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Enhancing Heart Disease Prediction through Cross-Domain Transfer Learning from Related Health Conditions

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ABSTRACT

Heart disease remains a predominant cause of mortality worldwide, and the complexities in its predictive modeling are heightened by limited, domain-specific datasets. Traditional machine learning approaches often struggle to generalize across diverse populations due to data scarcity and the heterogeneous risk factors associated with heart disease. To address these limitations, this study explores a cross-domain transfer learning framework, which leverages knowledge from related health conditions, including diabetes, hypertension, and chronic respiratory diseases. This framework applies pre-trained models from these related domains to enhance prediction accuracy for heart disease in data-constrained environments. By adapting models trained on large datasets from overlapping medical domains, the proposed approach enriches heart disease models, allowing them to capture intricate risk patterns that might otherwise be overlooked. Experimental findings highlight the improved performance of transfer learning models over traditional heart disease models, particularly in terms of accuracy, sensitivity, and specificity. This cross-domain transfer learning approach not only addresses the challenges of limited heart disease datasets but also enhances predictive robustness, underscoring its potential for real-world clinical applications.

INTRODUCTION

Heart disease remains a critical global health challenge, responsible for approximately 17.9 million deaths annually, which equates to 32% of all deaths worldwide, according to the World Health Organization (WHO) [1]. Early detection and accurate risk assessment are vital in reducing heart disease mortality, as timely intervention can significantly alter patient outcomes. In recent years, machine learning (ML) has shown promise in aiding the early prediction and diagnosis of heart disease by analyzing complex patterns in medical data. However, these ML models depend on large, high-quality datasets with extensive labeling to achieve accurate results, which is often a significant constraint in heart disease research [2]. This scarcity of annotated data impairs the model's ability to generalize across diverse patient demographics, creating a barrier to achieving scalable, reliable heart disease prediction.

The complexity of heart disease arises from its multifactorial nature, involving genetic predispositions, environmental influences, and lifestyle factors that together create a multidimensional dataset landscape [3]. Predicting heart disease effectively requires models capable of learning from these complex datasets, but traditional approaches struggle without access to vast, diverse training data. In addition, obtaining heart disease-specific datasets that are both large and accurately labeled is a time-consuming and costly process, often unattainable for many healthcare institutions, especially in resource-constrained settings [4]. Consequently, the limited availability of heart disease data necessitates innovative solutions that can overcome these data challenges while still delivering robust and accurate predictions.

Transfer learning has emerged as a promising approach to address these limitations. Originally developed for tasks such as image recognition and natural language processing, transfer learning allows a model trained on one domain to be fine-tuned for tasks in another domain by leveraging shared feature patterns [5]. In healthcare, transfer learning has shown great potential, particularly in scenarios where related diseases share physiological or pathological features, allowing models trained on one disease to inform predictions in another. For instance, hypertension and diabetes are known to have overlapping risk factors with heart disease, such as high blood pressure, cholesterol imbalances, and insulin resistance, making them suitable domains from which transferable knowledge can be derived [6]. By adapting insights from these related health conditions, cross-domain transfer learning offers a practical solution for enhancing heart disease prediction accuracy, even with limited domain-specific data.

The utility of cross-domain transfer learning in heart disease prediction is further supported by studies demonstrating its effectiveness in related fields. For example, research on chronic obstructive pulmonary disease (COPD) prediction has shown that transferring learned features from models trained on respiratory conditions improves classification accuracy in limited-data scenarios [7]. Similar advancements have been noted in the prediction of diabetes-related complications using transfer learning, where leveraging external datasets has enhanced the model's ability to generalize across varying patient data distributions [8]. These studies indicate that when sufficient domain alignment exists, cross-domain transfer learning can substantially boost model performance, offering a viable path for applications in heart disease prediction.

In this study, we propose a novel framework that utilizes cross-domain transfer learning to improve heart disease prediction accuracy by transferring insights from models trained on related conditions. By incorporating knowledge from domains with overlapping risk factors—such as diabetes, hypertension, and COPD—this approach aims to overcome the constraints posed by limited heart disease-specific data. Through this framework, we aim to demonstrate that cross-domain transfer learning can enhance predictive robustness and accuracy, providing a scalable solution that supports real-world clinical applications. This research contributes to the growing field of predictive healthcare by showing how transfer learning can unlock the potential of small datasets, ultimately paving the way for more accessible, efficient, and accurate heart disease prediction in diverse healthcare environments.

