X-Cardia: Phenotype-Guided Cross-Modal Alignment for Opportunistic Cardiac Screening on Routine Chest CT

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Abstract

Multimodal medical data offer an opportunity to learn general-purpose representations for cardiovascular diagnosis. We introduce X-Cardia, a cardiac phenotype-guided multimodal framework that uses structured data as intermediate supervision during pretraining. X-Cardia learns to extract cardiac information from non-contrast, non-gated chest CT scans by aligning CT features with tabular measurements derived from echocardiography (ECHO) and electrocardiography (ECG). Our method combines CLIP-style contrastive pre-training with a non-parametric Nadaraya—Watson (NW) prediction head that enforces phenotype-level similarity via exemplar-based alignment. Pre-training on 20,574 patients, followed by fine-tuning on ten cardiac abnormality prediction tasks, yields substantial performance gains. X-Cardia improves AUROC by up to 8% on the held-out test set and delivers an average 9.8% AUROC improvement in a 5-shot regime. These results demonstrate that explicit phenotype alignment produces interpretable, data-efficient representations and enables routine chest CT to support opportunistic cardiac screening. **Keywords:** Multimodal Alignment, Phenotype-Guided, Nadaraya—Watson head, Chest CT, Echocardiography, Electrocardiography.

1. Introduction

Modern cardiac diagnostics routinely use volumetric scans such as CT, together with structured clinical measurements (e.g., chamber dimensions, pressure estimates) derived from different modalities, such as echocardiography and electrocardiography (Ota et al., 2001; Jenkins et al., 2009). These modalities provide complementary information: imaging captures morphological patterns, while tabular measurements encode expert-derived phenotypes (Henry et al., 1980; Lau et al., 2023; Ghorbani et al., 2020; Castrejon et al., 2016). Despite this, current deep learning pipelines typically operate on a single modality or use

simple late fusion, leaving the rich semantic correspondence between modalities largely untapped. This limits robustness and underutilizes valuable clinical structure. Routine non-gated, non-contrast chest CT scans represent an especially challenging but impactful setting for opportunistic cardiac screening. These studies are acquired for non-cardiac indications, lack cardiac gating, and attenuate cardiovascular detail—making cardiac interpretation difficult even for experts. Yet many clinically meaningful phenotypes, such as chamber dilation or valvular dysfunction, manifest jointly as geometric patterns on CT and quantitative deviations in structured measurements. Leveraging these natural correspondences could enable models to extract cardiac information from routine thoracic imaging.

Cross-modal alignment (Wang et al., 2022; Jiang and Ye, 2023) provides a mechanism to learn such shared semantic structure. Aligning imaging and tabular representations allows gradients from cleaner, more structured phenotypes to regularize the image encoder, guiding it toward physiologically grounded features that generalize across tasks and modalities. Prior multimodal contrastive learning (MMCL) (Yuan et al., 2021; Radford et al., 2021) approaches have demonstrated the promise of contrastive alignment, but often produce global, mixed embeddings that offer limited interpretability and weak few-shot generalization. Moreover, they rarely enforce per-phenotype similarity, which is crucial in cardiology where findings are sparse and modalities may disagree.

These challenges are amplified when the goal is to infer cardiac status from routine chest CT. Without explicit phenotype guidance, models may rely on shortcut features or collapse toward modality-specific biases, especially in data-scarce settings. Effective cardiac—non-cardiac transfer therefore requires an approach that (i) tightly couples CT and structured measurements, (ii) grounds representations in clinically meaningful phenotypes, and (iii) supports exemplar-based reasoning. In this work, we introduce X-Cardia, a cardiac phenotype—guided multimodal framework for aligning chest CT with ECHO and ECG-derived measurements. X-Cardia integrates a CLIP-style contrastive objective with a non-parametric Nadaraya—Watson (NW) head (Cai, 2001; Wang et al., 2023; Wang and Sabuncu, 2022) that enforces phenotype-level similarity via a support bank of exemplar embeddings. This hybrid objective produces interpretable, data-efficient representations that transfer effectively to downstream cardiac prediction tasks on non-gated chest CT.

