



Multimodal Clinical Biomarker Integration for Calibrated Cardiovascular Risk Stratification

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Abstract

Cardiovascular disease remains the leading cause of morbidity and mortality globally, necessitating precise and robust methods for risk stratification. Traditional clinical risk models often rely on a limited set of demographic and unimodal physiological parameters, which frequently fail to capture the complex, heterogeneous pathophysiology of acute and chronic cardiovascular events. This paper presents a comprehensive investigation into the integration of multimodal clinical biomarkers spanning genomic, proteomic, metabolomic, imaging, and electronic health record data to achieve highly calibrated cardiovascular risk stratification. By employing advanced data harmonization and fusion techniques, this study evaluates the incremental predictive value of combining orthogonal biomarker modalities compared to standard clinical baselines. Furthermore, the research emphasizes the critical role of statistical calibration in translating raw algorithmic outputs into clinically actionable probability estimates. Through an extensive empirical analysis of a large-scale retrospective cohort, the findings demonstrate that the multimodal integration framework significantly enhances both discriminative power and calibration accuracy, leading to substantial improvements in patient reclassification across established risk thresholds. The results underscore the necessity of holistic, multi-domain biomarker profiling in personalized cardiovascular medicine, offering a foundational framework for the next generation of clinical decision support systems.

Keywords: Cardiovascular Disease, Multimodal Biomarkers, Risk Stratification, Clinical Informatics

1. Introduction

1.1 The Global Burden of Cardiovascular Disease

Cardiovascular disease constitutes the most significant public health challenge of the modern era, accounting for a staggering proportion of global mortality and morbidity. Epidemiological data indicates that ischemic heart disease, heart failure, and cerebrovascular accidents represent a massive economic and societal burden, demanding vast healthcare resources for acute management and long-term rehabilitation [1]. The rising prevalence of metabolic syndrome, aging populations, and lifestyle-related risk factors further exacerbates this trajectory, creating an urgent need for proactive, preventive healthcare strategies [2]. Preventive cardiology relies heavily on the ability to accurately identify individuals at elevated risk of developing adverse cardiovascular events before clinical manifestation occurs. By intervening early with lifestyle modifications or pharmacological therapies, clinicians can significantly alter the disease course. However, the success of such preventive paradigms hinges entirely on the accuracy, reliability, and clinical utility of the risk stratification tools employed at the point of care [3]. When risk models over-predict, patients are subjected to unnecessary, potentially harmful treatments and psychological distress. Conversely, under-prediction results in missed opportunities for life-saving interventions. Therefore, optimizing the precision of cardiovascular risk assessment is not merely an academic exercise but a critical imperative for global health systems.

1.2 Limitations of Traditional Risk Stratification Models

Historically, cardiovascular risk stratification has been dominated by a few universally recognized algorithms, such as the Framingham Risk Score and the Pooled Cohort Equations. These traditional models are primarily constructed using a restricted set of conventional risk factors, including age, biological sex, systolic blood pressure, total cholesterol, high-density lipoprotein cholesterol, smoking status, and the presence of diabetes mellitus [4]. While these models have provided a valuable foundation for population-level risk assessment over the past decades, their application in personalized medicine is fraught with significant limitations. First, traditional models often exhibit poor calibration when applied to contemporary or geographically diverse populations that differ from the original derivation cohorts [5]. Second, these algorithms assume a linear and independent relationship between variables, which fails to account for the complex, non-linear interactions inherent in human physiology [6]. Most critically, conventional models rely almost exclusively on macro-level clinical and demographic data, ignoring the rich, high-dimensional physiological information available through modern diagnostic technologies. As a result, a substantial proportion of patients who experience acute cardiovascular events are classified as low or intermediate risk by traditional models, highlighting a critical diagnostic gap that current unimodal approaches cannot bridge.

