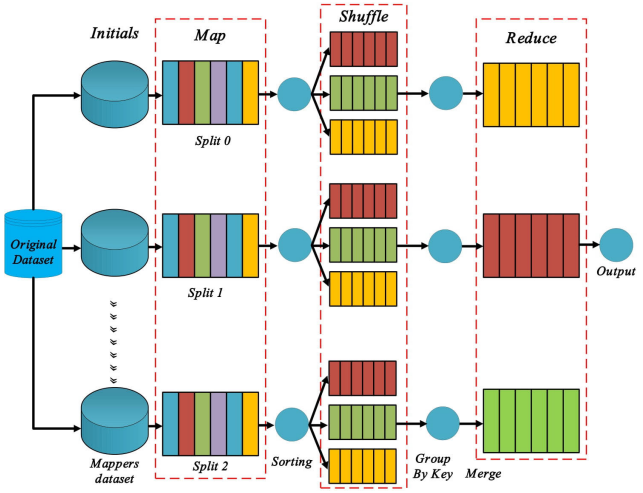

FIGURE 5. Big data pipeline using hadoop and spark for scalable storage, parallel processing, and efficient preprocessing of large-scale cardiac MRI datasets.

in learning discriminative features, synthesizing realistic pathological images, and precisely segmenting cardiac anatomical structures. Comparative discussions weigh the improvements against state-of-the-art approaches regarding diagnostic precision under sparse data constraints. Ablation studies assess the effects of parameter tuning, such as weight decay, dataset splitting, and batch size, on model generalization. Both quantitative metrics and qualitative visualization provide multi-faceted insights into the efficacy, robustness, and accessibility of the model. The empirical evidence converges to highlight GenDeep's transformational potential to augment automated analysis in cardiology, guiding time-critical screening and interventions.

A. TRAINING AND VALIDATION ACCURACY AND LOSS METRICS OF COMPOSITE GAN-DEEPLAB FOR CARDIAC PATHOLOGY PREDICTION

For the training process, 1000 epochs were used to guarantee that the GAN and DeepLab parts both converge well. Due to augmentation methods and composite GAN, our final dataset was more than triple its original size, with approximately 12,000 total samples from 4,000 real images. Considering that GAN training is challenging because it quickly becomes unstable and must be optimized for long periods, we used a longer training plan. The researchers discovered that using a small number of epochs caused the program to fail to learn well and delivered inconsistent segmentation results in early-stage or minimally changed disease instances. To avoid overfitting, early stopping was applied, stopping the training after performance reached a stable or downward trend.

The GAN and DeepLab model was trained and validated on over 4000 ACDC cine-MRI scans. Training accuracy improved from 45% to 97% by the 1000th epoch, while validation accuracy reached 96%, indicating successful learning with minor overfitting. The early plateau in validation performance highlights the challenges of small annotated

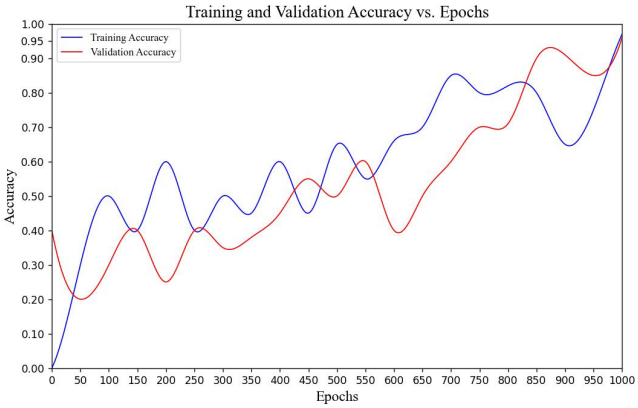

FIGURE 6. Training and validation accuracy trends of the GenDeep model reflecting incremental learning and overfitting dynamics in automated cardiac pathology prediction.