We pre-train on a large cohort of 20,574 patients and fine-tune the CT encoder on ten clinically relevant abnormalities derived from ECHO. X-Cardia substantially improves performance over strong baselines—including standard multimodal contrastive learning, achieving up to 8% AUROC gains in full-data settings and nearly 10% improvements in 5-shot regimes. These results indicate that explicit phenotype alignment is key to unlocking cardiac information from routine CT and enabling scalable opportunistic screening.

2. Related Works

2.1. Learning with Tabular Data

Conventional tabular models such as XGBoost (Chen and Guestrin, 2016) and Light-GBM (Ke et al., 2017) remain strong baselines, often outperforming early neural networks (Shwartz-Ziv and Armon, 2022). Recent attention-based architectures better capture feature dependencies: TabTransformer (Huang et al., 2020) introduces contextual embeddings, and TabNet (Arik and Pfister, 2021) applies sequential attention for feature selection.

Foundation models like TabPFN (Hollmann et al., 2022) and TabLLM (Hegselmann et al., 2023) enable few-shot reasoning through meta-learning or language-model serialization, producing transferable structured embeddings.

In medical applications, tabular representations offer complementary physiological information. Prior work has shown that contrastively coupling image and tabular encoders can enhance unimodal performance (Hager et al., 2023). Jiang et al. (Jiang et al., 2024a,b) extend this idea by aligning visual feature channels with clinical phenotypes using optimal transport and mutual information. These methods highlight the value of tabular data as a source of structured, expert-derived signals for guiding representation learning.

2.2. Cross-Modal Transfer

Cross-modal alignment learns a shared embedding space. For example, vision—language models such as CLIP (Radford et al., 2021), ALBEF (Li et al., 2021), IRRA (Jiang and Ye, 2023), CUSA (Huang et al., 2024), and UNITER (Chen et al., 2019) use contrastive or masked objectives to link image and text representations. Liang et al. (Liang et al., 2022) revealed a persistent modality gap formed by each encoder due to initialization and temperature dynamics.

In medical imaging, multimodal contrastive methods such as MMCL (Yuan et al., 2021; Hager et al., 2023), SimCLR-based approaches (Chen et al., 2020; Tang et al., 2020), and clinically grounded frameworks like CHARMS (Jiang et al., 2024a,b) demonstrate that structured signals can regularize visual encoders and improve data efficiency. The modality-focusing hypothesis (Xue et al., 2022) further suggests that cross-modal transfer succeeds when modalities share causal, modality-general features. Recent work on large vision–language models (Li et al., 2025) underscores the importance of aligning both latent spaces and model behavior.

Motivated by these, we perform cardiac-to-non-cardiac transfer by aligning chest CT with ECHO and ECG-derived phenotypes via a contrastive, phenotype-supervised objective, reducing modality gaps and yielding more data-efficient multimodal representations.

3. Methodology

We start with the basic setup in Sec. 3.1, followed by the encoders and representation fusion in Sec. 3.2. We then describe the Nadaraya–Watson head in Sec. 3.3, the support bank construction in Sec. 3.4, and the cross-modal alignment in Sec. 3.5. The training and evaluation details are described in Sec. 3.6. Finally, we present the supervised fine-tuning on cardiac binary targets in Sec. 3.7. An overview of the proposed cross-modal pre-training and fine-tuning framework is shown in Figure 1.

3.1. Problem Setup

We denote our multimodal training dataset as $\mathcal{D} = \{(\mathbf{x}_i^{\text{img}}, \mathbf{x}_i^{\text{tab}}, \mathbf{y}_i)\}_{i=1}^{|\mathcal{D}|}$, where $\mathbf{x}_i^{\text{img}} \in \mathcal{X} \subset \mathbb{R}^{D \times H \times W}$ is the 3D chest CT volume with D as number of slices, H and W as height and width. $\mathbf{x}_i^{\text{tab}} \in \mathcal{X} \subset \mathbb{R}^F$ is the structured tabular feature vector derived from ECHO and ECG with F as the number of features. $\mathbf{y}_i \in \{0,1\}^C$ is the multi-hot vector and C is the number of classes.