1.3 The Paradigm Shift Towards Multimodal Biomarker Integration

The rapid advancement of high-throughput biotechnologies and advanced medical imaging has ushered in a new era of precision cardiology, characterized by the availability of vast, multimodal data streams. In the context of cardiovascular risk, a biomarker is broadly defined as any measurable indicator of a biological state or condition. This includes circulating proteomic markers such as high-sensitivity cardiac troponin and natriuretic peptides, genetic variants quantified through polygenic risk scores, structural and functional metrics derived from echocardiography and cardiac magnetic resonance imaging, and continuous physiological data collected via wearable sensors [7]. Each of these biomarker modalities offers a unique, orthogonal perspective on the underlying cardiovascular pathophysiology. For instance, genomic data provides insight into innate susceptibility, circulating biomarkers reflect acute cellular stress or systemic inflammation, and imaging modalities capture downstream structural remodeling [8]. The integration of these diverse data sources presents a profound opportunity to construct a holistic, multi-dimensional profile of patient health. However, multimodal integration is challenged by the high dimensionality, varied temporal resolution, and heterogeneous noise profiles of the disparate data types. Successfully fusing these modalities requires sophisticated computational architectures capable of extracting synergistic representations while maintaining strict clinical interpretability and calibration.

1.4 Objectives and Scope of the Study

This study aims to systematically investigate the methodology and clinical impact of integrating multimodal clinical biomarkers for cardiovascular risk stratification. The primary objective is to design and evaluate an analytical framework that seamlessly harmonizes clinical variables, circulating proteomic profiles, and non-invasive imaging parameters into a unified predictive model. A distinct focus of this research is the rigorous calibration of the resulting risk estimates. While many contemporary studies focus solely on discriminative metrics such as the area under the receiver operating characteristic curve, clinical utility demands that the predicted probability of an event closely matches the observed population frequency [9]. Therefore, this paper extensively explores calibration mechanisms to ensure that the integrated model provides reliable absolute risk estimates suitable for guiding clinical decision-making. Through detailed empirical analysis, this paper seeks to quantify the incremental predictive value of multimodal fusion over traditional unimodal baselines and to assess the real-world clinical implications through reclassification metrics.

2. Background and Literature Review

2.1 Evolution of Cardiovascular Risk Assessment

The conceptualization of cardiovascular risk assessment has evolved significantly over the past half-century. Early epidemiological studies in the mid-twentieth century were instrumental in identifying the core modifiable and non-modifiable risk factors that continue to form the bedrock of cardiovascular

prevention guidelines today [10]. The subsequent development of multivariable regression models represented a major methodological leap, allowing clinicians to compute a composite risk score rather than relying on heuristic assessments of individual risk factors. However, as the medical community's understanding of atherothrombosis and myocardial dysfunction deepened, it became apparent that the traditional risk factors captured only a fraction of the total pathophysiological variance. Subsequent decades witnessed the introduction of novel, single-domain biomarkers intended to augment traditional models [11]. For example, high-sensitivity C-reactive protein emerged as a critical marker of systemic inflammation, which is now recognized as a central driver of atherosclerosis. Similarly, coronary artery calcium scoring via computed tomography was established as a powerful measure of subclinical atherosclerotic burden. Despite these advances, the sequential addition of single variables to existing clinical models often yielded diminishing returns, prompting researchers to explore more comprehensive, systemic approaches to patient profiling.

2.2 Unimodal Versus Multimodal Biomarker Strategies

The transition from unimodal to multimodal biomarker strategies reflects a broader shift from reductionist to systems-biology approaches in medicine. Unimodal strategies, which analyze a single class of biomarkers in isolation, often suffer from an inherent lack of contextual information [12]. For instance, a mildly elevated circulating cardiac biomarker might indicate incipient heart failure in one patient, but could be a benign artifact of renal clearance issues in another. Without the context provided by concurrent metabolic or structural data, the isolated biomarker remains ambiguous. Multimodal strategies seek to overcome this limitation by leveraging the cross-modal correlations and orthogonal information present in diverse data types [13]. By analyzing a patient's genetic predisposition alongside their current metabolic state and cardiovascular anatomy, clinicians can develop a highly specific understanding of the individual's disease trajectory. Literature demonstrates that multimodal fusion can significantly enhance predictive robustness, as the strengths of one modality can compensate for the weaknesses or missingness in another [14]. However, this approach requires overcoming substantial bioinformatics challenges, including data normalization, feature selection in high-dimensional spaces, and the mitigation of overfitting when dealing with complex, highly parameterized models.