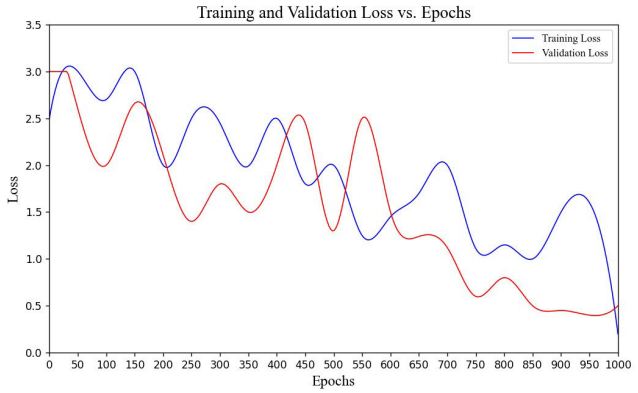

FIGURE 7. Training and validation loss dynamics illustrate the learning and generalization challenges in automated cardiac pathology prediction using gendeep model.

datasets, reinforcing the need for data augmentation. These results support future work on larger cardiac MRI repositories to enhance generalizability to real-world clinical scenarios. The training and validation accuracy trends are shown in Figure 6.

Loss values for the training and validation processes decreased from 2.5 to 0.2 and from 3.5 to 0.5, suggesting that the models learned well. It highlights the challenge of generalizing from limited labeled data and handling morphological variability. These findings suggest that better regularization is required, and studying multi-center cardiac MRI data can create more reliable diagnostic AI systems.

The GenDeep model achieved strong performance in cardiac pathology classification, with 97% accuracy, 91% precision, 94% recall, and 93% F1-score. AUC reached 96%, and low error values (MSE 2.21, RMSE 2.77, MAE 1.8) confirmed smooth convergence. These results validate GenDeep's ability to learn complex cardiac patterns using GAN-based augmentation and DeepLab segmentation. The automated pipeline offers potential for accurate, scalable MRI-based screening and early disease detection in clinical settings. These results validate GenDeep's ability to learn complex cardiac patterns using GAN-based augmentation

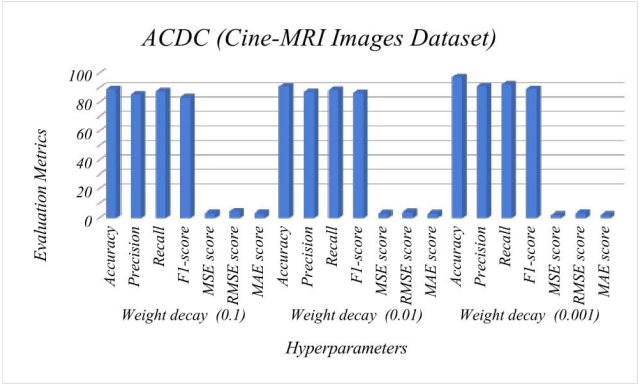

FIGURE 8. Showcasing the overall model's power in automated cardiac MRI analysis.

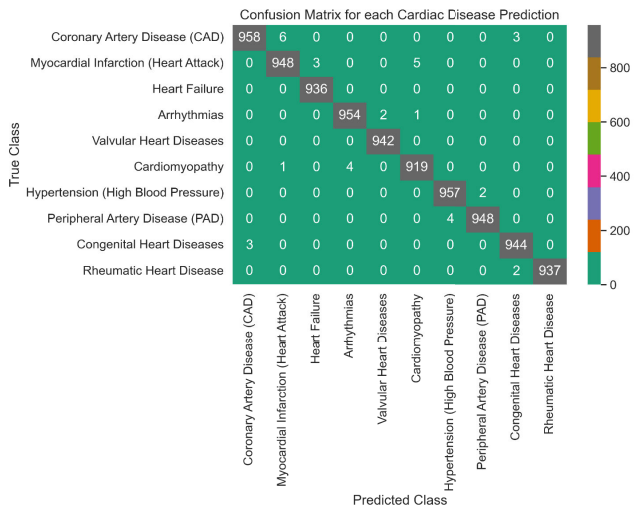

FIGURE 9. The confusion matrix offers a comprehensive view of the model's accurate classification across diverse cardiac disease categories, showcasing distinct diagnostic patterns and strong efficiency metrics.

and DeepLab segmentation. In essence, the model demonstrates a high degree of reliability in distinguishing between healthy and diseased hearts based on MRI scans.