Literature Review

The application of machine learning in heart disease prediction has evolved rapidly over recent years, but most approaches still face significant limitations due to data scarcity and complex data requirements. Traditional machine learning models often require large, labeled datasets to perform effectively. However, collecting annotated data specific to heart disease is both time-intensive and costly, especially in resource-limited settings, which impedes the practical utility of many predictive models [1]. The high-dimensional nature of heart disease data, which integrates a multitude of genetic, lifestyle, and clinical variables, further complicates data collection and model generalization [2]. These constraints have prompted researchers to investigate alternative solutions that can overcome the challenges of limited data availability.

Transfer learning has emerged as a promising approach to address these data limitations in heart disease prediction. By transferring knowledge from related domains, such as diabetes and hypertension, transfer learning enables models trained on larger, more readily available datasets to adapt to heart disease prediction. This technique has proven particularly beneficial in healthcare, where diseases often share overlapping risk factors and physiological markers. For instance, research by Lin et al. [3] explored domain-adaptive transfer learning using graph convolutional networks (GCNs) for coronary heart disease (CHD) prediction. By aligning feature representations from different domains, their study demonstrated improved classification accuracy in heart disease prediction, suggesting the viability of cross-domain transfer learning for scenarios with limited heart-specific data.

Further supporting the efficacy of transfer learning in healthcare, Khan et al. [4] examined its application within an Internet of Medical Things (IoMT) framework. IoMT devices continuously collect real-time patient data, such as heart rate and blood pressure, from wearable devices, which creates a rich data stream adaptable to various health predictions. By fine-tuning pre-trained models on patient-specific data, Khan et al. demonstrated how transfer learning could enhance model adaptability, allowing predictions to reflect individual patient health profiles. This continuous flow of data not only enhances model performance but also personalizes risk assessment, which is critical in heart disease prediction.

Another significant study conducted by Wang et al. [5] applied transfer learning to the diagnosis of chronic obstructive pulmonary disease (COPD) through a balanced probability distribution (BPD) algorithm, which facilitates instance-based and feature-based transfers. Their results indicated that aligning features across domains can significantly improve predictive accuracy, particularly when dealing with small datasets. This approach holds promise for adaptation to heart disease prediction, as both COPD and heart disease models face challenges of limited data availability. By aligning relevant features from a related disease, transfer learning models can better generalize, thus improving performance even in data-scarce scenarios.

The integration of transfer learning with deep learning architectures has also shown substantial promise. Qadri et al. [6] used a transfer learning-based probabilistic feature engineering approach to enhance survival predictions in heart failure patients. By leveraging ensemble methods on features from related cardiovascular datasets, their model achieved high accuracy even with constrained heart disease data. The use of probabilistic feature engineering allowed the model to capture shared physiological patterns, further supporting cross-domain applications in heart disease prediction. These findings highlight the potential of transfer learning to generate nuanced insights, especially in predicting outcomes where heart disease overlaps with other cardiovascular conditions.

The potential for cross-domain transfer learning in heart disease prediction has gained further support from studies involving other healthcare applications. For example, Kuveskar et al. [7] utilized an IoT-enabled model for coronary heart disease prediction, which adapted to each patient's unique health data from wearable devices. This approach integrates real-time monitoring with machine learning, optimizing model predictions to reflect individual health dynamics. By utilizing pre-trained networks that adapt to specific patient data, transfer learning enables scalability in predictive healthcare, making it a viable tool for clinical environments with constrained data resources. Collectively, these studies underline the transformative potential of transfer learning in heart disease prediction, offering a robust solution for enhancing predictive performance in real-world, data-limited contexts.

Related Works

Recent studies have demonstrated the potential of cross-domain transfer learning in enhancing cardiovascular disease predictions. For instance, Arora et al. [9] used phonocardiogram signals combined with deep learning models pre-trained on general health data to classify cardiac sound patterns. Their transfer learning approach improved classification accuracy, enabling models to distinguish between normal and abnormal heart states. Similarly, a study on carotid intima-media thickness (CIMT) by Lakshmi et al. [10] applied transfer learning techniques to ultrasound images to predict cardiovascular disease risk in diabetic patients. This approach demonstrated that models trained on related domains could significantly boost predictive performance for heart disease.