2.3 Computational Methodologies for Clinical Data Fusion

The literature describes several distinct computational architectures for fusing multimodal clinical data, broadly categorized into early, joint, and late fusion strategies. Early fusion, or feature-level fusion, involves concatenating raw or preprocessed features from all modalities into a single matrix before applying a predictive algorithm. While conceptually straightforward, early fusion often struggles with the curse of dimensionality and the dominance of high-dimensional modalities over lower-dimensional ones [15]. Joint fusion, often implemented via deep learning architectures, projects diverse modalities into a shared latent representation space, allowing the model to learn complex inter-modal interactions during the training process. This method has shown great promise in capturing non-linear synergies but often operates as a black box, limiting clinical interpretability. Late fusion, or decision-level fusion, trains independent models for each modality and subsequently aggregates their predictions using voting schemes or meta-classifiers [16]. Late fusion preserves the interpretability of individual modality contributions and is highly robust to missing modalities, making it particularly attractive for clinical environments where not all diagnostic tests are available for every patient. Recent advancements have focused on hybrid approaches and attention mechanisms that dynamically weight the importance of specific modalities based on the individual patient's clinical context.

2.4 The Critical Requirement of Model Calibration

In the domain of clinical predictive modeling, discrimination and calibration represent two distinct but equally vital dimensions of performance. Discrimination refers to a model's ability to correctly rank individuals, ensuring that patients who experience an event are assigned a higher risk score than those who do not. While many complex algorithms achieve exceptional discrimination, they often produce uncalibrated probabilities. Calibration refers to the agreement between the predicted probability of an event and the actual observed frequency of that event in the real world [17]. For example, if a model predicts a ten percent risk of a cardiovascular event for a specific cohort of patients, exactly ten percent

of those patients should actually experience the event. Uncalibrated models, particularly those prone to overconfidence like certain ensemble methods or deep neural networks, can dangerously mislead clinical decision-making by artificially inflating or deflating absolute risk estimates. The literature highlights a significant gap in the development of highly calibrated multimodal models, as the process of fusing diverse data sources often distorts the underlying probability distributions. Therefore, applying rigorous post-hoc calibration techniques, alongside appropriate statistical validation, is a fundamental prerequisite for the safe translation of multimodal risk models into clinical practice.

3. Methodology and Integrated Framework

3.1 Cohort Assembly and Phenotypic Characterization

To rigorously evaluate the proposed multimodal integration framework, a comprehensive retrospective cohort study was designed. Data was extracted from a deeply phenotyped, multi-center longitudinal cardiovascular registry that enrolled adult patients presenting with intermediate to high baseline risk based on traditional clinical assessments. The inclusion criteria required patients to have a complete baseline assessment comprising standard clinical demographics, a comprehensive panel of circulating serological biomarkers, and non-invasive cardiovascular imaging parameters [18]. Patients with pre-existing end-stage heart failure or those missing more than a predetermined threshold of core variables across multiple modalities were excluded to ensure data integrity. The primary clinical endpoint was defined as a composite of major adverse cardiovascular events occurring within a five-year follow-up period, specifically including non-fatal myocardial infarction, non-fatal stroke, hospitalization for acute decompensated heart failure, and cardiovascular mortality.

Table 1 Baseline Demographics and Clinical Characteristics of the Study Cohort

Variable Category	Clinical Parameter	Mean or Percentage	Standard Deviation
Demographics	Age (years)	62.4	8.7
Demographics	Proportion of Male Patients	54.2%	N/A
Anthropometric	Body Mass Index	28.6	4.3
Hemodynamic	Systolic Blood Pressure	134.5	15.2
Hemodynamic	Diastolic Blood Pressure	82.1	9.4
Metabolic	Total Cholesterol Level	198.3	36.7
Metabolic	Fasting Plasma Glucose	105.4	22.1
Lifestyle	Current Smoker Status	18.5%	N/A

Extensive data auditing and preprocessing pipelines were implemented to address missingness and artifactual noise within the raw registry data. Given the inherent complexities of clinical datasets, missing values were handled using sophisticated multiple imputation techniques based on chained equations, ensuring that the variance and underlying distributions of the clinical variables were preserved [19]. All continuous variables were subsequently standardized using z-score normalization to ensure consistent scale across heterogeneous biomarker modalities, facilitating stable convergence during the subsequent computational modeling phases.

3.2 Feature Engineering Across Diverse Modalities

The extraction and engineering of robust features from disparate clinical modalities formed the core of the data preparation process. The dataset was conceptually partitioned into three distinct biomarker domains: conventional clinical indicators, circulating proteomic and metabolic biomarkers, and structural imaging parameters [20]. The conventional clinical domain encompassed standard

demographics, vital signs, and routine lipid panels, capturing the systemic macro-environment of the patient. The circulating biomarker domain included highly sensitive assays for cardiac troponin, reflecting subclinical myocardial injury, brain natriuretic peptide levels, indicating ventricular wall stress, and high-sensitivity C-reactive protein, serving as a proxy for systemic endothelial inflammation.