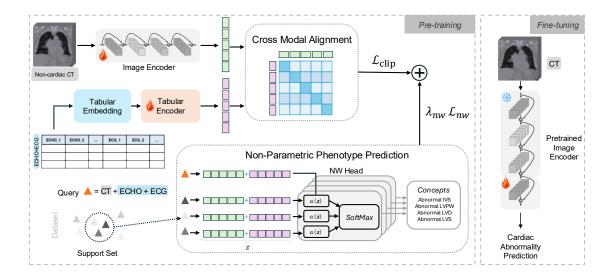


Figure 1: Overview of proposed X-Cardia. During pre-training (left), multimodal alignment is learned across chest CT and tabular features (ECHO and ECG) using a CLIP-style contrastive loss $\mathcal{L}_{\text{clip}}$ and cardiac supervision via a Nadaraya–Watson (NW) head with loss \mathcal{L}_{nw} . Flame icon means learnable, whereas snowflake icon means frozen. During fine-tuning (right), only the last layer of pre-trained CT encoder is optimized to predict cardiac abnormalities from non-cardiac chest CTs, leveraging the aligned and phenotype-guided latent space obtained during pre-training.

3.2. Encoders and Representation Fusion

Image encoder. We denote image encoder (3D ResNet-50 (He et al., 2016; Hara et al., 2017; Wang et al., 2018)) as $f_{\theta} : \to \mathbb{R}^d$ mapping $\mathbf{x}_i^{\text{img}}$ to a d-dimensional embedding:

$$\mathbf{e}_i^{\text{img}} = f_{\theta}(\mathbf{x}_i^{\text{img}}) \tag{1}$$

where θ represents the learnable parameters of the image encoder and $\mathbf{e}_i^{\text{img}} \in \mathbb{R}^d$ is the image embedding after Global Average Pooling (GAP) and MLP head.

Tabular encoder. We adopt a FT-Transformer (Gorishniy et al., 2021) based architecture. We define a tokenizer h_{ψ} and encoder g_{ϕ} that map the input $\mathbf{x}_{i}^{\mathrm{tab}} \in \mathbb{R}^{F}$ to an embedding $\mathbf{e}_{i}^{\mathrm{tab}} \in \mathbb{R}^{d}$. The tokenizer h_{ψ} projects each scalar feature to form a sequence of embeddings. The encoder g_{ϕ} processes this sequence via Transformer layers, aggregates the output via GAP, and applies a final projection head:

$$\mathbf{e}_i^{\text{tab}} = g_\phi \big(h_\psi(\mathbf{x}_i^{\text{tab}}) \big), \tag{2}$$

where ψ and ϕ are learnable parameters.

Embedding fusion. We further fuse $\mathbf{e}_i^{\text{img}}$ and $\mathbf{e}_i^{\text{tab}}$ to obtain a shared representation for phenotype prediction. We define the fusion operation as follows:

$$\mathbf{z}_{i} = \frac{\mathbf{e}_{i}^{\text{img}} \oplus \mathbf{e}_{i}^{\text{tab}}}{\left\|\mathbf{e}_{i}^{\text{img}} \oplus \mathbf{e}_{i}^{\text{tab}}\right\|_{2}}$$
(3)

where \oplus denotes element-wise summation and $\|\cdot\|_2$ is ℓ_2 norm.

3.3. Non-Parametric Phenotype Prediction (Nadaraya-Watson Head)

We adopt a Nadaraya–Watson (NW) estimator (Cai, 2001; Wang et al., 2023; Wang and Sabuncu, 2022) on fused embedding \mathbf{z}_i for phenotype prediction. The NW head is non-parametric and has no learnable parameters; it uses support bank $\mathcal{D}_{sup} = \{(\hat{\mathbf{z}}_k, \hat{\mathbf{y}}_k)\}_{k=1}^{|\mathcal{D}_{sup}|}$, where $\hat{\mathbf{z}}_k$ is fused embedding and $\hat{\mathbf{y}}_k$ is the multi-hot phenotype label of sample k. Given a query embedding \mathbf{z}_i , we first compute temperature-scaled similarities,

$$\alpha_k(\mathbf{z}_i) = \frac{\exp\left((\mathbf{z}_i \cdot \hat{\mathbf{z}}_k)/\tau_{\text{nw}}\right)}{\sum_{j=1}^{|\mathcal{D}_{sup}|} \exp\left((\mathbf{z}_i \cdot \hat{\mathbf{z}}_j)/\tau_{\text{nw}}\right)},\tag{4}$$

