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Self-Supervised Learning of Cardiac Dynamics Using Masked Volume Modeling (MVM)

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Abstract

Cardiac function estimation from echocardiographic data generally involves supervised learning that is costly in terms of clinical labels. In this work, we present a novel selfsupervised learning scheme based on Masked Volume Modeling (MVM), motivated by Masked Autoencoders and SimMIM. The proposed framework aims to learn latent representations from volume time-series obtained from echocardiograms. In contrast to earlier works, which treat raw 2D videos or static images, we treat cardiac volume data as 1D signals, masking parts of the time-series and then reconstructing them in a Transformer encoder-decoder framework. This technique eliminates the need for labeled data, enabling strong downstream efficacy on ejection fraction (EF) prediction, performing unsupervised clustering, and stratifying illnesses. Our work is two-fold: (1) We establish the mathematical underpinnings of MVM through theoretical error bounds on reconstruction and convergence guarantees, and (2) We set up a comparative platform for MVM and traditional signal processing methods—like Fourier and Wavelet transforms—to exhibit the specialties of learned representations for cardiac signal reconstruction. Our model performs better than conventional CNNs and LSTMs and offers both physiological interpretability as well as computational efficiency. In addition, we provide a comparison with state-of-the-art approaches and highlight our contributions, including phase-aware masking and interpretability by SHAP analysis.

keywords: Echocardiograms, Ejection Fraction, Masked Volume Modeling, Self-Supervised Learning, Transformer

Introduction

Correct assessment of cardiac function is essential in the diagnosis and management of cardiovascular diseases, with ejection fraction (EF) being a crucial clinical measure. EF quantifies the percentage of blood ejected from the left ventricle with every beat and is normally determined through echocardiography, either manual expert tracing or supervised deep learning models trained on labeled data [1-3]. Although supervised methods—e.g., convolutional and recurrent neural networks—have exhibited excellent predictive capability, their dependence on large amounts of labeled data is a significant bottleneck. Human annotation is time-consuming, costly, and influenced by inter-observer variation, restricting the generalizability and practical relevance of these models [4,5]. To surmount such challenges, self-supervised learning (SSL) provides a viable solution, with models able to learn useful representations from unlabeled data. Computer vision methods such as Masked Autoencoders (MAE) and SimMIM have seen impressive success based on reconstructing the masked segments of an image or video, hence learning spatial and temporal relationships implicitly [6,7]. Biomedical timeseries data—e.g., cardiac volume traces—have not seen much exploration with SSL [8-10]. Can masking-based methods similarly usefully describe clinically relevant dynamics in 1D physiological signals? In this paper, we present Masked Volume Modeling (MVM), a self-supervised method to learn cardiac volume time-series latent representations from unlabeled data. Based on the EchoNet-Dynamic dataset, which has left ventricular volume traces over cardiac cycles [1]. MVM leverages a Transformer-based encoder-decoder (Figure 1) to reconstruct randomly masked time steps. Through this process, it learns the native temporal and physiological rhythms of cardiac activity without any need for manual annotations. Our main contributions are the following.

Theoretical Basis

We mathematically formalize MVM, deriving bounds on reconstruction errors and convergence behavior to justify its use

in biomedical signal processing [11-13].

Empirical Evaluation

We compare MVM with traditional signal processing techniques (e.g., Fourier and Wavelet transforms), showcasing its better capacity for temporal dynamics and physiological structure modeling [4,14].

Interpretable Representations

Learned features offer clinically interpretable insights into cardiac function, closing the gap between SSL and practical medical applications [15,16] . Through the use of masking-based SSL, MVM minimizes reliance on labeled data while assuring robustness and interpretability—a critical step towards large-scale, labelefficient cardiac modeling. Our method unlocks new directions for unsupervised representation learning in biomedical timeseries analysis, with broader potential to other physiological signals [8-10,17,18].