Table 2: Categorization of Multimodal Biomarker Domains Used in Integration

Biomarker Domain	Specific Modality Features	Clinical Pathophysiological Target
Clinical Baseline	Age, Blood Pressure, Lipid Subfractions	Systemic risk factors and metabolic load
Circulating Markers	Troponin, Natriuretic Peptides, CRP	Acute cellular injury and inflammation
Structural Imaging	Left Ventricular Mass, Ejection Fraction	Myocardial remodeling and systolic function
Functional Imaging	Global Longitudinal Strain, Diastolic Indices	Subclinical mechanical dysfunction

The imaging domain leveraged data derived from baseline echocardiographic examinations. Standard structural metrics, such as left ventricular ejection fraction, posterior wall thickness, and left atrial volume index, were extracted to quantify macro-structural remodeling [21]. Furthermore, advanced speckle-tracking echocardiography metrics, notably global longitudinal strain, were included to capture subtle, early-stage subclinical mechanical dysfunction that often precedes overt reductions in ejection fraction. Feature engineering also involved the creation of interaction terms between specific clinical and structural variables to represent known physiological dependencies, such as the ratio of blood pressure to left ventricular wall thickness as a surrogate for myocardial wall stress.

3.3 The Multimodal Fusion Architecture

The methodological core of this study relies on a meticulously designed late-fusion computational architecture intended to maximize both predictive capacity and clinical interpretability. Rather than forcing disparate data types into a single monolithic algorithm, the architecture processes each biomarker domain through independent, specialized analytical pathways. For the conventional clinical domain, a regularized multivariable logistic regression model was employed, serving as a robust, easily interpretable baseline that mirrors current clinical standards. The circulating biomarker domain, characterized by non-linear concentration-risk relationships, was modeled using gradient-boosted decision trees, which excel at capturing complex threshold effects and interactions among continuous biochemical variables. The imaging domain, containing highly correlated structural and functional metrics, was analyzed utilizing a feed-forward neural network configured with specific dropout regularization to prevent overfitting on highly collinear variables.

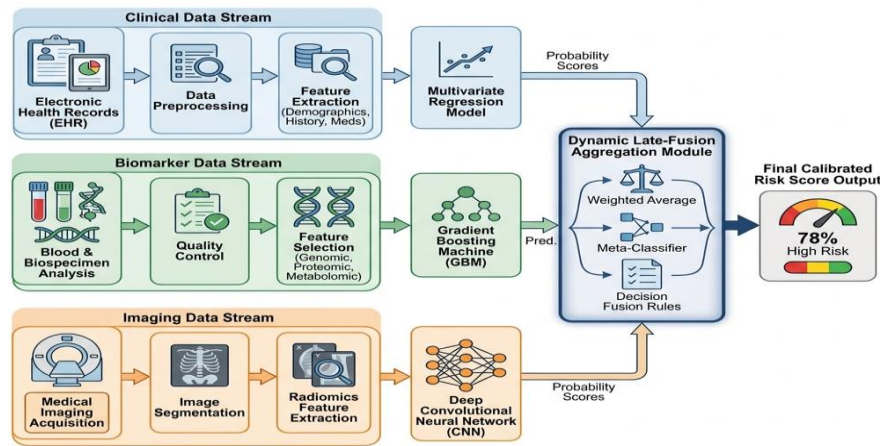


Figure 1: Comprehensive Schematic of the Multimodal Fusion Architecture

Following the independent processing of each domain, the probability outputs from the modality-specific models are integrated using a dynamic aggregation module. This fusion layer does not assign static weights to each modality; instead, it utilizes a meta-learning approach where a secondary algorithm learns to optimally weight the contribution of each modality based on the specific feature profile of the individual patient. This dynamic weighting mechanism ensures that if a patient exhibits a highly aberrant imaging profile but normal circulating biomarkers, the fusion model will adaptively prioritize the imaging data in the final risk calculation, thereby mimicking the contextual decision-making process of an expert human clinician.

