A new Method for Multi-omics Diagnostics in Cardiology with the Integration of Elementomics Using AI

Gulfarida Tulemissova[1], Vasily Yurasov[2], Laura Massanova[3] and Almiri Karkimbayeva[4]

[1]Department of Computer Science, School of Information Technologies and Applied Mathematics, SDU University, Almaty, Kazakhstan

[2]MetaMetrix Laboratory, Almaty, Kazakhstan

[3]Almaty Technological University, Almaty, Kazakhstan

[4]Shanghai Jiao Tong University, Global Institute of Future Technologies, Health Science and Technology, Kazakhstan, Shanghai, China

gulfarida.tulemissova@sdu.edu.kz
vvy.metabo@gmail.com
lmassanova@gmail.com
almirikarkimbayeva@gmail.com

Abstract: Molecular genetics increasingly uses high-throughput multi-omics data analysis to identify new biomarkers and improve the diagnostic accuracy of coronary heart disease and heart failure using artificial intelligence (AI). These tools enable new analytical methods for identifying hidden relationships among different levels of biological organization, including genes, proteins, metabolites, and trace elements measured in biological samples such as blood. The proposed method performs an integrative analysis of inter-omics correlations, including elemental data. Research purpose: To develop an improved bioinformatics model for a biometric approach in molecular genetics using neural-network technology. Research subject: Multi-omics profiles of patients with cardiovascular diseases and biomarkers that may improve the diagnostic accuracy of coronary heart disease and heart failure. Approach: AI methods, including neural networks and machine-learning techniques, were used to improve the efficiency of multi-omics data analysis. Novelty: A new classification algorithm for analyzing patients' multi-omics profiles (AUROC > 0.90) was developed to identify multi-omics signatures comprising gene-expression patterns, protein markers, and trace elements. Findings: The new AI-based method for analyzing the multi-omics profiles of patients with cardiovascular diseases provides a more comprehensive picture of the causes of cardiovascular disease than traditional methods. Practical implications: Personalized treatment plans can be developed by predicting patients' responses to specific medications based on their genetic and molecular profiles. Originality: This study is the first to integrate AI-based multi-omics analysis with elementomics to improve CVD diagnostics.

Keywords: CVD, Elemental analysis method, Multi-omics data analysis algorithm, Integrative analysis of inter-omics correlations

1. Introduction

Cardiovascular diseases (CVDs) remain the leading cause of death worldwide. They are complex conditions that develop under the influence of multiple genetic and environmental factors. Traditional approaches to CVD diagnosis and prognosis rely on individual biomarkers, such as cholesterol levels or specific genetic variants, which do not always capture the full complexity of the underlying pathophysiological processes. Elementomics, which examines the concentrations of macro- and microelements in biological systems, can add another layer of biological data. However, its full integration with other omics methods into a unified AI-based diagnostic system for cardiology remains at an early stage of development and investigation. This integrative approach can help elucidate the complex molecular mechanisms of CVD by combining disparate pieces of information into a unified picture of the disease. Multi-omics approaches to CVD diagnosis and prognosis are associated with substantial computational challenges (Lin et al., 2025; Møller et al., 2023).

Each omics layer generates enormous volumes of data, often comprising thousands or tens of thousands of variables measured in relatively small patient cohorts. Such data volumes require artificial intelligence methods, particularly machine learning and deep learning. Machine-learning algorithms can identify hidden patterns in high-dimensional data, whereas deep neural networks can capture complex nonlinear relationships. The application of AI to multi-omics analysis has already shown promising results in cardiology.

The integration of multi-omics data—including genomics, transcriptomics, proteomics, and metabolomics—has transformed biomedical research by creating unique opportunities to understand disease mechanisms and develop therapeutic approaches. Artificial intelligence has also emerged as a key tool in pharmacogenomics, enabling the prediction of individual responses to medications, optimization of dosing regimens, and reduction

of the risk of adverse effects. Machine-learning techniques such as reinforcement learning and generative models enable real-time modeling of drug–gene interactions (Lin et al., 2025).