where τ_{nw} is a temperature hyperparameter controlling the sharpness of the attention distribution over support, $\alpha_k(\mathbf{z}_i)$ denotes the weight assigned to query embedding \mathbf{z}_i over support bank. The predicted phenotype probabilities are then given by:

$$\hat{\mathbf{p}}_i = \sum_{k=1}^{|\mathcal{D}_{sup}|} \alpha_k(\mathbf{z}_i) \,\hat{\mathbf{y}}_k,\tag{5}$$

where $\hat{\mathbf{p}}_i$ is the *C*-dimensional vector of phenotype probabilities for query \mathbf{z}_i , which can be viewed as weighted average of the support-label vectors in phenotype space. For training the NW head, we use binary cross-entropy (BCE) loss \mathcal{L}_{nw} applied to all cardiac phenotypes and averaged over the training set.

3.4. Support Bank Construction

We maintain a non-parametric support bank for Nadaraya–Watson inference on embeddings. At initialization, all training samples are encoded and up to K positive examples per phenotype are selected: if a phenotype has fewer than K positives, we keep all; otherwise, we run k-means with K clusters and retain the samples closest to each centroid. The resulting normalized support embeddings are stored in the NW head and used to compute cosine similarities between query and support embeddings, and the bank is rebuilt every M epochs to track the evolving representation.

3.5. Cross-Modal Alignment

To align image and tabular modalities in a shared embedding space, we employ a CLIP-style symmetric contrastive loss (Oord et al., 2018; Radford et al., 2021; Hager et al.,

2023). We define scaled similarities as $s_{ij} = (\mathbf{e}_i^{\text{img}} \cdot \mathbf{e}_j^{\text{tab}})/\tau_{\text{clip}}$ where, τ_{clip} is a temperature hyperparameter controlling sharpness of the similarity distribution. Cross-modal loss is,

$$\mathcal{L}_{\text{clip}} = -\frac{1}{2|\mathcal{D}|} \left[\sum_{i=1}^{|\mathcal{D}|} \log \frac{\exp(s_{ii})}{\sum_{j=1}^{|\mathcal{D}|} \exp(s_{ij})} + \sum_{j=1}^{|\mathcal{D}|} \log \frac{\exp(s_{jj})}{\sum_{i=1}^{|\mathcal{D}|} \exp(s_{ji})} \right]$$
(6)

which encourages each matched image—tabular pair (the diagonal terms s_{ii}) to have higher similarity than all non-matching pairs within the batch.

3.6. Training and Evaluation

The overall objective combines cross-modal alignment and phenotype supervision as:

$$\mathcal{L}_{\text{total}} = \mathcal{L}_{\text{clip}} + \lambda_{\text{nw}} \, \mathcal{L}_{\text{nw}},\tag{7}$$

The weighting term λ_{nw} is tuned to balance alignment and phenotype learning. Training uses AdamW with cosine-annealed learning rate. Optimization runs for up to 100 epochs with early stopping criteria. In all the comparison studies, MMCL is actually our model (X-Cardia) without NW head and trained using only \mathcal{L}_{clip} loss.

3.7. Supervised Fine-Tuning on Cardiac Binary Targets

We fine-tuned the pre-trained image encoder (3D ResNet-50 (He et al., 2016; Wang et al., 2018; Hara et al., 2017)) on the labeled cohort to predict ten binary cardiac phenotypes directly from non-cardiac chest CT. To leverage the learned alignment, we froze the lower convolutional blocks and jointly optimized the remaining layers and task-specific heads with a multi-task, masked binary cross-entropy loss, reporting AUROC for all targets.

Table 1: Performance (AUROC) by label on the test set under different training strategies (**bolded** values indicate best result; <u>underlined</u> values indicate second-best).