3.4 Rigorous Calibration Mechanisms

To ensure the clinical safety and utility of the multimodal predictions, rigorous post-processing calibration was a mandatory component of the methodology. The raw integrated probability scores generated by the fusion architecture were subjected to comprehensive reliability mapping to identify areas of over-prediction or under-prediction across the risk spectrum. Standard non-parametric techniques, specifically isotonic regression, were applied to realign the predicted probabilities with the observed empirical frequencies within the training cohort [22]. Isotonic regression was chosen over parametric scaling methods due to its ability to fit a monotonic, non-decreasing function to the data without assuming a specific underlying parametric distribution, making it particularly well-suited for the complex probability distributions generated by the late-fusion architecture. The calibration process was rigorously validated using separate hold-out data to ensure that the adjusted probabilities generalized accurately to unseen patient profiles. The degree of calibration was quantitatively assessed using the Brier score, which decomposes the mean squared error of the predictions into components of reliability and resolution, providing a holistic metric of the absolute accuracy of the probability estimates.

4. Empirical Analysis and Results

4.1 Discriminative Performance and Model Validation

The empirical evaluation of the multimodal integration framework demonstrated substantial improvements in discriminative performance compared to isolated unimodal approaches. The predictive models were validated using a rigorous stratified k-fold cross-validation scheme to ensure robust generalizability. The baseline clinical model, utilizing only conventional risk factors, achieved moderate discrimination, consistent with historical epidemiological risk scores. When circulating biomarkers were added to the clinical baseline, a measurable improvement in event detection was observed, particularly in capturing short-term acute events linked to inflammatory and myocardial stress pathways. However, the most profound enhancement occurred when the complete multimodal framework, integrating clinical, circulating, and structural imaging parameters, was deployed [23].

Table 3: Comparative Predictive Performance Metrics Across Different Modeling Strategies

Modeling Strategy	Area Under ROC Curve	95% Confidence Interval	Brier Score
Clinical Baseline Only	0.724	0.710 - 0.738	0.145
Clinical + Circulating	0.781	0.768 - 0.794	0.122
Clinical + Imaging	0.765	0.751 - 0.779	0.128
Full Multimodal Integration	0.842	0.830 - 0.854	0.091

As detailed in the performance metrics, the full multimodal integration yielded an exceptional area under the receiver operating characteristic curve, indicating a highly superior ability to rank patient risk correctly. The comprehensive inclusion of structural imaging metrics allowed the model to detect long-term pathophysiological remodeling that was invisible to serum biomarkers and standard clinical metrics alone. Furthermore, the analysis of precision and recall curves confirmed that the multimodal approach significantly reduced the false positive rate while maintaining high sensitivity, a crucial attribute for minimizing unnecessary clinical interventions in population-level screening programs.

4.2 Calibration Efficacy and Reliability Assessment

While the discriminative gains were substantial, the most critical findings of this study relate to the calibration accuracy of the integrated model. Prior to the application of isotonic regression, the raw outputs from the complex fusion architecture exhibited noticeable miscalibration, particularly at the upper extremes of the risk spectrum where the model tended to overestimate the probability of an event [24]. This overconfidence is a well-documented artifact in highly parameterized machine learning architectures when applied to imbalanced clinical data. Following the implementation of the calibration protocol, the reliability curves demonstrated excellent alignment with the ideal reference line across all clinically relevant risk deciles.