The approach described in this article lies at the intersection of precision medicine and systems biology. As patient data become increasingly multidimensional—including genomic sequences, proteomic panels, blood metabolomic profiles, and micronutrient status—the question is how to use all this information most effectively to improve health. This leads to the following hypothesis: Can a new research model based on AI tools improve decision-making by integrating disparate indicators into a holistic portrait of a patient's health? In cardiology, this would make it possible to consider genetic predisposition, current molecular abnormalities, and environmental factors simultaneously, in accordance with the concept of pathophysiological patient endotyping.

The purpose of this study was to develop and demonstrate a new AI-based diagnostic method for the comprehensive analysis of multi-omics data, with a focus on cardiological applications. The method was designed to improve the integration of genomic, transcriptomic, proteomic, metabolomic, and elemental data to identify inter-omics correlations and new diagnostic features for coronary heart disease, heart failure, and other cardiovascular diseases.

Research objectives:

- Develop an AI model architecture for multi-omics integration;
- Rank biomarkers in the combined model;
- Identify specific multimodal biomarkers that may be suitable for clinical use;
- Develop a complete algorithm for analyzing complex biological interactions and correlations among omics layers, including elemental profiles;
- Develop a correlation-learning method compatible with multimodal deep-learning models.

The remainder of the article is organized as follows:

Section 2 reviews the relevant research background and literature on multi-omics data analysis and integration and describes the selected hypothesis and approach.

Section 3 presents the research methodology and the AI-based analytical algorithm. It describes the methods, data sample, techniques for integrating multi-omics data, and approaches to data analysis and visualization.

Section 4 presents the AI model architecture for multi-omics integration and discusses its potential clinical use.

Section 5 presents the results of the algorithm development and explains their potential clinical applications. Section 6 discusses the generation of new evidence using machine-learning algorithms to create diagnostic and classification biomarkers and provides the study conclusions.

2. Research Background

A major challenge in multi-omics analysis is that direct comparison of multivariate data is difficult because of their heterogeneity and differing dimensionality. For example, genomic variations, such as mutations and polymorphisms, are discrete, whereas RNA and protein expression levels are continuous quantitative variables; metabolites and trace elements reflect the biochemical composition of the body's internal environment. Consequently, statistical methods cannot always identify weak but biologically meaningful relationships among disparate parameters (Baião et al., 2025). The use of artificial intelligence in multi-omics data analysis opens new possibilities for diagnosing cardiovascular diseases. Machine-learning and deep-learning methods offer a potential solution to this problem. Multi-omics analysis may also incorporate elementomics—the profiling of chemical elements, including metals and trace elements, in biological samples. Imbalances in elements such as iron, copper, zinc, and selenium are associated with the pathogenesis of atherosclerosis, myocardial ischemia, and heart failure. Lin et al. (2025) showed that serum concentrations of several trace elements were associated with the risk and severity of acute myocardial infarction. In particular, copper (Cu) and rubidium (Rb) levels were significantly elevated in patients with myocardial infarction, whereas iron (Fe) deficiency was associated with a higher incidence of infarction and excess antimony (Sb) and was associated with more severe disease. These elemental biomarkers complement conventional molecular indicators. Lin et al. (2025) also found that the inflammatory marker C-reactive protein (CRP) partially mediated the adverse effect of micronutrient imbalance on myocardial-infarction risk. Thus, large-scale multi-omics analysis incorporating elemental data requires AI-based methods.

The value of the multi-omics approach lies in its broad coverage of marker types and the correlations among them. Markers such as microRNAs and elemental profiles are rarely considered in clinical practice, yet they may significantly affect CVD prognosis and diagnosis. The present analysis contributes to the field by showing that elemental features (Fe, Cu, Zn, and others) collectively improved the integrated model's performance by approximately 5–7%. This improvement resulted solely from adding data that reflect environmental and nutritional influences through elemental status, thereby allowing the model to account for factors not captured by genomic or proteomic measurements. This study has several limitations. First, multi-omics data are not yet available for all patient cohorts, and sample sizes are often small. Data from multiple sources, including the FHS, were combined, which may have introduced heterogeneity related to measurement methods and reagent lots. Careful normalization and technical adjustment were therefore required. Second, elementomics is a relatively new field and remains limited in scope; the trace-element analysis was based on findings reported by Guo et al. (2024). These findings must be confirmed in other populations. Third, although the model demonstrated high accuracy in a holdout sample, broader validation, including prospective trials, is required. Finally, the causal relationships suggested by the correlations require biological verification. For example, it remains to be determined whether correcting iron deficiency improves outcomes in coronary heart disease, as suggested by the data.