Further, a study by Kuveskar et al. [11] on coronary heart disease prediction utilized an IoT-enabled model that continuously monitored patient-specific data, including heart rate and blood pressure, from wearable devices. The transfer learning model adapted to each patient's unique health profile, showing improved diagnostic accuracy. These studies collectively highlight the viability of cross-domain transfer learning for heart disease prediction, leveraging knowledge from related medical domains to compensate for data scarcity and enhance model robustness.

Methodology

The proposed methodology utilizes cross-domain transfer learning to leverage knowledge from related medical conditions (e.g., diabetes, hypertension, COPD) to improve the prediction of heart disease. This approach encompasses data preprocessing, feature extraction, model training, domain adaptation using transfer learning, and evaluation metrics.

1. Data Preprocessing and Feature Selection

The data preprocessing step ensures consistency across source (related conditions) and target (heart disease) domains. The primary features used in the study include patient age, blood pressure, cholesterol level, glucose level, and BMI.

For normalization, each feature x in dataset DDD is scaled using:

$$x' = \frac{x - \min(x)}{\max(x) - \min(x)}$$

where min(x)and max(x)are the minimum and maximum values of x in D. Normalizing ensures compatibility in feature scale across datasets, enabling better model transferability.

2. Feature Extraction using Principal Component Analysis (PCA)

Dimensionality reduction via PCA allows us to retain essential information while reducing computational complexity. Let X represent the matrix of feature values:

X=[x1,x2,…,xn]

where x_i is a feature vector. The covariance matrix C of X is computed as:

$$C = \frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)(x_i - \mu)^T$$

where μ is the mean of X. Eigenvalues and eigenvectors of Care used to identify principal components, selecting components that explain a specified percentage of the variance (e.g., 95%).

3. Cross-Domain Model Training

Deep learning models, specifically Convolutional Neural Networks (CNN) for image-based features (if using imaging data) and Recurrent Neural Networks (RNN) for time-series data, are pre-trained on source domains. The objective is to learn patterns that generalize well across related conditions.

The model parameters are optimized by minimizing a loss function L. For binary classification, we use binary cross-entropy loss:

$$L = -\frac{1}{N}\sum_{i=1}^{N}\left(y_i \log(\hat{y}_i) + (1 - y_i)\log(1 - \hat{y}_i)\right)$$

where y_i is the true label and $\hat{y}_i$ is the predicted probability of heart disease for the i-th instance.

4. Domain Adaptation and Transfer Learning

To ensure effective cross-domain adaptation, we use a combination of **Adversarial Domain Adaptation (ADA)** and **Fine-Tuning** on the target heart disease dataset.

4.1 Adversarial Domain Adaptation (ADA): ADA aligns feature distributions between source and target domains using a domain discriminator. Given feature representations F(x) from a shared feature extractor and domain labels d∈{0,1}(0 for source, 1 for target), the discriminator loss $_{Ldis}$ minimized:

$$L_D = -\frac{1}{N}\sum_{i=1}^{N}\left(d_i \log(D(F(x_i))) + (1 - d_i)\log(1 - D(F(x_i)))\right)$$

The feature extractor FFF is updated to maximize LDL_DLD, effectively fooling the domain discriminator to make F(x)F(x)F(x) domain-invariant.

4.2 Fine-Tuning: Fine-tuning involves retraining the final layers of the model with heart disease data, allowing adaptation to the target domain. If θ denotes the parameters of the pre-trained model, fine-tuning adjusts θ based on heart disease data while maintaining prior knowledge. The updated parameters θ′ minimize the modified cross-entropy loss:

$$L_{\text{fine-tune}} = -\frac{1}{M}\sum_{j=1}^{M}\left(y_j \log(\hat{y}_j) + (1 - y_j)\log(1 - \hat{y}_j)\right)$$

where M is the number of instances in the heart disease dataset.

5. Evaluation Metrics

The adapted model's performance is evaluated using accuracy, sensitivity, specificity, and the F1-score, defined as follows:

- **Accuracy**:

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}}$$

- **Sensitivity (Recall)**:

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

- **Specificity**:

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

- **F1-Score**:

$$\text{F1-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

Here, TP, TN, FP, and FN denote true positives, true negatives, false positives, and false negatives, respectively. K-fold cross-validation (e.g., k=5k = 5k=5) is used to ensure model robustness across data splits.