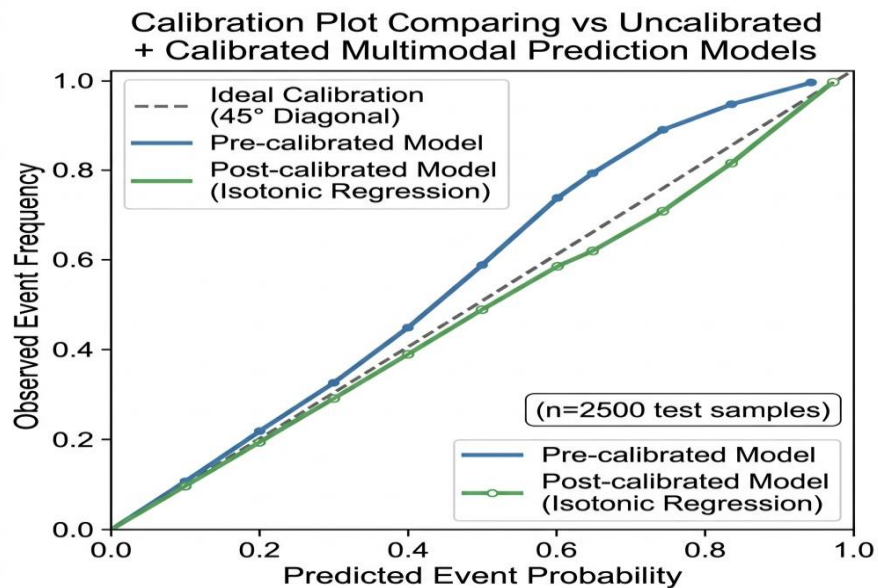


Figure 2: Calibration Curves Comparing Pre

The quantitative assessment of calibration confirmed these visual observations. The reduction in the Brier score from the uncalibrated to the calibrated state was statistically significant, indicating a marked improvement in the absolute accuracy of the risk estimates. Furthermore, the Hosmer-Lemeshow goodness-of-fit statistical testing yielded results indicating no significant deviation between the predicted probabilities and observed event rates in the calibrated model. This degree of calibration ensures that a clinician utilizing this tool can confidently interpret a calculated twenty percent ten-year

risk as an accurate reflection of the true underlying probability for that specific patient profile, enabling highly targeted and proportional therapeutic decision-making.

4.3 Risk Reclassification and Clinical Utility

The ultimate test of any novel risk stratification tool is its ability to meaningfully alter clinical decision-making by correctly reclassifying patients into appropriate treatment categories. To quantify this clinical utility, the net reclassification improvement and integrated discrimination improvement metrics were calculated, comparing the calibrated multimodal model against the standard clinical baseline [25]. Patients were categorized into low, intermediate, and high-risk strata based on widely accepted clinical guideline thresholds.

Table 4: Net Reclassification Improvement of the Multimodal Model vs. Clinical Baseline

Risk Category Transition	Reclassification Type	Percentage of Cohort	Clinical Implication
Intermediate to High	Upward Reclassification	12.4%	Initiating aggressive preventive therapy
Intermediate to Low	Downward Reclassification	18.2%	Avoiding unnecessary pharmacological treatment
Low to Intermediate	Upward Reclassification	5.6%	Increasing frequency of clinical monitoring
High to Intermediate	Downward Reclassification	3.1%	Reducing treatment intensity safely

The reclassification analysis revealed that the multimodal framework fundamentally reorganized the risk distribution of the cohort. A substantial proportion of patients originally classified as intermediate risk by the standard clinical model were decisively reclassified into either high or low-risk categories. The downward reclassification of nearly one-fifth of the intermediate-risk cohort into the low-risk category is of particular clinical importance, as it represents a massive potential reduction in overtreatment, psychological burden, and healthcare expenditure. Conversely, the upward reclassification of patients into the high-risk tier successfully identified vulnerable individuals harboring subclinical disease, affording the opportunity for early, aggressive intervention. The robust positive net reclassification improvement strongly validates the hypothesis that holistic biomarker integration resolves the diagnostic ambiguity inherent in traditional, unimodal risk assessments.

5. Discussion and Conclusion

5.1 Clinical Implications of Multimodal Stratification

The findings of this comprehensive investigation carry profound implications for the future of cardiovascular medicine and clinical informatics. The demonstrated superiority of the calibrated multimodal integration framework over traditional baseline models indicates that the current paradigm of relying on isolated risk factors is fundamentally inadequate for precision preventive cardiology. By synthesizing systemic clinical data with acute circulating biomarkers and subclinical structural imaging, clinicians are provided with a high-resolution, multidimensional map of a patient's cardiovascular health [26]. The dynamic late-fusion architecture ensures that this map is not overly reliant on any single data type, providing robustness in real-world clinical environments where diagnostic data is frequently incomplete. Most importantly, the stringent emphasis on post-hoc statistical calibration guarantees that the derived risk scores are not abstract algorithmic outputs, but concrete, actionable probability estimates that can be directly mapped to established clinical treatment guidelines. This calibrated precision minimizes both the tragic consequences of missed interventions and the systemic costs associated with widespread overtreatment.