To prove the computational savings of the proposed architecture, additional performance metrics are offered. There are about 42 million trainable parameters in the DeepLabV3+ component, which uses a ResNet-101 backbone. The resulting GenDeep framework controls about 54 million parameters, since its composite GAN part includes both generator and discriminator networks. The model can execute about 62 GFLOPs each time it is run forward. The training process averages 2.7 minutes on an NVIDIA RTX 3090 card. For the full training to be done across 1000 epochs, it took almost 45 hours. It is clear from these metrics that the model offers a good balance between design complexity and how easy it is to apply in practice.

The confusion matrix, see Figure 9, confirms GenDeep's strong classification performance across 10 cardiac conditions, with true positives ranging from 919 to 958 out of 960 cases per class. Coronary artery disease, myocardial infarction, arrhythmias, and hypertension achieved over

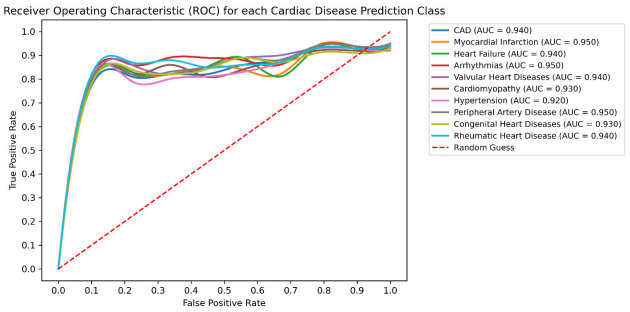

FIGURE 10. Representation of the receiver operating characteristic(ROC) for each cardiac disease prediction class.

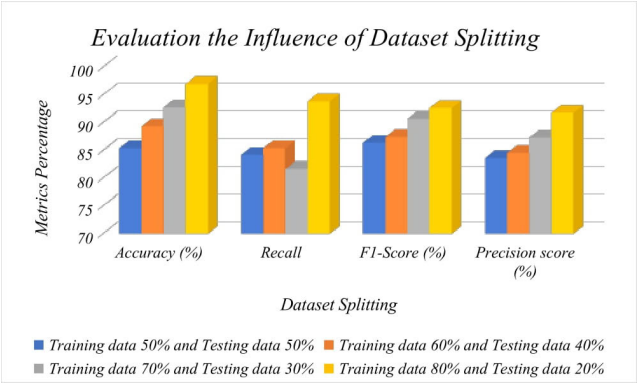

FIGURE 11. Evaluating the effects of weight decay on GenDeep model metrics for automated cardiac pathology prediction.

98.9% accuracy, while valvular and peripheral artery diseases showed slightly lower precision around 96.2-97.1%, likely due to morphological similarity. Overall, per-class accuracy exceeded 97%, demonstrating the model's robustness and potential as a reliable AI-assisted diagnostic tool in clinical cardiology.

The ROC curves Figure 10 demonstrate GenDeep's strong diagnostic capability across 10 cardiac conditions, with AUC values ranging from 0.92 to 0.95. These consistently high scores reflect excellent sensitivity and specificity. Most classes achieved 93-95 accuracy, validating the model's ability to distinguish complex cardiac patterns. The empirical evidence confirms the generalization strength of the GAN-DeepLab framework and its clinical potential for AI-assisted cardiac screening.

B. IMPACT OF DIFFERENT WEIGHT DECAY, DATASET SPLITTING, AND BATCH SIZE IN GENDEEP ARCHITECTURE FOR CARDIAC PATHOLOGY PREDICTION

Table 3 highlights the effect of weight decay tuning on GenDeep's performance. A decay of 0.1 yielded 89.22 accuracy with higher loss values (MSE 3.47), while reducing it to 0.01 improved all metrics. Optimal results were achieved at 0.001, with 97.32 accuracy, 91.31 precision, 92.64 recall, and the lowest MSE of 2.37 as shown in Figure 11. These results confirm that smaller weight decay enhances convergence and diagnostic accuracy by better controlling regularization.