Label	No pre-training	MMCL	SimCLR	NW+MMCL
LVEF $\leq 45\%$	0.76	0.75	0.60	0.77
$LVWT \ge 13 \text{ flag}$	0.67	0.69	0.62	0.72
Aortic Stenosis	0.73	0.76	0.54	0.79
Aortic Regurgitation	0.66	0.66	0.61	0.74
Mitral Regurgitation	0.76	0.73	0.61	0.75
Tricuspid Regurgitation	0.74	0.72	0.65	0.75
Pulmonary Regurgitation	0.73	0.80	0.57	0.79
$PASP \ge 45 \text{ flag}$	0.70	0.67	0.63	0.70
$TR_{max} \geq 32 \text{ flag}$	0.69	0.66	0.66	0.69
SHD flag	0.74	0.74	0.63	0.74

4. Experiments and Results

4.1. Dataset Overview

We assembled a large-scale multimodal cardiac imaging dataset from Columbia University Irving Medical Center and Weill Cornell Medicine comprising non-gated chest CT, ECHO, ECG, and demographic data. CT studies were temporally matched to corresponding ECHO and ECG exams using unique patient identifiers, yielding a pre-training cohort of 20,574 patients with non-contrast chest CT, ECHO, and ECG acquired within six months of the CT scan. This cohort was split at the patient level into 16,459/4,115 patients (80/20) for training and validation, and used to pre-train the cross-modal alignment and phenotype prediction framework in Section 3. For supervised downstream training, we curated a separate labeled cohort of 7,553 patients with 16,357 chest CT studies annotated for cardiac structural and functional abnormalities derived from ECHO. We defined ten binary cardiac targets, including reduced LVEF ($\leq 45\%$), increased LV wall thickness (≥ 13 mm), valve stenosis/regurgitation (aortic, mitral, tricuspid, pulmonary), elevated PASP (≥ 45 mmHg), increased TR_{max} (≥ 32 m/s), and structural heart disease (SHD) presence (Poterucha et al., 2025). The fine-tuning cohort was split 80/20 into training and validation subsets, with an independent test set of 2,266 patients (4,861 CT studies) held out for final evaluation.

4.2. Implementation Details

Training and validation were conducted using PyTorch on NVIDIA A100 GPUs with mixed-precision optimization. All CT volumes were resampled to 2 mm isotropic resolution and center-cropped to 164^3 voxels. Both the image encoder and tabular encoder were randomly initialized (Xavier for all linear layers) and trained end-to-end during pre-training. Tabular features were standardized per column. Missing entries in $\mathbf{x}_i^{\text{tab}}$, were then imputed with a k-nearest neighbors (k = 5) imputer fitted on the training split and subsequently applied to the validation and test splits. For contrastive pre-training, batch size was set to 12 with temperature τ_{clip} =0.07. The Nadaraya–Watson head was initialized with K=20 exemplars per phenotype and refreshed every M=5 epochs. All reported metrics were computed on held-out patient-level splits to ensure independence across train, validation, and test cohorts.

4.3. Results

Table 1 summarizes performance across ten cardiac prediction tasks on the held-out chest CT test set. Our proposed framework (NW+MMCL) consistently outperformed both no-pre-training and standard multimodal contrastive learning approaches (Hager et al., 2023; Chen et al., 2020) across most of the prediction tasks (Table 1). Here, one of the baselines, MMCL denotes an ablation of X-Cardia without the NW Head. Our method improved AUROC by 0.03-0.08 over the no-pre-training baseline, except for mitral regurgitation. Improvements were also observed relative to standard MMCL, particularly in valvular disease tasks where physiological phenotypes yield clearer cross-modal correspondence. In the few-shot evaluation (Table 2), NW+MMCL exhibited the largest relative gains, achieving an average improvement of 9.8% AUROC over MMCL and 33.7% AUROC over SimCLR. Few-shot gains were most pronounced for Aortic Stenosis and SHD Flag, demonstrating

the effectiveness of phenotype-guided pre-training for detecting structural abnormalities. Additional experiments varying the fraction of labeled CT studies used for fine-tuning (Appendix C, Table C.1) show that NW+MMCL consistently outperforms the baseline across all data regimes, highlighting its strong sample efficiency.

Table 2: Test performance (AUROC) by label across different training strategies in 5-shot learning. (**bolded** values indicate best result; <u>underlined</u> values are second-best).