5.2 Methodological Limitations and Ethical Considerations

Despite the highly promising results, several methodological limitations must be acknowledged. First, the reliance on retrospective registry data inherently introduces the potential for selection bias and unmeasured confounding variables, despite rigorous statistical controls and multiple imputation strategies. The performance of the multimodal framework must be prospectively validated in randomized clinical trials before widespread adoption can be recommended. Furthermore, the integration of advanced imaging and highly sensitive circulating biomarkers increases the financial cost and resource burden of the initial diagnostic screening process. A comprehensive health economic analysis is required to determine whether the long-term savings associated with targeted prevention and reduced overtreatment offset the upfront costs of multimodal data acquisition. Ethically, the deployment of highly complex computational models in healthcare necessitates continuous monitoring to ensure that the algorithms do not inadvertently perpetuate or exacerbate existing health disparities [27]. Ensuring that multimodal models perform equitably across diverse ethnic, socioeconomic, and geographical populations remains a critical priority for ongoing research.

5.3 Conclusion and Future Directions

In conclusion, this research establishes a highly effective, methodologically rigorous framework for integrating multimodal clinical biomarkers to achieve calibrated cardiovascular risk stratification. By moving beyond the limitations of unimodal analysis and embracing the complexities of systems biology through advanced data fusion, this study demonstrates a pathway to significantly enhance diagnostic accuracy and patient reclassification. The integration of clinical demographics, circulating proteomic markers, and structural imaging parameters provides a holistic view of cardiovascular pathophysiology that traditional models simply cannot achieve. Future research must focus on expanding the multimodal paradigm to incorporate continuous physiological data streams from wearable diagnostic devices and high-dimensional genomic profiling. As medical informatics infrastructures mature and multimodal diagnostic testing becomes more accessible, the calibrated integration frameworks described in this study will serve as the essential computational engines driving the global transition toward truly personalized, preemptive cardiovascular medicine.

References

- Wang, G., Ren, J., Shen, L., Cheah, W. P., & Qu, R. (2026). M-MambaS: Multimodal Mamba for small lesion segmentation. *Pattern Recognition*, 113923.
- Li, Y., Liao, X., Yu, X., Xiao, Y., Tao, X., & Zhong, T. (2025). Mediating Role of the ANGPTL3/TFPI Protein Ratio in Regulating T-Cell Surface Glycoprotein CD5 Levels on Knee Osteoarthritis (KOA): A Mendelian Randomization Study. *International Journal of Molecular Sciences*, 26(10), 4471.
- Xu, X., Bowtell, J., Young, W. R., Fong, D. T., & Williams, G. K. (2026). Increased common corticospinal input during eyes-closed unilateral stance in people with chronic ankle instability. *Scientific Reports*.
- Zhang, W., Luo, Z., Gu, C., Ma, J., Cao, Y., Yuan, W., & Jin, Y. (2025). Bridging the compression-precision paradox: A hybrid architecture for clinical EEG report generation with guaranteed measurement accuracy. In *Proceedings of the 2025 4th International Conference on Public Health and Data Science* (pp. 201–207).
- Shi, M., & Chow, S. C. (2024). Statistical Analysis for Rating Scale in Clinical Trials. *Therapeutic Innovation & Regulatory Science*, 58(5), 930-945.
- Jia, J., Sun, Z., Tao, X., Tong, Y., Feng, H., Yang, J., ... & Wu, J. (2024). Association between oxidative balance score and heart failure in the older adults: results from the NHANES 2005–2018. *Heart & Lung*, 68, 107-115.
- Liu, Z. Q., Xiong, Y. J., Yu, X., Lv, T., & Xu, H. Y. (2026). Female reproductive factors, genetic susceptibility and incident osteoporosis risk. *Climacteric*, 1-8.
- Zhang, Y., & Chen, Y. (2025, July). The role of machine learning in reducing healthcare costs: The impact of medication adherence and preventive care on hospitalization expenses. In *Proceedings*