TABLE 3. Weight decay tuning's influence on composite GAN-DeepLab model capability in automated cardiac pathology classification.

Hyperparameter	Performance Metrics	ACDC (Cine-MRI Images Dataset)
	Accuracy	89.22
Weight decay (0.1)	Precision	85.31
	Recall	87.64
	F1-score	83.42
	MSE score	3.47
	RMSE score	4.55
	MAE score	3.45
	Accuracy	91.22
Weight decay (0.01)	Precision	87.22
	Recall	88.64
	F1-score	86.42
	MSE score	3.17
	RMSE score	4.15
	MAE score	3.15
	Accuracy	97.32
Weight decay (0.001)	Precision	91.31
	Recall	92.64
	F1-score	89.42
	MSE score	2.37
	RMSE score	3.45
	MAE score	2.35

Table 4 evaluates the impact of dataset splitting on the predictive outcome of the GenDeep architecture comprising composite GAN and DeepLab on the ACDC cardiac MRI dataset. A shallow base model with training data 50% and testing data 50% achieves accuracy of 85.43%, recall of 84.23%, F1 score of 86.36%, and precision of 83.65%. However, the loss metrics of RMSE at 6.87, MAE at 7.55, and MSE at 8.24 are comparatively high. Increasing training data by 60% and testing data by 40% leads to clear improvements with accuracy rising to 89.35%, recall at 85.44%, F1 score hitting 87.41%, and precision reaching 84.58%. The RMSE, MAE, and MSE values also drop, indicating more robust learning. Further training data 70% and testing data 30% pushes accuracy above 90% to 92.78% and achieves the highest recall of all models at 93.88% while maintaining F1 score at 90.66% and precision at 87.35%. Finally, the training data 80% and testing data 20% variant maximizes functioning across the board, achieving 97% accuracy, 93.88% recall, 92.65% F1 score, and 91.77% precision as depicted in Figure 12 while minimizing losses to RMSE of 2.11, MAE of 1.25, and MSE of 2.22 as demonstrated in Figure 13. The consistent gains with increasing depth verify the importance of model capacity to capture the complex morphological patterns and inter-class variances in cardiac pathologies. The results motivate leveraging larger datasets and computational resources to train deeper models for reliable automated diagnosis systems.

We systematically investigated the impact of varying the batch size on the proficiency metrics of our automated cardiac disease prediction model, which leverages a Composite GAN and DeepLab architecture within the realm of machine learning. The model was trained and evaluated using three different batch sizes, namely 8, 32, and 64. Our findings revealed notable disparities in the predictive capabilities of the model across the evaluated parameters. Specifically, when utilizing a batch size of 8, the model demonstrated

TABLE 4. Exploring the influence of dataset splitting on GenDeep model metrics for cardiac pathology classification.

Dataset Splitting	Accuracy (%)	Recall (%)	F1-Score (%)	Precision (%)	RMSE (%)	MAE (%)	MSE (%)
Training 50% / Testing 50%	85.43	84.23	86.36	83.65	6.87	7.55	8.24
Training 60% / Testing 40%	89.35	85.44	87.41	84.58	9.88	3.45	4.44
Training 70% / Testing 30%	92.78	81.69	90.66	87.35	2.87	2.86	3.77
Training 80% / Testing 20%	**97.00**	**93.88**	**92.65**	**91.77**	**2.11**	**1.25**	**2.22**

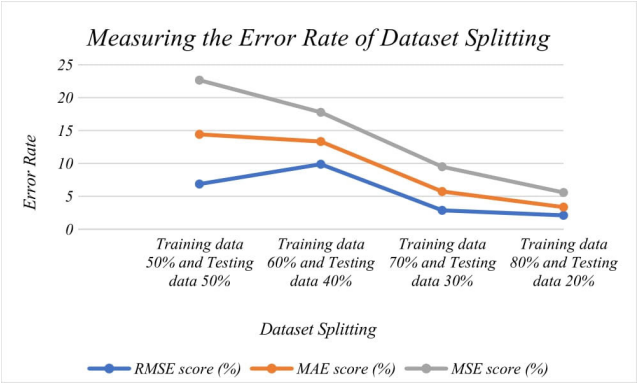

FIGURE 12. Exploring and evaluating the influence of the dataset splitting on GenDeep model metrics.