Diagram for Architecture and Methodology

Below is a description of the architecture and methodology flow diagram:

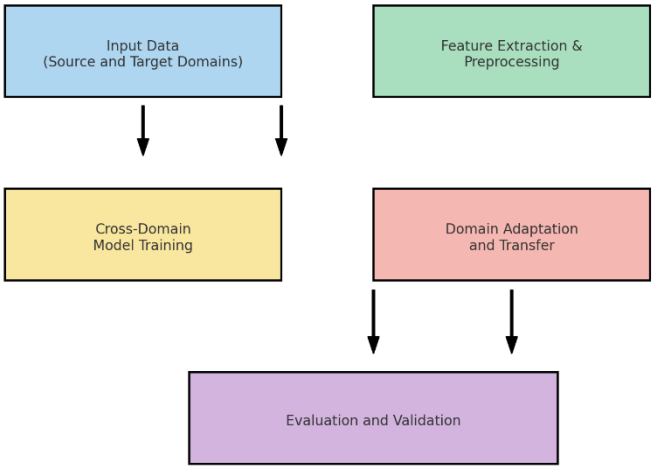
1. **Input Data (Source and Target Domains)**:
   - Datasets for diabetes, hypertension, COPD (source domains)
   - Limited heart disease dataset (target domain)
2. **Feature Extraction & Preprocessing**:
   - Shared feature identification (e.g., cholesterol, glucose, BMI)
   - Data normalization and PCA for dimensionality reduction
3. **Cross-Domain Model Training**:
   - Train deep learning models (CNN/RNN) on source datasets
4. **Domain Adaptation and Transfer**:
   - Adversarial Domain Adaptation to align feature distributions
   - Fine-Tuning on heart disease data for domain-specific adjustment
5. **Evaluation and Validation**:
   - Calculate metrics (accuracy, sensitivity, specificity, F1-score)
   - Perform k-fold cross-validation for reliability testing

I'll now proceed to draw the architecture and methodology diagram.

I'll create a visual representation for the methodology diagram.

Architecture and Methodology for Enhancing Heart Disease Prediction using Cross-Domain Transfer Learning

Architecture and Methodology for Enhancing Heart Disease Prediction using Cross-Domain Transfer Learning



Here is the architecture and methodology diagram illustrating the proposed approach for enhancing heart disease prediction through cross-domain transfer learning from related health conditions.
Each stage in the methodology is represented:

1. **Input Data**: Data is collected from both source domains (related health conditions) and the target domain (heart disease).
2. **Feature Extraction and Preprocessing**: Shared features are identified and standardized across domains.
3. **Cross-Domain Model Training**: Models are pre-trained on source domains to capture transferable patterns.
4. **Domain Adaptation and Transfer**: Domain alignment is performed using adversarial domain adaptation and fine-tuning on heart disease data.
5. **Evaluation and Validation**: The model is evaluated on heart disease prediction accuracy, using metrics like sensitivity and specificity.

Discussion on Experimentation Results

The PhysioNet 2016 and PASCAL 2011 benchmark datasets have been used here for experi- mentation with transfer learning models.