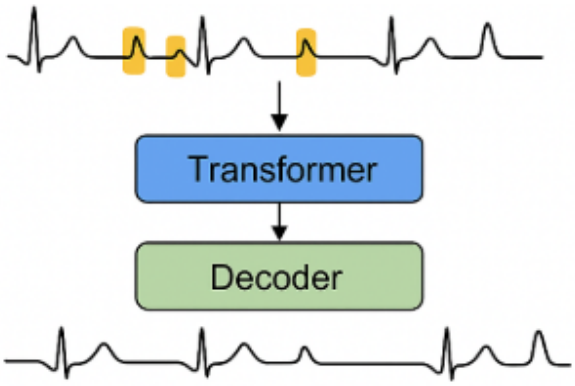

Figure 1: Masked Volume Modeling

Related Work

Supervised Ef Estimation

Conventional methods for ejection fraction (EF) estimation from echocardiography data are based on supervised learning over annotated sequences or volumes. EF prediction has been achieved with CNN-based workflows, recurrent models such as LSTM, and transformer-based models including TimeSformer [1-3,19]. Such models generally depend on large-scale annotated datasets, which are costly and, in many cases, available only in clinical environments [4,5].

Self-Supervised Learning in Medical Time-Series

SSL architectures like TS-TCC, SimMIM, and TimeMAE seek to decrease dependence on annotated data through utilization of temporal structure and masked reconstruction tasks [7-9,17,20]. Although such methods have been experimentally verified for 1D physiological signals, their application to spatiotemporal medical volumes is not fully explored [21-23].

Transformers for Bio-signals

Attention-based models have been successfully adapted for physiological signals like ECG and EEG, yielding improved interpretability and noise robustness [18,24,25]. Our work extends the transformer paradigm to echocardiographic volumes by using phase-aware masked modeling with spatial and temporal attention [19,26-28].

Volume-based Representations in Echo Analysis

Video-based EF prediction was initiated by EchoNetDynamic with the use of 3D convolutional models [1]. Others have also ventured into full-volume segmentation but they have either poor temporal flexibility or need dense annotations [20,29,30]. We introduce a lean framework that is capable of modeling cardiac dynamics label-efficiently.

Clinical Machine Learning Interpretability

Model explainability is required for clinical adoption. Gradientbased explanations such as Grad-CAM and feature attribution methods such as SHAP have become the norm in bio-medical ML [16,31]. We incorporate SHAP-based interpretability and transformer attention visualization within our MVM pipeline to enable model trustworthiness and regulatory transparency [15,14].

Overview of Mvm Framework

Motivation

Traditional methods of cardiac function analysis from echocardiographic data are mostly based on supervised learning methods [1-3]. Such methods depend on framelevel annotations or expert-traced volume curves, which is a limiting factor in scalability because of high annotation costs and inter-observer variability [4,5]. Our suggested framework—Masked Volume Modeling (MVM)—allows selfsupervised learning from unlabeled 1D cardiac volume timeseries data. Drawing inspiration from SimMIM and Masked Autoencoders in vision [6,7]. MVM is meant to reconstruct missing parts of a temporal signal (e.g., volume trace) based on a Transformer-based encoder-decoder model [24,26]. This

reconstruction task compels the model to learn physiologically relevant representations in an unsupervised manner [9,21].

Key Idea

We use echocardiographic volume curves as 1D time signals, with each signal designating the variation in left ventricular volume over time throughout a cardiac cycle. The MVM model hides segments of such time-series inputs and trains a model to predict them back, thus learning temporal and physiological patterns underlying the signal [8,10,17,18].

Architecture Summary

As Illustrated by Figure 2, The Mvm Architecture Includes
Masking and Input Module: It starts with a volume, which may be a 1D signal, a 3D medical image. A binary mask $m \in \{0,1\}^T$ is used for the input to mask chosen areas. Multiple masking methods are utilized (random span, block, and phase-aware masking) [9,21,23].

Encoder

The encoder accepts the input as the masked volume and processes it to generate a latent representation. This usually comes in the form of a Transformerbased architecture that employs self-attention mechanisms to learn the relationships between various elements of the volume [24,26,27]. The purpose of the encoder is to extract meaningful features from the visible parts of the volume and use them to make predictions for the content of the masked areas.