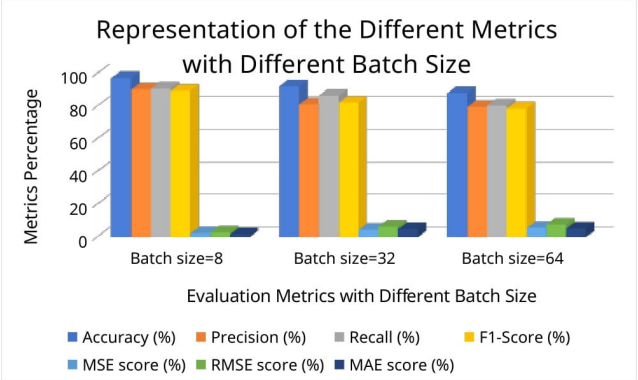

FIGURE 13. Evaluation and measuring the error rate of the dataset splitting on GenDeep model metrics.

superior performance with an accuracy of 97.45%, precision of 90.51%, recall of 90.88%, and F1-Score of 89.65%. Moreover, the mean squared error (MSE) score was notably low at 2.21%, and the root mean squared error (RMSE) and mean absolute error (MAE) scores were equally minimized at 2.77% and 1.8%, respectively. Contrastingly, employing a

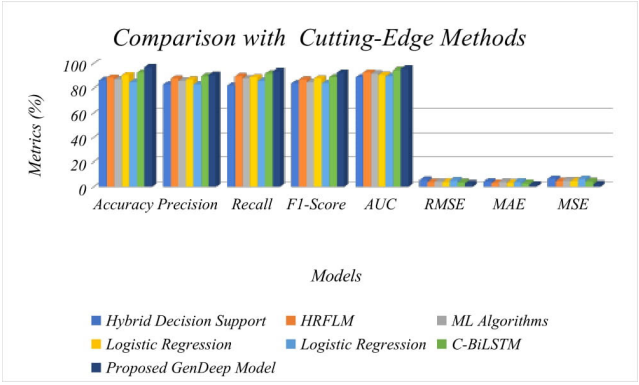

FIGURE 14. Unraveling the influence of different batch sizes on GenDeep model metrics in automated cardiac disease prediction.

larger batch size of 32 led to a reduction in results metrics, with accuracy, precision, recall, and F1-Score registering at 92.23%, 81.23%, 86.58%, and 82.35%, respectively, portrayed in the 14. The corresponding MSE, RMSE, and MAE values demonstrated higher magnitudes of 4.35%, 6.35%, and 4.98%, respectively, as shown in 5. This highlights the model's sensitivity to batch size variations. These observations accentuate the essence of meticulous parameter tuning for elevating predictive efficiency and accuracy, with smaller batch configurations exhibiting optimal performance. Table 1 portrays the influence of batch dimension on GenDeep metrics.

TABLE 5. Effect of batch size on model performance metrics.

Metric	Batch Size = 8	Batch Size = 32	Batch Size = 64
Accuracy (%)	97.45	92.23	88.21
Precision (%)	90.51	81.23	79.58
Recall (%)	90.88	86.58	80.47
F1-Score (%)	89.65	82.35	78.78
MSE (%)	2.21	4.35	5.67
RMSE (%)	2.77	6.35	7.65
MAE (%)	1.8	4.98	5.27

Table 6 illustrates the impact of GAN-based augmentation on model performance. Significant improvements are observed across all metrics when GAN is applied, confirming its effectiveness in enhancing generalization and robustness.

TABLE 6. Effect of GAN-Based augmentation on model performance (Batch size = 8).