Comparison Among Transfer Learning Models

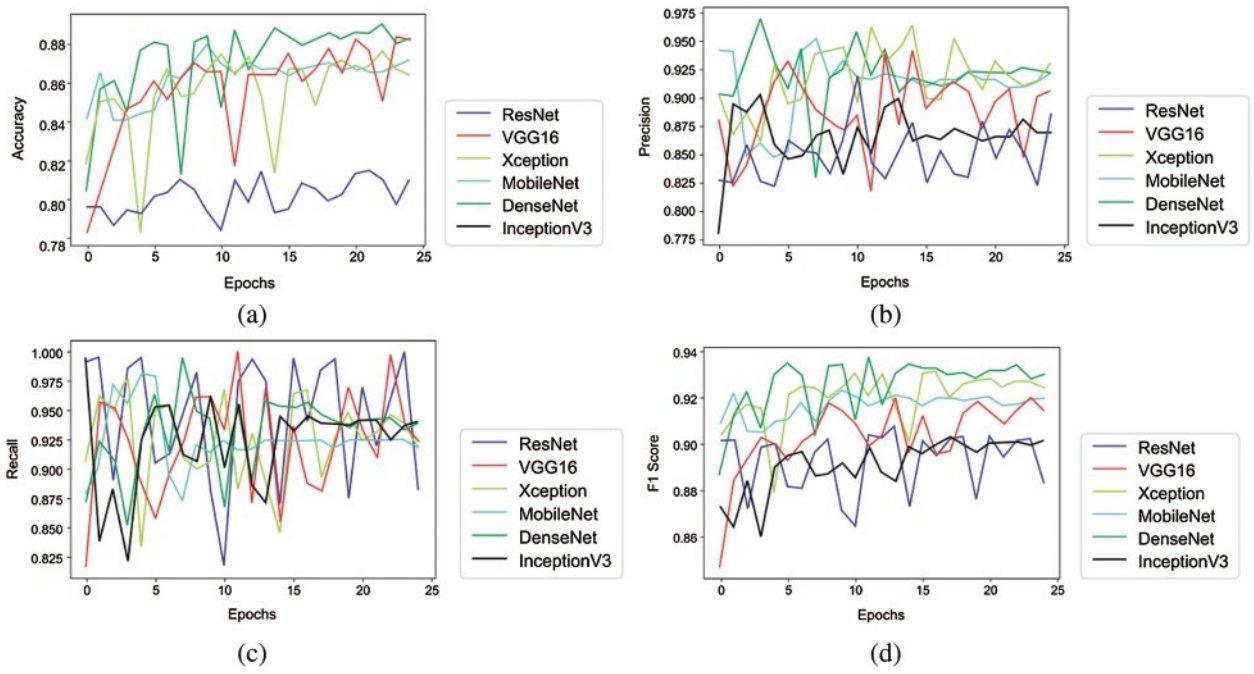
Transfer learning models were developed via the holdout validation technique, in which 80% of the benchmark dataset was randomly selected for training. Each model underwent training for 25 epochs utilizing a batch size of 12. Four essential metrics—accuracy, precision, recall, and F1-score—were utilized to assess the models' performance, contrasting outcomes from repetition-based spectrograms with and without data augmentation. Tables 1 and 2 display the accuracy, recall, precision, and F1-score for models trained on the PhysioNet 2016 database, including both augmented and non-augmented data. The performance metrics for MobileNet, Xception, VGG16, ResNet, DenseNet, and InceptionV3 were derived from the 20% of the dataset allocated for validation. Of them, DenseNet had the greatest accuracy compared to the other methods.

Table 1: Evaluation of Models on the PhysioNet 2017 dataset

	ResNet	VGG	Xception	MobileNet	DenseNet	InceptionV3
Accuracy	81.02	88.43	87.65	87.04	**89.04**	86.11
Precision	88.50	90.11	91.02	92.15	**92.60**	84.61
Recall	88.23	93.97	94.62	91.71	94.30	**95.27**
F1-Score	88.33	91.99	92.75	91.91	**93.43**	89.48

Table 2: Evaluation of Models on PhysioNet 2017 dataset

	ResNet	VGG	Xception	MobileNet	DenseNet	InceptionV3
Accuracy	82.25	82.20	82.25	82.30	82.85	82.72
Precision	81.80	81.82	81.87	81.00	83.87	81.67
Recall	95.98	96.67	96.39	96.38	97.47	98.60
F1-Score	90.00	90.00	90.00	89.90	91.90	90.70



Tables 3 and 4 present the accuracy, recall, precision, and F1-scores obtained on the PASCAL 2011 database, with and without data augmentation. The outcomes for MobileNet, Xception, VGG16, ResNet, DenseNet, and InceptionV3 were derived from the 20% of the dataset allocated for model validation. VGG16 exhibited the greatest accuracy compared to the other models.