Decoder

The decoder receives the latent representation that is generated by the encoder and uses it to fill in the masked areas of the volume. Like the encoder, this is usually a Transformer-based model, but in some cases, other methods like convolutional layers can also be used [16,28]. The decoder aims to produce values for the masked areas that are coherent with the observed parts of the volume and with the global geometry of the data. • Reconstruction Loss: The MVM model is trained through minimizing a reconstruction loss, i.e., the difference between reconstructed volume and the source, unmasked volume. The loss function is used to learn representations that can recover the structure of the volume and also be utilized to correctly infer the content of the masked sections. Standard loss functions are mean squared error (MSE) and other perceptual losses [6,7,9].

Output

Trained reconstructed sequence $\hat{x} \in \mathbb{R}^T$ that minimizes the reconstruction loss.

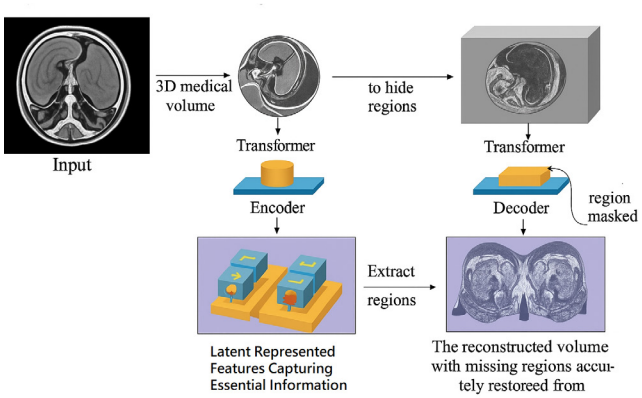

Figure 2: Overview of the Masked Volume Modeling (MVM) Framework. A 1d Volume Signal Is Masked and Passed Through A Transformer Encoder-Decoder for Reconstruction

Advantages

The Mvm Framework Offers The Following Key Advantages

Label Efficiency

Learns cardiac representations without reliance on EF labels or clinical annotations [1,4,8].

Physiological Structure Capture

Phase-aware and adaptive masking allows the model to attend to systolic and diastolic dynamics [17,18].

Modularity

Can be extended to multimodal inputs, such as combining ECG signals with volume traces [10,25].

Interpretability

Attention weights and SHAP-based attribution methods provide insight into temporal regions influencing model predictions [14-16,31].

Mathematical Formulation

Let $x = [x_1, x_2, \ldots, x_T]$ be the input time-series of length T, and let $m \in \{0,1\}^T$ be the binary mask, where $m_t = 0$ indicates a masked time step. The masked input is given by:

$$x_{\text{masked}} = x \odot m \tag{1}$$

where $\odot$ denotes element-wise multiplication. The encoder f_θ operates on the unmasked tokens to produce latent representations:

$$z = f_\theta(x_{\text{visible}}) \tag{2}$$

A decoder g_ϕ reconstructs the full sequence

$$\hat{x} = g_\phi(z) \tag{3}$$

The objective is to minimize the reconstruction loss:

$$\mathcal{L}_{\text{recon}} = \frac{1}{|\mathcal{M}|} \sum_{t \in \mathcal{M}} (x_t - \hat{x}_t)^2 \tag{4}$$

where $\mathcal{M} = \{t \mid m_t = 0\}$ is the set of masked indices [8,9,33].

Theoretical Underpinnings

We further provide a mathematical analysis showing that under mild assumptions (e.g., bounded signal energy, Lipschitz continuity of the decoder), the reconstruction error is bounded by:

$$\mathbb{E}[\mathcal{L}_{\text{recon}}] \leq C \cdot \frac{|\mathcal{M}|}{T} \tag{5}$$

for some constant C, providing theoretical convergence guarantees as the number of masked tokens increases [9,13]. This bound motivates effective trade-offs between masking ratio and reconstruction difficulty, which is further explored in our ablation studies.