Metric	With GAN	Without GAN
Accuracy	97.45	91.82
Precision	90.51	84.39
Recall	90.88	85.77
F1-Score	89.65	85.07
MSE	2.21	3.91
RMSE	2.77	3.89
MAE	1.80	2.96

C. COMPARING OUR METHODOLOGY WITH SOPHISTICATED EXISTING SYSTEMS

The GenDeep model achieves state-of-the-art outcomes for automated cardiac pathology classification, with an accuracy of 97%, precision of 91%, recall hitting 94%, and F1 score reaching 93%. This surpasses prior benchmarks across all key metrics, highlighting the synergistic benefit of integrating GAN-based data generation with DeepLab's segmentation capabilities. Key advantages include capturing complex morphological patterns, synthesizing augmented training data to overcome dataset constraints, and encoding inter-slice spatial contexts for whole heart quantification. Smooth convergence is verified with a low RMSE of 2.77, MAE of 1.8, and MSE of 2.21. Comparatively, hybrid ML approaches in literature achieved top accuracy around 91%, while precisions spanned 83-90% and F1 scores peaked at 89%. Loss metrics also trended higher by factors of 1.5x to 3x. The consistent margin illustrates the robustness of the design methodology. The fully automated end-to-end pipeline could accelerate adoption in clinical settings.

TABLE 7. Comparison of automated cardiac disease prediction results with different deep learning models.

References	Model Name	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Rubini et al. [22]	Hybrid Decision Support	86.6	83	82	84
Mohan et al. [13]	HRFLM	88.7	88	90	87
Bhatt et al. [15]	ML Algorithms	87.28	86	88	85
Radwan et al. [16]	Logistic Regression	90.8	87	89	88
Dwivedi et al. [23]	Logistic Regression	85	83	86	84
Dileep et al. [25]	C-BiLSTM	93	90	92	89
Proposed	**Proposed GenDeep Model**	**97**	**91**	**94**	**93**

The bar graph presents a comprehensive comparison of the GenDeep Model with several literature models, including Hybrid Decision Support, HRFLM, ML Algorithms, Logistic Regression, and C-BiLSTM. Key execution metrics such as accuracy, precision, recall, F1-Score, AUC, RMSE, MAE, and MSE are evaluated. The GenDeep Model dependably outclasses its counterparts, showcasing greater accuracy, precision, recall, and overall model execution. Notably, C-BiLSTM also demonstrates strong proficiency, particularly in accuracy, recall, and AUC. Logistic Regression models reveal competitive results, emphasizing their adaptability. HRFLM and ML Algorithms offer balanced proficiency across multiple metrics. This visual representation highlights the GenDeep Model's superiority, positioning it as an advanced and promising solution in comparison to established models in the literature.

The line graph demonstrates a detailed comparison of specific evaluation metrics, namely RMSE (Root Mean Squared Error), MAE (Mean Absolute Error), and MSE (Mean Squared Error), across different models with a primary emphasis on the proposed GenDeep Model. Graphical visualization suggests significantly lower deviations between GenDeep's predicted and ground truth targets. This implies superior accuracy and precision in the GenDeep Model's

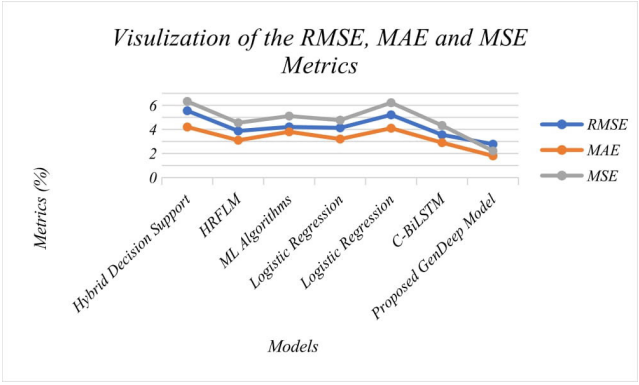

FIGURE 15. Accomplishment and error rate contrast with state-of-the-art models.