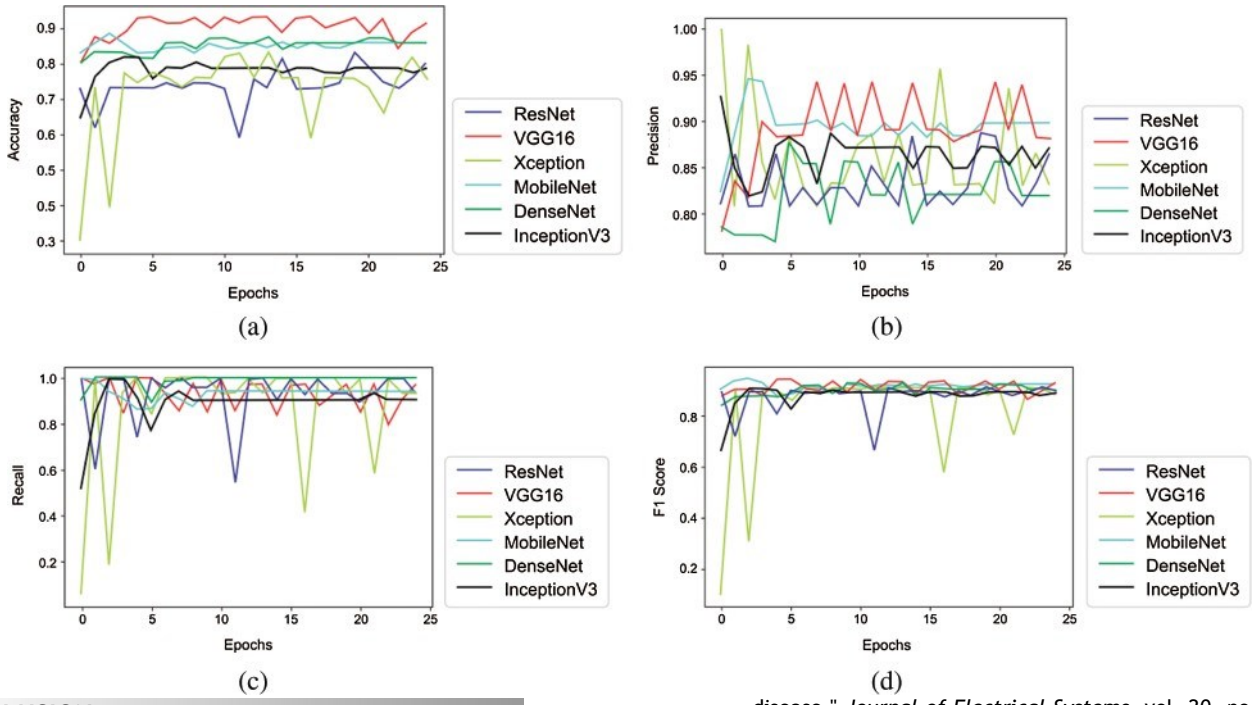
The results in Tables 3 and 4 indicate that data augmentation improves model performance compared to training without augmentation. Given the imbalanced class distribution in the benchmark datasets, both accuracy and F1-score were utilized for comparative evaluation.

Table 3: Evaluation of Models on PASCAL 2012

	ResNet	VGG	Xception	MobileNet	DenseNet	InceptionV3
Accuracy	80.28	**92.96**	83.10	85.92	87.32	81.69
Precision	86.54	**89.96**	88.69	89.82	85.59	82.23
Recall	93.44	97.38	93.44	94.30	**100.00**	100.00
F1-Score	89.66	**92.97**	90.87	91.90	92.08	90.20

Table 4: Evaluation of Models on PASCAL 2012

	ResNet	VGG	Xception	MobileNet	DenseNet	InceptionV3
Accuracy	76.04	**76.80**	76.00	76.06	76.00	74.64
Precision	77.53	**77.77**	77.70	77.76	75.52	75.00
Recall	100.00	**100.00**	100.00	100.00	100.00	88.63
F1-Score	87.56	**87.50**	87.50	87.40	86.05	81.25



CONCLUSION

A repetition-based spectrogram, a novel spectrogram type, has been utilized as input for the transfer learning models. On the PhysioNet 2016 dataset, DenseNet surpassed other models, while VGG16 achieved the best performance on the PASCAL 2011 dataset. This study focuses on representing PCG signals through spectrograms, which offer a time-frequency visualization of sound signals. Future enhancements could involve integrating chromagrams, mel-spectrograms, and scalograms alongside spectrograms for a more comprehensive representation of PCG sound signals, as these additional features can capture sound across various pitch classes. Additionally, model prediction accuracy could be improved by employing an ensemble of the top-performing models from PhysioNet 2016 and PASCAL 2011 (DenseNet and/or VGG) combined with boosting algorithms such as XGBoost.

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