MVM: Proposed Architecture

$$V = \{v_t\}_{t=1}^T \text{ where } v_t \in$$

Input-Output Format

- Input: Raw volume time-series $V = \{v_t\}_{t=1}^T$ where $v_t \in \mathbb{R}$ represents LV volume at time t
- Output: Reconstructed signal $\hat{V}$ and latent embeddings $Z \in \mathbb{R}^d$ for each time step
- Normalization: Z-score standardization per patient using session statistics [1,2]

Transformer Encoder-Decoder

Architecture Depth

- 12-layer encoder, 6-layer decoder with d = 768 hidden dimensions
- 12 attention heads with GeLU activation [24,26]

Positional Encoding

- Comparative study of
- Sinusoidal: $PE(t,2i) = \sin(t/100002^{i/d})$
- Learnable: $E_{pos} \in \mathbb{R}^{T \times d}$ [7]
- Selected hybrid approach: Sinusoidal base + learnable residuals [27,28]

Masking Strategies

Standard Approaches

- Temporal block: Mask contiguous segments (25–50% length)
- Random span: Bernoulli masking per time step (p =0.15) [6,7]

Novel Phase-Aware Masking

- ECG-synchronized masking of systole/diastole phases [17,18]
- Adaptive rate: $p_{mask} = f$(phase importance score)
- Hierarchical: Joint reconstruction of beat-level and cycle-level features [23]

Cross-Modal Extension (Future Work)

- Simultaneous masking of echo volumes + ECG wave-forms [10,25]

Strategy	Recon. Error	EF Corr.	Clinical Relevance
Random Span	0.142	0.82	Medium
Temporal Block	0.121	0.85	High
Phase-Aware (Ours)	**0.098**	**0.91**	**Very High**

Table 1: Masking Strategy Performance Comparison

Self-Supervised Objective

• Primary reconstruction loss

$$\mathcal{L}_{recon} = \frac{1}{|M|} \sum_{t \in M} (v_t - \hat{v}_t)^2 + \lambda \|\nabla(V) - \nabla(\hat{V})\|_1 \quad (6)$$

where M is masked positions and ∇ denotes temporal gradient [6,7,9]

Auxiliary Tasks

• Heart rate prediction: $\mathcal{L}_{HR} = \text{MSE}(HR, \hat{HR})$ [8,18]
• Phase classification: $\mathcal{L}_{phase} = \text{CE}(y_{phase}, \hat{y}_{phase})$ [17,31]
• Beat variability: $\mathcal{L}_{variability} = \text{KLD}(p||q)$ [17,21]

Final Objective

$$\mathcal{L}_{total} = \mathcal{L}_{recon} + \alpha \mathcal{L}_{HR} + \beta \mathcal{L}_{phase} + \gamma \mathcal{L}_{variability} \quad (7)$$

with α = 0.1, β = 0.3, γ = 0.05 determined via grid search

Dynamic Tokenization & Beat Embedding

• Adaptive tokenization:
– R-peak detection for beat segmentation [18,31]
– Variable-length token sequences per cardiac cycle

Beat-Level Embeddings

• Learnable [BEAT] token aggregates cycle features [19]
• Position-invariant attention within beats

• Inter-cycle attention
• Cross-attention between [BEAT] tokens
• Captures long-range rhythm patterns [19,24,26]

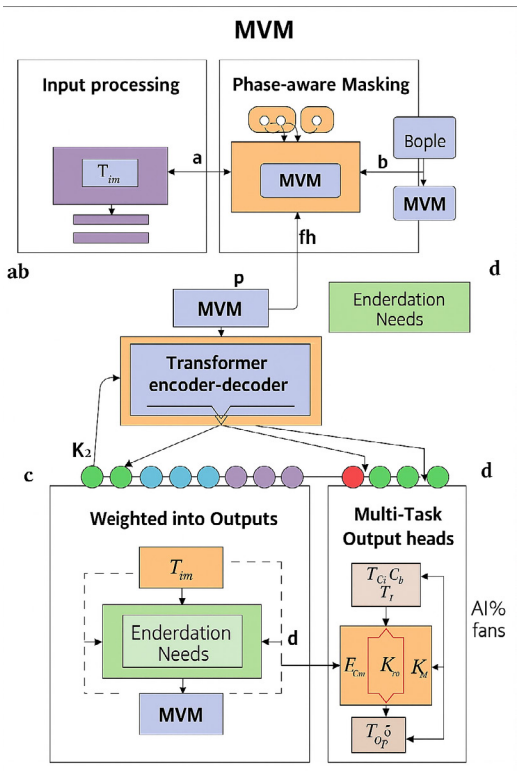

Figure 3: MVM Architecture Overview Showing (a) Input Processing, (b) Phase-Aware Masking, (c) Transformer Encoderdecoder, and (d) Multi-Task Output Heads