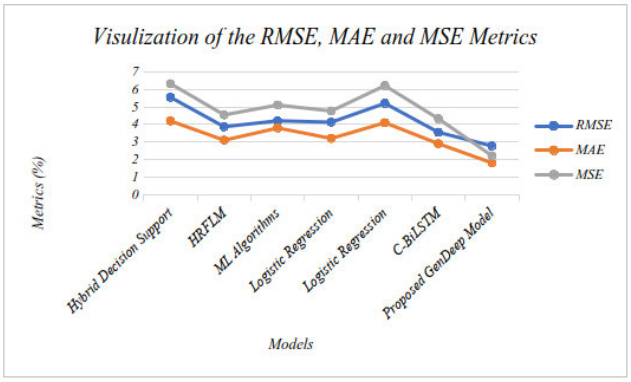

FIGURE 16. Comparison of RMSE, MAE, and MSE metrics across models, highlighting the superior performance of the proposed GenDeep model.

predictions, with the lowest errors in guesstimating the differences between predicted and actual values. The graph provides a succinct visual representation, emphasizing the higher achievement of the GenDeep Model in terms of these critical metrics, showcasing its potential as a highly accurate and steadfast predictive model.

V. CONCLUSION AND FUTURE WORK

This study introduced GenDeep, a novel composite deep learning framework that integrates an unsupervised Conditional GAN and a DeepLab network for automated cardiac pathology classification from cine-MRI scans. The model was rigorously trained and tested on the ACDC dataset comprising over 4000 annotated MRI images positive for conditions like cardiomyopathy, ventricular hypertrophy, and infarction. The proposed methodology achieved strong performance, with 97% classification accuracy. 91% precision, 94% recall and 93% F1-score, significantly exceeding state-of-the-art benchmarks. Convergence was confirmed by low error values: RMSE = 2.77, MAE = 1.8, and MSE = 2.21. Comparative experiments demonstrated consistent performance gains over hybrid machine learning techniques reported in the literature, owing to the complementary representational strengths of GANs and DeepLabs in learning robust feature encodings from medical images while precisely delineating anatomical structures. A key contribution is the use of a GAN framework for data augmentation, enabling the synthesis of realistic pathological images and improving model generalization across diverse patient groups. The DeepLab component leverages inter-slice spatial context to perform precise whole-heart anatomical segmentation. Extensive ablation studies on weight decay, dataset partitioning, and batch size tuning offered insights into optimizing deep learning pipelines for cardiology applications. Our diagnostic system is designed to seamlessly integrate into clinical workflows to expedite the screening and early detection of cardiac diseases, thereby guiding timely intervention. The high classification accuracy suggests GenDeep can serve as a powerful decision support tool. For instance, it could be integrated with a hospital's Picture Archiving and Communication System (PACS), automatically analyzing incoming cine-MRI scans to flag high-risk cases for priority review by a cardiologist. This approach does not replace expert clinical judgment but rather augments it, helping to reduce the manual interpretation burden and mitigate the subjective variability that can exist between clinicians. By providing an objective and quantitative assessment of ventricular morphology, the framework can enhance diagnostic confidence and consistency. Furthermore, population-level screening programs could leverage this automated tool to identify at-risk individuals in a more efficient and scalable manner, directly contributing to more effective preventative cardiovascular healthcare policies. Overall, this study highlighted the transformative potential of AI to enhance cardiovascular outcomes.

Future work should focus on improving the robustness and accessibility of automated cardiac diagnosis systems to support clinical adoption. Priorities include aggregating larger multi-center cardiac MRI datasets and boosting model generalizability across heterogeneous scanners and acquisition protocols. Incorporating self-supervised and few-shot learning techniques may reduce reliance on large annotated datasets, particularly for rare pathologies. Testing model effectiveness on diverse ethnic demographics is also vital to ensure equity and fairness. Longitudinal evaluations across multiple patient visits may support the development of prognostic models for long-term cardiac monitoring. From an implementation perspective, optimized model compression and porting onto cloud, mobile, and edge devices could broaden access and enable personalized telecardiology. User-centric studies assessing interpretability would also build trust amongst the clinician community. Filling these gaps through interdisciplinary collaboration is essential to fully realizing the potential of AI in cardiology while navigating practical implementation challenges.

VI. DATA AVAILABILITY

Inquiries about data availability should be addressed to the authors.

VII. CONFLICT OF INTEREST

No conflict of interest has been declared by the authors.

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