Label	No pre-training	MMCL	SimCLR	NW+MMCL
$LVEF \le 45\%$	0.52	0.63	0.50	0.65
$LVWT \ge 13 \text{ flag}$	0.53	0.61	0.51	0.65
Aortic Stenosis	0.54	0.63	0.51	0.85
Aortic Regurgitation	0.54	0.61	0.51	0.60
Mitral Regurgitation	0.58	0.59	0.50	0.68
Tricuspid Regurgitation	0.56	0.59	0.44	0.67
Pulmonary Regurgitation	0.68	0.67	0.48	0.70
$PASP \ge 45 \text{ flag}$	0.59	0.58	0.50	0.60
$TR_{max} \geq 32 \text{ flag}$	0.63	0.50	0.53	0.64
SHD flag	0.64	0.62	0.49	0.74

Table 3: Phenotype prediction performance with NW head versus standard linear head.

Evaluation Metric	NW Head	Linear Head
AUROC F1 Score Cosine Similarity	$0.66 \\ 0.60 \\ 0.72$	$0.63 \\ 0.55 \\ 0.76$

4.4. Ablation Study

We conducted ablations to evaluate the contributions of, (i) training with NW head vs. Linear head, (ii) the quality of cross-modal embedding alignment, and (iii) the interpretability of the support-bank representations.

NW Head. Empirically, Table 3 shows that a learnable linear head on the fused embeddings underperforms the non-parametric, parameter free NW head on phenotype prediction, even though it achieves similar or slightly higher global cosine similarity. This suggests that the NW objective promotes more discriminative, phenotype-aligned decision boundaries: because the NW head has no learnable parameters, the encoders themselves must adapt to align CT and tabular embeddings, whereas a parametric head can partially bypass one modality by relying more heavily on the cleaner signal. Qualitative Grad-CAM comparisons between the NW head and a linear head further support this effect, with the NW head producing more focused cardiac attention maps (Appendix D, Figure D.1).

Quality of embedding alignment. PCA visualization (Figure 2) demonstrates that only the NW + MMCL pre-training strategy yields substantial embedding alignment between chest CT and tabular features (ECHO and ECG), forming a coherent cross-modal

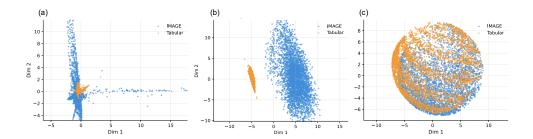


Figure 2: PCA visualization of image (blue) and tabular (orange) modality embeddings under different pre-training strategies. (a), (b), and (c) are SimCLR, MMCL, and NW + MMCL, respectively. SimCLR and MMCL show weak alignment whereas, NW + MMCL enhances alignment by integrating phenotype-level supervision, promoting structured semantic consistency across modalities and reducing modality gaps.

latent space. In contrast, SimCLR and MMCL exhibit weak or partial alignment, highlighting the necessity of phenotype-level supervision to bridge modality-specific representation gaps. These results support our hypothesis that integrating physiological phenotypes enables more effective cross-modal embedding fusion.

Interpretability of the support-bank representations. Support examples formed coherent manifolds with smooth phenotype gradients, and Grad-CAM maps (Figure 3) show that the pre-trained CT encoder focuses on cardiac regions despite non-cardiac, non-gated scans, indicating successful multimodal transfer of cardiac information, though chamber diameters remain harder to predict than wall thickness.

4.5. Discussion and Limitations

Our proposed phenotype-guided multimodal alignment framework demonstrates several significant advantages. By enforcing consistency between cardiac measurements and CT-derived embeddings during pre-training, the model learns physiologically relevant representations that transfer effectively to non-gated chest CT. This leads to strong gains across all cardiac prediction tasks and is especially beneficial in data-scarce scenarios, where our approach consistently outperforms standard contrastive pre-training and no pre-training baselines.

Additionally, the non-parametric Nadaraya—Watson head serves as a structural safe-guard against modality collapse. In contrast to parametric classifiers that can implicitly down-weight the noisier signal in favor of cleaner features, the NW head has no learnable parameters and therefore cannot internalize the supervision itself. This places the optimization burden entirely on the encoders, encouraging the CT backbone to shape its embedding geometry to align with the phenotype-support prototypes. The exemplar-based formulation also offers a more transparent link between predictions and representative cases, helping to anchor the latent space in clinically meaningful phenotypes. Notably, despite the CT scans not being acquired for cardiac indications, the pre-trained model learns to focus on cardiac

regions, suggesting effective transfer of structural information from ECHO and ECG into CT-based representations.