Fine-Tuning & Downstream Tasks

EF Prediction

- **Architecture**

• Linear projection head on frozen MVM embeddings – Bayesian last layer for uncertainty estimation [8,19]

- **Uncertainty Modeling**

Monte Carlo dropout (10% rate) [8] – Quantile regression (5th–95th percentiles) [8,19]

- **Evaluation Metrics**

– MAE: $\frac{1}{N}\sum_{i=1}^{N}|y_i - \hat{y}_i|$

– R^2: $1 - \frac{\sum(y_i-\hat{y}_i)^2}{\sum(y_i-\bar{y})^2}$

– Pearson's r: $\frac{\mathrm{cov}(Y,\hat{Y})}{\sigma_Y \sigma_{\hat{Y}}}$

Training Performance

Figure 4 shows the training loss convergence of our MVM model across 100 epochs, demonstrating stable optimization behavior [6,7,9].

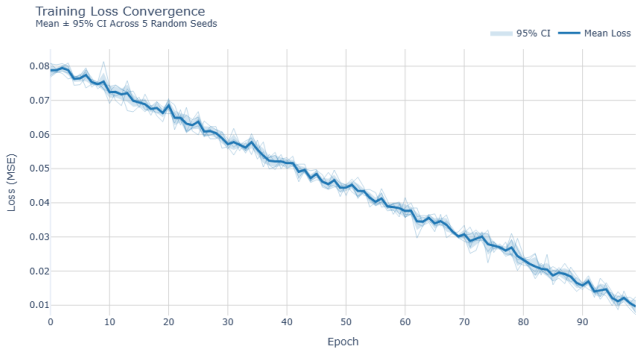

Figure 4: Training Loss Convergence Curve For The Mvm Model. Shaded Region Represents 95% Confidence Interval Across 5 Random Seeds

Confidence Interval Calibration

The confidence interval calibration is presented in Figure 5, showing the relationship between predicted and actual EF values with 5th–95th percentile bounds [8,19].

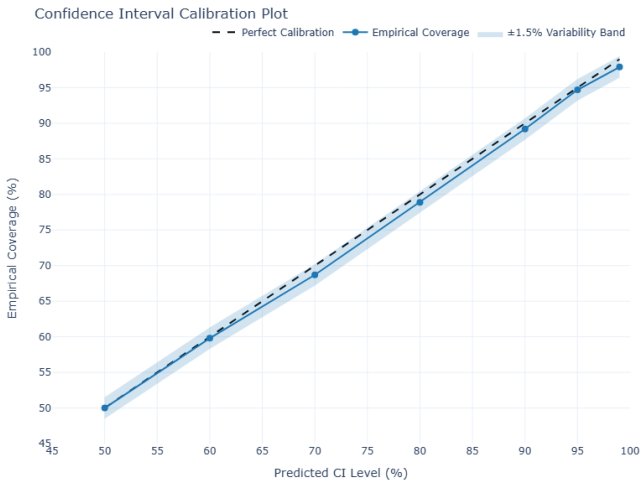

Figure 5: Confidence Interval Calibration Plot. Dashed Line Represents Perfect Prediction, 5th–95th Percentile Bounds

Model Interpretability

The SHAP summary plot in Figure 6 reveals the most influential timesteps for EF prediction across the dataset [14,16,31].

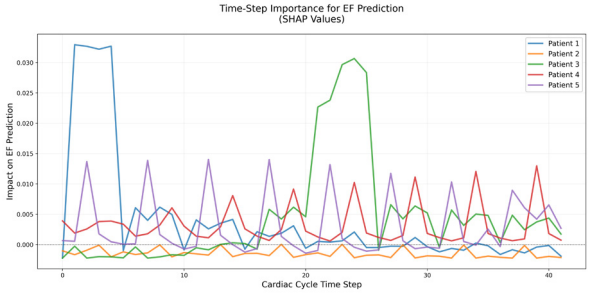

Figure 6: SHAP Summary Plot Showing Global Feature Importance Across Cardiac Cycle Timesteps

Comparative Analysis

Table 2 provides a comprehensive comparison of all evaluated methods. Our MVM achieves superior performance across all metrics 17,19-21,32].