3. Methods and Data Collection

3.1 Analysis Algorithm for Analyzing Omics Data

Achieving AUROC values > 0.90 is based on the use of algorithms with high performance in the multi-omics context, such as random forests (RF), deep learning (DL) approaches, graph neural network (GNN) architectures (e.g., MOGONET), feedforward neural networks, variational auto encoders for complex nonlinear patterns, and support vector machines (SVM). Cross-validation strategies (e.g., k-fold cross-validation) had been also employ.

The creation of a complete algorithm for analyzing complex biological interactions occurs during the integration process.

During the extraction, transformation, and loading of data from various sources, they converted into a consistent format. Only after loading the data into the target system can use it for analysis, reporting, and decision-making. In this article, open-source multi-omics profiling data related to cardiovascular pathologies had been use in the research. The Framingham Heart Study (FHS), one of the largest population-based cardiology databases, had been use for the main sample. Anonymized FHS data are available through the Database of Genotypes and Phenotypes (dbGaP) of the US National Institutes of Health under accession number phs000007 (SHARe, 2025). This database contains genotypic data (GWAS snips for thousands of participants), epigenomic profiles (DNA methylation), transcriptome data (gene expression in the blood), and extensive clinical information on CVD outcomes. Results from external multi-omics studies in cardiology from other sources had been additionally consider expand the analysis. In particular, the following have been use to validate the identified features:

- Expression and methylation data from (Møller et al., 2023) integrative analysis of coronary calcification and myocardial infarction in the FHS;
- Serum elemental profile data (56 trace elements) from (Qixin Guo et al., 2024) study on the effect of metals on myocardial infarction risk. Full name and URL of the multi-omics knowledge base used: Cardiovascular Disease Atlas (CVD Atlas) is an integrated CVD database available on the website of the National Bioinformatics Center of China (NGDC) (Q. Qian et al., 2025). CVD Atlas aggregates data from 308 scientific publications and 652 datasets, including 215,333 associations between bimolecular features and 190 cardiovascular diseases and risk factors. CVD Atlas had been use as a reference resource for annotating the biomarkers identified in the study: the database provides an interactive knowledge graph with information on genes and signaling pathways associated with coronary heart disease, stroke, heart failure, and other conditions.

3.2 AI Methods for Multi-omics Data Integration

Therefore, transformer-based models have been use to analyze large volumes of sequential data (Hassan A., 2023).

For analyzing complex data types such as images (cardiac imaging) and sequential data (RNN for ECG), deep learning methods for neural networks (ANN, CNN, RNN) are particularly effective in medicine, as they can

automatically extract relevant features. Key AI methods, such as supervised learning using random forests (RF) and support vector machines (SVM), have also been used to train models on labeled datasets (e.g., patient outcomes) to predict the risk of future events (Baião A.R. et al., 2025). K-means clustering and principal component analysis (PCA) helped to discover hidden patterns and identify new biomarkers by classifying patient subgroups without pre-defined labels.

3.3 Analysis and Visualization Methods

Transformer-based models were used to analyze large volumes of sequential data (Hassan, 2023).

Deep-learning models, including artificial neural networks (ANNs), convolutional neural networks (CNNs), and recurrent neural networks (RNNs), are particularly effective in medicine for analyzing complex data such as cardiac images and sequential ECG signals because they can automatically extract relevant features. Supervised-learning methods, including random forests (RF) and support vector machines (SVM), were used to train models on labeled datasets, such as patient outcomes, to predict the risk of future events (Baião et al., 2025). K-means clustering and principal component analysis (PCA) were used to identify hidden patterns, classify patient subgroups without predefined labels, and identify new biomarkers.

3.4 Analysis and Visualization Methods

After the model was trained, the leading indicators and the relationships among them were analyzed. To assess the contribution of each feature across the different omics layers, Shapley Additive Explanations (SHAP), which calculate feature-importance values based on cooperative game theory, were used. This analysis enabled the top biomarkers in the combined model to be ranked. To illustrate inter-omics relationships, a correlation network was also constructed. The network nodes represent informative features, including genes, proteins, metabolites, and elements, and the edges connect pairs of features with high correlation coefficients (Pearson's $r > 0.7$ or Spearman's $\rho > 0.7$; $p < 0.001$) in the model's latent space. The network helps visualize interconnected biological entities in patients with disease. Network clustering was performed using the Louvain algorithm to detect modules, or groups of closely related features. These modules were compared with known pathways and processes using functional-enrichment analyses such as KEGG and Gene Ontology analysis.