Despite these strengths, several limitations should be considered. The multimodal alignment depends on exams occurring within six months of the CT scan, during which a patient's cardiac condition may change, potentially introducing misalignment. Phenotype labels were derived using threshold-based binarization, which may simplify complex physiological conditions. Furthermore, the current support bank does not dynamically adapt to rare or evolving phenotypes. Finally, our evaluation focused on binary classification tasks; future extensions could explore continuous severity prediction, temporal modeling for deeper clinical insight.

5. Conclusion

This work presents a phenotypically supervised multimodal alignment framework that unifies cardiac and non-cardiac imaging by leveraging tabular cardiac features as alignment signals. By integrating CLIP-style cross-modal contrastive learning and a Nadaraya-Watson non-parametric head, the method produces semantically grounded, interpretable embeddings that transfer effectively to chest CT for cardiac abnormality prediction. Extensive experiments demonstrate consistent improvements across ten cardiac tasks, strong data efficiency, and substantial few-shot gains. Together, these results highlight phenotype-level alignment as a promising direction for multimodal representation learning in medical imaging, particularly when labeled data are scarce or modalities differ in diagnostic intent.

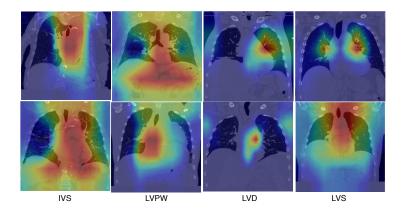


Figure 3: Qualitative Grad-CAM maps on cardiac CT slices from the final support set after cross-modal pre-training. Each column corresponds to one phenotype: IVS (interventricular septal thickness), LVPW (left ventricular posterior wall thickness), LVD (left ventricular internal diameter in diastole), and LVS (left ventricular internal diameter in systole), and each image shows a different case from the final support set. The pre-trained encoder attends to anatomically relevant cardiac regions, indicating transferable structural priors before downstream fine-tuning.

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Appendix A. Test set overview

Table A.1: Label distribution and missingness rate in the test cohort across ten cardiac abnormalities. Counts represent positive (pos), negative (neg), and rate of missing labels per class.

Label	Pos	Neg	Missing (%)
LVEF $\leq 45\%$	553	4304	0.1
$LVWT \ge 13 \text{ flag}$	624	3691	11.2
Aortic stenosis	126	3470	26.0
Aortic regurgitation	75	4575	4.3
Mitral regurgitation	196	4428	4.9
Tricuspid regurgitation	363	4267	4.8
Pulmonary regurgitation	15	3334	31.1
$PASP \ge 45 \text{ flag}$	886	1920	42.3
$TR_{max} \geq 32 \text{ flag}$	422	1733	55.7
SHD flag	1942	170	56.6

Appendix B. Effect of NW Head Loss Weighting (λ_{nw})

Varying the NW loss weight (Table B.1) revealed that excessively small values underutilize phenotype structure, while very large values can overconstrain the representation. The optimal range lies between 0.4 and 0.6, balancing alignment and phenotype smoothing.

Table B.1: Performance (AUROC) on the test set by label using different λ_{nw} values in the loss.

Label	$\lambda_{nw} = 0.2$	$\lambda_{nw} = 0.4$	$\lambda_{nw} = 0.6$	$\lambda_{nw} = 0.8$	$\lambda_{nw} = 1.0$
$LVEF \le 45\%$	0.74	0.74	0.73	0.74	0.74
$LVWT \ge 13 \text{ flag}$	0.72	0.69	0.70	0.69	0.71
Aortic Stenosis	0.89	0.90	0.87	0.88	0.88
Aortic Regurgitation	0.72	0.67	0.65	0.68	0.73
Mitral Regurgitation	0.73	0.73	0.72	0.72	0.75
Tricuspid Regurgitation	0.66	0.69	0.66	0.65	0.70
Pulmonary Regurgitation	0.81	0.73	0.77	0.72	0.66
$PASP \ge 45 \text{ flag}$	0.67	0.68	0.67	0.68	0.69
$TR_{max} \ge 32 \text{ flag}$	0.64	0.65	0.65	0.67	0.65
SHD flag	0.77	0.76	0.76	0.75	0.75