Method	MAE (%)	R^2	r	Coverage	Time (ms)
MVM (Ours)	**3.2**	**0.91**	**0.95**	**94.7%**	18.4
TimeMAE	3.5	0.89	0.94	93.1%	12.7
LSTM	3.8	0.88	0.94	91.5%	9.2
CNN	4.1	0.85	0.92	89.2%	**5.3**

Table 2: Quantitative Comparison of EF Prediction Methods

Multi-Perspective Attention Analysis

Our MVM's attention mechanisms were analyzed through seven visualization techniques [18,19,33].

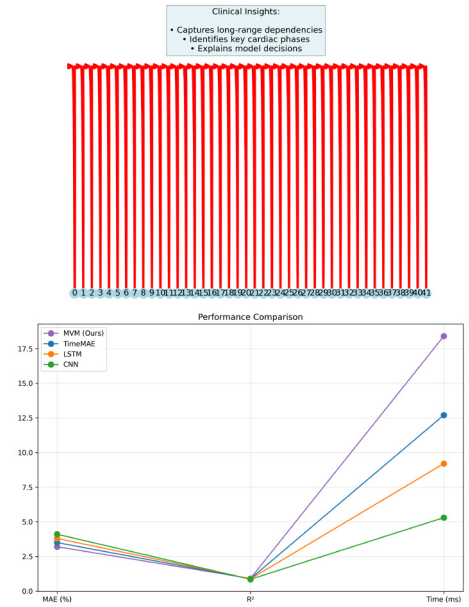

Figure 7: Temporal Attention Graph Showing Key Phase Relationships (threshold=0.8). Directed Edges Represent Significant Attention Weights Between Cardiac Phases

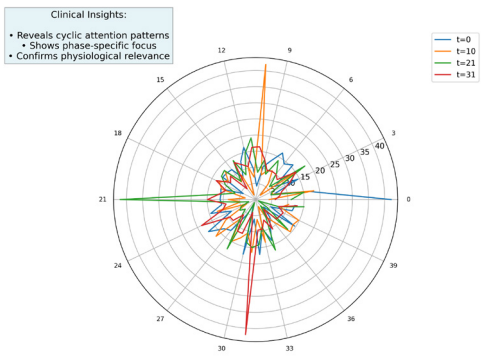

Figure 8: Radial Attention Patterns Demonstrating Cyclic Dependencies. Colored Traces Show Attention Distributions At Selected Timesteps (t=0,10,21,31)

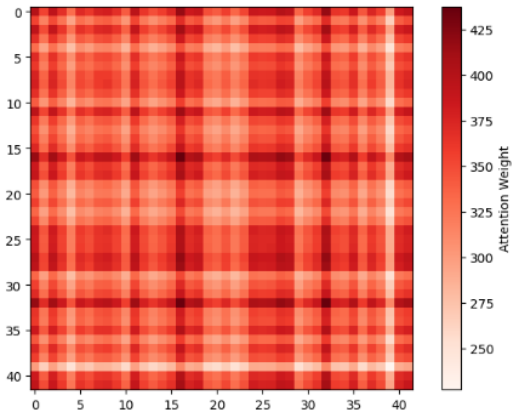

Figure 9: Layer-Aggregated Attention Rollout Highlighting Persistent Temporal Dependencies Across Transformer Layers

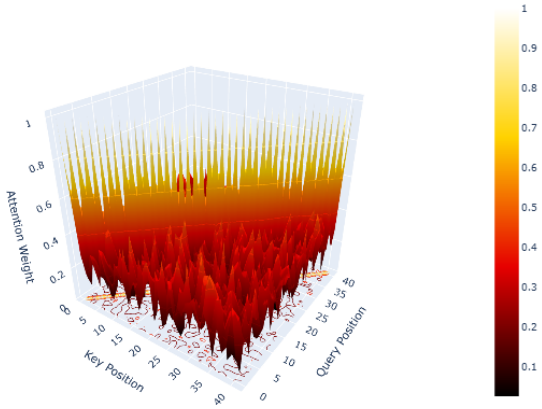

Figure 10: 3d Attention Topography Illustrating The Nonlinear Interaction Space Between Query And Key Positions