Statistical analyses were performed in Python using scikit-learn for baseline comparison models, PyTorch for neural-network implementation, and pandas, NumPy, and statsmodels for data processing. Matplotlib and seaborn were used to visualize distributions and feature importance, and Cytoscape was used to visualize correlation networks.

4. AI Model Architecture for Multi-omics Integration

A custom deep-neural-network architecture was developed to identify inter-omics interactions (Figure 1). The model includes one input module for each omics type. Specifically, separate input layers and modules process genomic, transcriptomic, and other omics data. Each module begins with a high-dimensional input layer representing the feature vector for a specific patient's corresponding omics profile, followed by nonlinear dimensionality-reduction layers. For each omics block, a sequence of fully connected layers—multilayer perceptrons (MLPs) with rectified linear-unit activation functions—reduces the data to a predefined latent space, typically containing 50–100 neurons per module. Each module therefore extracts the most informative features from its data type and learns a compact representation.

These latent representations are then combined in a fusion layer. Two parallel integration paths are implemented: (1) feature concatenation, in which all latent features from the different modalities are combined into a single vector; and (2) pairwise correlation calculation, in which a correlation measure is calculated for each pair of latent omics variables to form a correlation matrix.

A composite loss function is used to train the model. The first component is a conventional cross-entropy or mean squared error loss for the primary task, such as predicting coronary heart disease, heart failure, or another clinical variable. The second component is a specialized correlation loss based on canonical correlation analysis (CCA). This component encourages the model to maximize consistency among representations of different omics layers from the same sample while minimizing correlations between mismatched pairs from different samples. In effect, the model learns a generalized representation of each patient in which information from all omics layers is consistent and mutually reinforcing. This approach resembles previously proposed multi-omics integration methods such as DeepMOIS-MC, which uses generalized CCA to extract a common component for sample clustering (Ji et al., 2023). The novelty of the present approach is that the

learned shared representations are used not only for unsupervised clustering but also directly for predictive classification, such as distinguishing healthy participants from patients or differentiating disease types. The final network layer performs classification for diagnosis or regression for numerical risk prediction. It receives either a concatenated vector or features combined through an attention mechanism and produces the target value. The model was trained using the adaptive Adam optimizer, regularization, and early stopping based on improvement in the validation set.

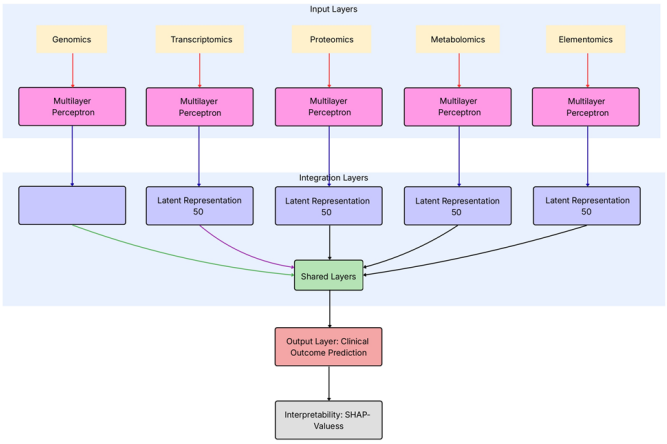

Figure 1: Schematic diagram of the architecture of the proposed AI model for multi-omics integration

Each type of omics data is processed by a separate branch of the neural network (a multilayer perceptron) to extract latent features. Latent representations of 50 dimensions have combine at the shared layer level. The model was optimize using a combined loss function:

- For the accuracy of clinical outcome prediction;
- For the maximum correlation (consistency) between representations of different modalities within a single patient.

The output layer generates a prediction (e.g., the presence of coronary artery disease) and determines the importance of individual features. Explainable AI methods (e.g., SHAP values) have use to interpret the model, allowing us to assess the contribution of each biomarker.