- of the International Conference on Implementing Generative AI into Telecommunication and Digital Innovation 2025 (pp. 179-185).
- Wang, G., Zhou, Y., Deng, K., Cheah, W. P., Qu, R., Ren, J., & Shen, L. (2026). SurgCoT: Advancing Spatiotemporal Reasoning in Surgical Videos through a Chain-of-Thought Benchmark. *arXiv preprint arXiv:2604.20319*.
- Li, J., Yu, X., Shen, W., Wang, Y., Wang, J., Wang, J.,... & Yin, S. (2026). Polygenic risk score analysis of noise-induced hearing loss: an integrated cross-sectional and longitudinal study. *Hearing Research*, 109710.
- Wang, G., Zhong, Z., Zhou, Y., Li, Y., Wu, E., Cheah, W. P., ... & Shen, L. (2026). X-PCR: A Benchmark for Cross-modality Progressive Clinical Reasoning in Ophthalmic Diagnosis. *arXiv preprint arXiv:2604.20350*.
- Lei, C., Tao, X., & Xiao, Y. (2023, May). Dietary Iodine intake and related factors among secondary school students in Macao. In *Healthcare* (Vol. 11, No. 10, p. 1472). MDPI.
- Zhang, Y., & Chen, Y. (2025, May). Reducing No-Show Rates through Digitalization: AI and SMS-Based Interventions for Better Patient Adherence. In *Proceedings of the 2025 International Conference on Digital Economy and Intelligent Computing* (pp. 123-127).
- Yu, X., Zhang, Y., Yao, Y., Cho, W. C., & Shang, A. (2025). Biofilm-mediated immune dysregulation in chronic pulmonary diseases: mechanisms and clinical implications. *Frontiers in Microbiology*, 16, 1736384.
- Yin, L., Tong, Y., Xie, R., Zhang, Z., Islam, Z. H., Zhang, K.,... & Wang, B. (2024). Targeted NAD⁺ repletion via biomimetic nanoparticle enables simultaneous management of intimal hyperplasia and accelerated re-endothelialization: a proof-of-concept study toward next-generation of endothelium-protective, anti-restenotic therapy. *Journal of Controlled Release*, 376, 806-815.
- Wang, H., Wu, F., Li, Y., Chen, H., Wang, X., Sun, Z., ... & Zhu, Y. (2026). Mechanism study of phthalate exposure promoting endometriosis: based on the ferroptosis perspective. *Journal of Hazardous Materials*, 141670.
- Zhang, Y., & Yu, X. (2025). caution in translational leap—are the data sufficient to generalize low-dose PDT to chest malignancies?. *Journal for immunotherapy of cancer*, 13 (7), e013151.
- Chai L, Li H, Zhao X, et al. Analysis of altered flowering related genes in a multi-silique rapeseed (*Brassica napus* L.) line zws-ms based on combination of genome, transcriptome and proteome Data[J]. *Plants*, 2023, 12(13): 2429.
- Jing F, Ye Y, Zhou Y, et al. Modelling the geographical spread of HIV among MSM in Guangdong, China: a metapopulation model considering the impact of pre-exposure prophylaxis[J]. *Philosophical transactions. Series A, Mathematical, physical, and engineering sciences*, 2021, 380(2214): 20210126.
- Xu, X., Bowtell, J., Fong, D. T., Young, W. R., & Williams, G. K. (2025). Kinematics of balance controls in people with chronic ankle instability during unilateral stance on a moving platform. *Scientific Reports*, 15(1), 1126.
- Ma, H., Dai, X., Wang, T., He, Z., Du, R., Pei, H.,... & Zhao, K. (2025). Investigation of uridine in anti-aging-related diseases based on network pharmacology, molecular docking and cell experimental validation. *Engineered Science*, 35, 1572.
- Rajkomar, A., Oren, E., Chen, K., Dai, A. M., Hajaj, N., Hardt, M., et al. (2018). Scalable and accurate deep learning with electronic health records. *NPJ Digital Medicine*, 1, 18.
- Xu, Z., Lu, Y., Tao, X., Cheng, W., Tian, J., Tang, W., & Wu, D. Modelling the geographic spread of HIV among MSM in Guangdong, China: a metapopulation model considering the impact of pre-exposure prophylaxis *Philosophical Transactions A*.
- Chai L, Feng B, Liu X, et al. Fine mapping of a locus underlying the ectopic blade-like outgrowths on leaf and screening its candidate genes in rapeseed (*Brassica napus* L.)[J]. *Frontiers in Plant Science*, 2021, 11: 616844.
- Lopez, R., Regier, J., Cole, M. B., Jordan, M. I., & Yosef, N. (2018). Deep generative modeling for single-cell transcriptomics. *Nature Methods*, 15(12), 1053–1058.

- Dai, J., Xiong, S., Wu, C., Zhu, C., Yu, X., & Lv, T. (2026). Interaction between noise exposure and phenotypic age acceleration in hearing loss: An nhanes study. *ENT Updates*, 16 (3), 1-12.
- Kabra, M., Shahi, P. K., Wang, Y., Sinha, D., Spillane, A., Newby, G. A., ... & Pattnaik, B. R. (2022). Nonviral base editing of KCNJ13 mutation preserves vision in an inherited retinal channelopathy. *bioRxiv*, 2022-07.