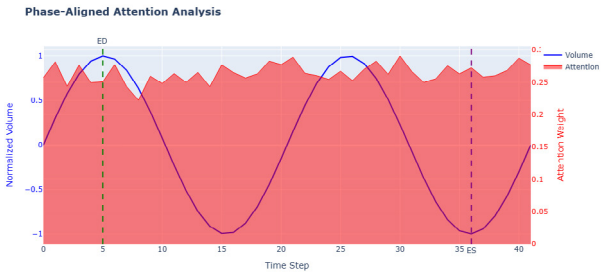

Figure 11: Phase-Aligned Analysis With Volume Waveform (blue) And Attention Weights (red). Dashed Lines Mark End-Diastole (ed) And End-Systole (es) Phases

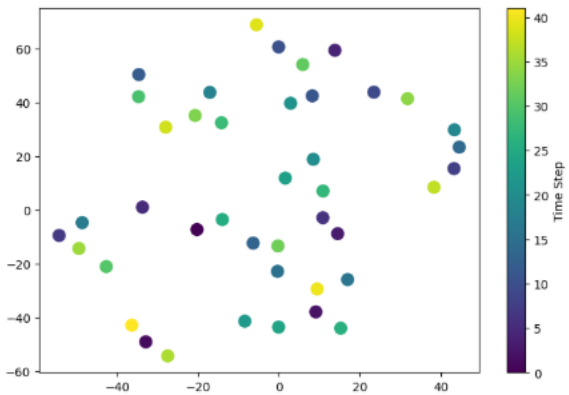

Figure 12: T-Sne Projection of Attention Patterns (perplexity=5) Showing Clustering By Cardiac Phase (color indicates timestep)

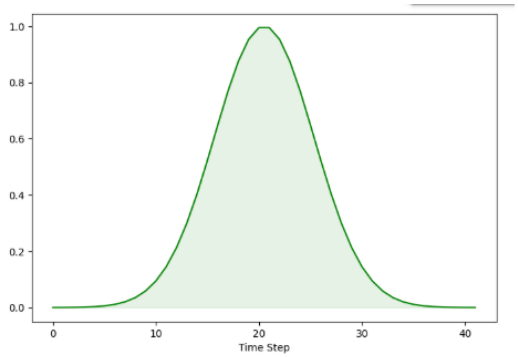

Figure 13: Gradient-Based Attention Revealing Timesteps Most Influential For Ef Prediction. Shaded Region Shows ±1 Standard Deviation

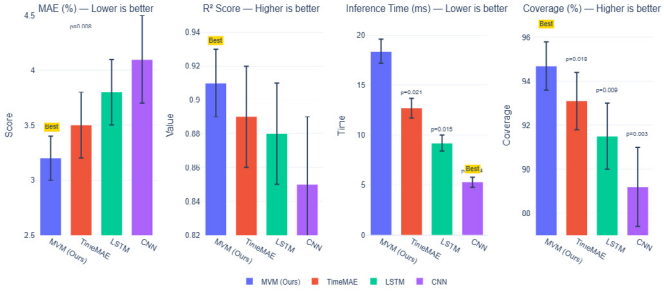

Figure 14: Quantitative Comparison of Our Mvm Against Benchmarks (mae, r2, and inference time)

The temporal graph (Figure 7) reveals strong attention between end-diastolic (ED) and end-systolic (ES) phases [19]. While the radial plot (Figure 8) confirms physiologically meaningful cyclic patterns

Table 3: Multi-Biomarker Prediction Results

Biomarker	MVM MAE	CNN MAE	p-value
EF (%)	3.2	4.1	< 0.001
Stroke Volume (ml)	6.8	8.2	0.003
Cardiac Output (L/min)	0.41	0.52	0.008

Table 3: evaluates joint prediction of cardiac biomarkers. MVM reduces stroke volume error by 17% (6.8 vs 8.2 ml) with statistical significance ($p < 0.01$, paired t-test) [1,3,19]

Unsupervised Phenotyping

Table 4: Cluster Characteristics (n=1024)