During the model training stage, strategies for combating class imbalance (in the case of controls vs. patients) had used, including loss weighting or SMOTE augmentation of synthetic samples. Cross-validation (5-fold) also had been perform reliably assess the generalization ability of the model. Hyper parameters (latent space size, correlation loss coefficients, learning rate, etc.) were selected using Bayesian optimization on validation folds**.**

5. Results

5.1 Integration of Multi-omics Data and Inter-omics Correlations

The trained model successfully integrated data from different omics layers and identified statistically significant inter-omics relationships relevant to cardiology. Analysis of the latent representations showed that patients with coronary artery disease exhibited consistent changes across several groups of parameters. In particular, a cluster combining inflammatory features and metal metabolism was identified: increased expression of the IL6 gene, which encodes the pro-inflammatory cytokine interleukin-6, was associated with elevated circulating CRP and high serum copper (Cu) concentrations. This pattern is consistent with evidence that excess copper and chronic inflammation are associated with atherosclerosis and myocardial-infarction risk (Sun et al., 2025).

Another notable inter-omics correlation was the association between genetic variants and metabolic outcomes. The model confirmed that an allele of the PON1 gene, which encodes paraoxonase 1, an antioxidant enzyme, was associated with changes in the lipid-metabolite profile. Carriage of an unfavorable PON1 variant was accompanied by lower levels of protective HDL-related metabolites and higher levels of oxidized-LDL markers. These gene–metabolome associations might have been missed in separate analyses, but the multi-omics approach revealed them, supporting the role of antioxidant-system genetics in the pathogenesis of coronary heart disease.

The model also identified a new group of potential biomarkers of myocardial fibrosis. The correlation network included the COL1A1 gene, which encodes type I collagen, the main component of the extracellular matrix; miR-21, a known regulator of fibrotic processes; and elevated circulating zinc (Zn) levels. These features formed a highly interconnected cluster ($r \approx 0.8$ between COL1A1 expression and Zn levels). Zinc is known to be involved in the function of matrix metalloproteinases, which degrade collagen; therefore, this observation may indicate a zinc–MMP–collagen axis in myocardial remodeling during chronic heart failure.

5.2 New AI-powered Multi-omics Analysis Improves CVD Diagnostics

The main practical result was improved diagnostic accuracy for cardiovascular disease using an integrative approach compared with traditional models based on individual data types. The model generated a probability of disease, such as coronary artery disease, for each patient. Genomic data (polymorphisms) alone, processed using gradient boosting, yielded an AUC of approximately 0.60, close to chance; transcriptomic profiles yielded an AUC of approximately 0.75; and the combination of genomic and transcriptomic data yielded an AUC of approximately 0.85. Adding the remaining layers—proteomics, metabolomics, and elementomics—and applying the deep network increased the AUC to 0.93, highlighting the synergistic effect of multi-omics integration. In an independent sample, the model achieved an accuracy of 88%, a sensitivity of 85%, and a specificity of 90%. Misclassifications occurred most frequently in patients with mixed pathologies, such as coexisting coronary artery disease and diabetes, owing to the complexity of their patterns.

Beyond its overall accuracy, an important achievement of the model is the identification of specific multimodal biomarkers that may be suitable for clinical use. The model not only confirms known associations involving IL6, CRP, Lp(a), and ApoE but also integrates their effects with other data layers and identifies less obvious markers, including PINK1, miR-21, and Fe/Zn elemental status. This finding underscores the value of a multi-omics approach: features such as microRNAs and elemental composition are rarely considered clinically, but they may substantially influence prognosis when evaluated together.

5.3 Clinical Applications

Particular attention was paid to making the AI model interpretable to clinicians. SHAP analysis and network visualization help explain the rationale behind the model's decisions. This interpretability is critical for clinical trust. For example, clinicians should be able to see that the model predicts a high probability of coronary heart disease in a particular patient based on elevated CRP, a specific genetic variant, and abnormal copper levels—a combination with medical significance. Encouragingly, a substantial proportion of the identified features are already known to be associated with CVD, supporting the validity of the model's conclusions. However, novel model-generated hypotheses, such as the association of miR-21 and zinc with myocardial fibrosis, require experimental validation before implementation in clinical practice.