Appendix C. Effect of Training Size

Table C.1 reports performance as the labeled training set is reduced to 2%, 4%, 6%, and 10% of available CTs. NW+MMCL outperformed the baseline at every fraction and for every label. In extremely low-supervision settings (e.g., 2%), the method improved AUROC by up to 57% for Aortic Stenosis and 48% for Mitral Regurgitation than the no-pre-training baseline. These results indicate that phenotype-guided multimodal alignment yields strong sample efficiency.

Table C.1: Performance (AUROC) by disease label across models at different fractions of the training set. Best per percent per row is bolded.

2%		2%	% 4%			6%		10%	
Label	Base	NW+MMCL	Base	NW+MMCL	Base	NW+MMCL	Base	NW+MMCL	
Aortic Regurgitation	0.56	0.73	0.51	0.71	0.56	0.72	0.62	0.66	
Aortic Stenosis	0.49	0.77	0.53	0.79	0.43	0.78	0.62	0.78	
LVEF $\leq 45\%$	0.58	0.69	0.61	0.73	0.54	0.73	0.50	0.74	
$LVWT \ge 13 \text{ flag}$	0.56	0.64	0.63	0.69	0.52	0.69	0.54	0.68	
Mitral Regurgitation	0.49	0.73	0.56	0.74	0.56	0.73	0.56	0.71	
$PASP \ge 45 \text{ flag}$	0.47	0.65	0.50	0.67	0.54	0.66	0.63	0.67	
Pulmonary Regurgitation	0.72	0.73	0.58	0.69	0.55	0.61	0.65	0.69	
SHD flag	0.46	0.72	0.61	0.71	0.52	0.73	0.63	0.72	
$TR_{max} \ge 32 \text{ flag}$	0.46	0.64	0.51	0.63	0.52	0.63	0.62	0.63	
Tricuspid Regurgitation	0.57	0.71	0.50	0.70	0.57	0.69	0.63	0.69	

Appendix D. Non-Parametric vs. Learnable Heads for Phenotype Prediction

In this appendix (Figure D.1), we qualitatively examine how the choice of prediction head influences the spatial focus of the pre-trained CT encoder. Grad-CAM visualizations for four key phenotypes show that the non-parametric NW head, when combined with multimodal contrastive pre-training, consistently drives the encoder to attend to anatomically relevant myocardial and chamber regions, in line with the underlying ECHO-derived measurements. In contrast, replacing the NW head with a linear classifier yields more scattered and occasionally extra-cardiac attention patterns. These examples support our hypothesis that the non-parametric NW head better enforces phenotype-level alignment between CT and tabular representations, leading to more interpretable and physiologically grounded image features.

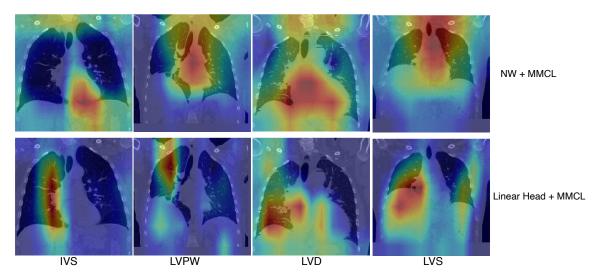


Figure D.1: Comparison of Grad-CAM attention maps on cardiac CT volumes for the non-parametric Nadaraya—Watson (NW) head versus a learnable linear head after cross-modal pre-training. Each column corresponds to one of four phenotypes—IVS (interventricular septal thickness), LVPW (left ventricular posterior wall thickness), LVD (left ventricular internal diameter in diastole), and LVS (left ventricular internal diameter in systole). The NW + MMCL model (top row) produces sharper, more localized attention over ventricular walls and chambers, whereas the Linear Head + MMCL model (bottom row) exhibits more diffuse and off-target responses, indicating weaker phenotype alignment in the learned image features.