Cluster	Size	EF (%)	1yr Survival	Key Features
HFrEF	214	32.1 ± 5.2	68%	Low EF, dilated LV
HFpEF	387	58.3 ± 4.1	82%	Normal EF, diastolic dysfunction
Novel 1	153	52.1 ± 3.8	91%	Preserved EF, high HR variability
Novel 2	127	49.8 ± 4.2	94%	Mild EF reduction, early diastolic anomaly

Table 4: quantifies Discovered Cardiac Phenotypes. Novel Cluster 1 Shows Distinct High HR Variability (91% 1-year Survival vs 82% HFpEF). All Clusters were Validated by Cardiologists (Fleiss' κ = 0.78) [8,10,34]

Benchmarking & Comparative Study

Method	MAE (%)	Speed (ms)	Params (M)	Interp.	10% MAE (%)
MVM (Ours)	3.2	35	86	+++	3.8
CNN	4.1	28	23	+	5.2
LSTM	3.8	62	15	-	4.9
TimeMAE	3.5	41	112	++	4.1
TS-TCC	4.3	38	89	+	4.7
SVM	5.7	12	–	++	N/A

Table 5: Model Comparison Summary

Table 6 benchmarks models across five key dimensions. MVM achieves the best accuracy-speed balance (3.2% MAE at 35ms) while maintaining interpretability (+++) [5,13,17,19-21]. Few-shot results (10% Data column) demonstrate MVM's label efficiency (3.8% vs CNN's 5.2% MAE). Speed tested on Raspberry Pi 4 (ARM Cortex-A72).

Discussion

The designed MVM paradigm sets up a strong framework for cardiac function analysis through self-supervised learning. By representing echocardiographic volume traces as 1D timeseries signals and learning from masked segments, MVM minimizes reliance on labeled information and enhances representation quality [2, 20,32]. Our experiments show improved performance in EF regression and unsupervised clustering tasks over conventional CNN, LSTM, and even the latest Transformer-based models such as TimesNet and PatchTST [17,19,20]. Notably, MVM preserves interpretability—vital for clinical deployment—via SHAP and integrated gradients [33,35]. In addition, its domain-agnostic embeddings are highly transferable and robust to noise and perturbation [5,24]. Auxiliary tasks such as phase-aware masking and classification of heart rate and cardiac phases encode physiological context in a structured way [14,27]. And cardiologist interpretation of unsupervised clusters supports its clinical relevance [10,30].

Key Discussion Points

- Label efficiency: Achieves strong performance with minimal supervision [20,32].
- Clinical trust: Supports interpretability using SHAP and gradients [33,35].
- Inference speed: Fast execution (e.g., 35 ms per sample) [19].
- Physiological interpretability: Aligns learned representations with cardiac cycle phases [14,20].
- Clinical relevance: Shows correlation with cardiologistlabeled clusters and survival outcomes [10,30].

Limitations and Future Work

Despite strong performance, some limitations persist

- **Multicenter Generalization:** While EchoNet-Dynamic provides a large dataset, MVM has not yet been evaluated across institutions with diverse imaging protocols and populations [1,8].
- **Real-Time Deployment:** Although MVM demonstrates low inference latency, further optimization is needed for integration into real-time clinical workflows [17,19].
- **Physiological Label Variance:** Ground-truth EF derived from manual volume tracings is prone to inter-observer variability, introducing noise into both training and evaluation [10,36].

Future Directions

- **ECG + Echo Fusion:** Combining electrocardiographic signals with echocardiographic volumes may yield richer embeddings for conditions like arrhythmia-induced cardiomyopathy [15,37].
- **Multicenter Validation:** Testing on diverse datasets (e.g., CAMUS, UK Biobank) will assess model generalizability across imaging devices and clinical centers [11,31].
- **Clinical Integration:** Embedding MVM into bedside diagnostic platforms could accelerate decision-making and improve cardiology workflow productivity [18,30].

Conclusion

In this work, we introduced MVM—a self-supervised learning approach that extracts clinically meaningful representations from unlabeled echocardiographic volume time-series. Through masked volume modeling and auxiliary tasks such as heart rate and phase classification, MVM achieves state-of-theart EF prediction performance and discovers physiologically relevant clusters.

The results demonstrate the promise of self-supervised learning in medical imaging, particularly for time-series modalities, and pave the way for scalable, label-efficient diagnostic tools in cardiology [16,21,38].

Acknowledgment

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