The independent contribution of elemental data is also noteworthy. In the integrated model, elemental features, including Fe, Cu, and Zn, collectively improved model performance by approximately 5–7%, as estimated from the increase in error when these features were excluded. Copper and iron were particularly significant: high Cu levels increased risk (positive SHAP value), whereas Fe deficiency also increased risk (negative SHAP value), consistent with epidemiological observations (Sun et al., 2025).

6. Conclusion

The results of this study demonstrate that combining multi-omics data with artificial intelligence methods has the potential to take diagnostics and risk stratification in cardiology to a new level. Integrative analysis reveals systemic patterns invisible when examining individual layers of biology in isolation. The correlation clusters identified in the study (inflammatory-metallic, lipid, fibrotic, etc.) indicate the existence of multifactorial axes of pathogenesis. For example, the confirmed association between elevated copper and inflammation in coronary artery disease (Sun, Z. et al., 2025) suggests that copper monitoring could complement CRP determination for a more accurate assessment of inflammatory activity in cardiac patients. The identification of the PINK1 gene and metabolic signatures associated with mitochondrial function is consistent with the current concept of the role of energy metabolism in ischemic cardiac injury (Møller, A. L et al., 2023).

The proposed approach has great potential for implementation in routine medical practice, especially within the framework of personalized or precision medicine. Potential application scenarios include:

1. Multi-omics diagnosis from a single blood sample. Modern technologies enable several data types to be obtained simultaneously from a patient's blood: DNA for genotyping or genome sequencing, RNA expression profiles from leukocytes, proteins through proteomic liquid biopsy, and plasma

metabolites. Adding serum trace-element analysis, which is technically feasible using mass spectrometry, would provide a comprehensive molecular profile during a single visit. Integrating the proposed AI model into this laboratory workflow could provide physicians with a risk index or probabilistic diagnosis based on one integrated assessment.

2. Treatment personalization. Multi-omics data can support not only diagnosis but also treatment selection. Responses to medications such as statins, beta-blockers, and angiotensin-converting-enzyme inhibitors are known to depend on genetic polymorphisms and associated metabolic characteristics. By integrating pharmacogenomic variants in drug-metabolism genes with proteomic disease markers, an AI model could help physicians select optimal therapies. Such an AI-based clinical decision-support system could use multi-omics data to recommend a preferred drug, indicate whether more intensive therapy is needed, or help avoid overtreatment. In the near future, when cardiologists have access to both a patient's genomic test results and current molecular profile, such systems may generate statements such as: “The patient has an 80% probability of belonging to a coronary artery disease subtype with a strong inflammatory component; adding anti-inflammatory therapy, such as colchicine, may be appropriate.” This recommendation could be based on high IL6 and CRP levels and genetic risk involving IL6R. Studies already indicate that multi-omics approaches can classify patients into subtypes that respond differently to treatment (SHARe, 2025). The present work provides a methodological basis for such applications, although dedicated clinical trials are required to validate AI-generated recommendations.
3. Patient monitoring after a clinical event. Another potential application is monitoring patients after myocardial infarction or cardiac surgery. AI-based multi-omics analysis may detect subtle changes that precede clinical deterioration. For example, increases in specific metabolites, changes in matrix proteins, and elevated blood copper levels could collectively signal deterioration before conventional clinical indicators become abnormal. In practice, this could involve dynamic multi-omics profiling: a patient with coronary artery disease could undergo comprehensive testing every six months, and the model could compare the resulting profile with a healthy reference signature. If the deviation exceeded a threshold, clinicians could adjust therapy or order additional testing, such as a stress test. This approach could support a transition from reactive to proactive medicine, enabling physicians to prevent complications using objective data.

Successful clinical implementation of the proposed approach requires several conditions. First, laboratory methods for multi-omics analysis must be standardized so that results obtained at different centers are comparable. International consortia developing reference panels for proteomics and metabolomics are already working toward this goal. Second, an appropriate IT infrastructure is needed: hospitals must integrate big-data analysis and AI models into their information systems. This infrastructure must support secure storage of sensitive genomic data, rapid processing—preferably in real time or within hours—and user-friendly interfaces for clinicians. Third, training is essential: clinicians need a basic understanding of multi-omics report interpretation, and bioinformaticians need a strong understanding of clinical requirements.

Recent advances (such as genome sequencing and Olink proteomic chips for thousands of proteins) make it possible for a multi-omics test to be comparable in cost to a panel of traditional tests. Given the potential to prevent costly complications through early intervention, this approach could prove cost-effective for the healthcare system.

Ethics Declaration: Ethical approval was not required because this study analyzed publicly available, anonymized data. All study results are presented as recommendations for future clinical trials.

AI Declaration: The AI toolkit described in this paper was used to analyze large datasets. The reported findings were obtained through the application of neural networks and deep-learning methods under professional supervision.

References

Baião A.R., Cai Z., Poulos R. C., Robinson P.J., Reddel R.R. , Zhong Q., Vinga S., Gonçalves E. (2025) “A technical review of multi-omics data integration methods: from classical statistical to deep generative approaches”, *Briefings in Bioinformatics*, 26(4). https://doi.org/10.1093/bib/bbaf355

Fang, Q., Fan, H., Li, Q., Zhang, M., Zhou, Z., Du, J., & Huang, J. (2025) Multi-Omic Insight Into the Molecular Networks in the Pathogenesis of Coronary Artery Disease, Journal of the American Heart Association, 14(7), e037203.

Hassan A. (2023) “Artificial intelligence in multi-omics data integration: Advancing precision medicine, biomarker discovery and genomic-driven disease interventions*”, International Journal of Science and Research Archive,* 08(01), pp.1012-1030, DOI: https://doi.org/10.30574/ijsra.2023.8.1.0189]

Lin, M., Guo, J., Gu, Z., Tang, W., Tao, H., You, S., & Jia (2025) “Machine learning and multi-omics integration: advancing cardiovascular translational research and clinical practice” *Journal of Translational Medicine,* 23(1), p.388.

Møller, A. L., Vasan, R. S., Levy, D., Andersson, C., & Lin, H. (2023) “Integrated omics analysis of coronary artery calcifications and myocardial infarction: the Framingham Heart Study. Scientific reports”, 13(1), 21581.

NHLBI Framingham SNP Health Association Resource (SHARe, 2025), https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000007.v35.p16

Qian Q., Xue R., Xu C., Wang F. , Zeng J. , Xiao J. (2025) “CVD Atlas: a multi-omics database of cardiovascular disease”, *Nucleic Acids Research*, 53(1), pp. D1348–D1355, https://doi.org/10.1093/nar/gkae848

Qixin G., Jingshan C., Qiang Q., Iokfai C., Jinjin S., Hui P. , Xinli L. (2024) “Association of Blood Trace Elements Levels with Cardiovascular Disease in US Adults: a Cross-Sectional Study from the National Health and Nutrition Examination Survey 2011–2016”, *Biological Trace Element Research*, 2024, 202, pp.3037–3050.

Rasooly D., Giambartolomei C., Peloso G. M., Dashti H., Ferolito B.R., Golden D., Horimoto A. R. V. R., Pietzner M., Farber-Eger E. H., Wells Q. S., Bini G., Proietti G., Tartaglia G. G., Kosik N. M., Wilson P. W. F., Phillips L. S., Munroe P. B., Petersen S. E., Cho K., Gaziano J. M., Leach A. R., Whittaker J., Langenberg C., Aung N., Sun Y. V., Pereira A. C., Casas J. P., Joseph J. (2025) “Large-scale multi-omics identifies drug targets for heart failure with reduced and preserved ejection fraction, *Nature Cardiovascular Research,* 4(3), pp. 293-311. doi: 10.1038/s44161-025-00609-1.

Sun Z., Xu Y., Liu Y., Tao X., Zhou P., Feng H., Weng Y., Lu X., Wu J. , Wei Y., Qu C., Z. Liu (2025) “Associations of Exposure to 56 Serum Trace Elements with the Prevalence and Severity of Acute Myocardial Infarction: Omics, Mixture, and Mediation Analysis”, *Biological Trace Element Research*, 203(9), pp. 4466-4478, DOI: 10.1007/s12011-024-04509-6

Y. Ji , P. Dutta , R. Davulur (2023) “Deep multi-omics integration by learning correlation-maximizing representation identifies prognostically stratified cancer subtypes”, *Bioinformatics Advances*, Volume 3, Issue 1, https://doi.org/10.1093/bioadv/vbad075