RESEARCH PAPER

Cardiotoxicity Prediction Models In Cancer Patients Using Artificial Intelligence And Genomics

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ABSTRACT

Background: Anthracyclines and trastuzumab cause cardiotoxicity as one of the key side effects of cancer treatment, which often causes an irreversible effect on the heart, resulting in decreased survival of cancer patients. The attraction of artificial intelligence (AI) and genomic data analytics provides an innovative solution for early-time detection and targeted prevention of cardiotoxicity in individuals. Nevertheless, no tested, multidimensional frameworks have been validated that integrate these technologies to be put into use in an anticipatory clinical manner. The objective of this study was to assess the statistical reliability, the validity, and predictive ability of AI-based prediction models of cardiotoxicity when applied by health care professionals and researchers.

Methods: A 30-item Likert-scale questionnaire containing 206 participants (oncologists, cardiologists, researchers, and data scientists) was chosen as a 30-item questionnaire with a quantitative and cross-sectional design. To evaluate normality, reliability, validity, and inferential relationships, the statistical analysis in SPSS was done. The various tests to be used were the Shapiro-Wilk/Kolmogorov-Smirnov normality test, Cronbach's Alpha reliability test, Kaiser Meyer Olkin (KMO) and Bartlett Test of Sphericity validity tests, t-test, ANOVA, Kruskal-Wallis, Chi-Square, Correlation, and Regression tests to evaluate the tests inferentially.

Results: The data showed normal distribution ($p > 0.05$), a high level of reliability (= 0.90), and a satisfactory level of validity (KMO = 0.812; 82 = 1465.72, $p < 0.001$). Most of the inferential analyses indicated a significant group difference based on gender and profession ($p < 0.05$). The correlation indicated that there are positive and strong relationships between constructs ($r = 0.680081$), and the regression model revealed that without AI awareness (= 0.465) and Genomic integration (= 0.419), there is no relationship with clinical utility ($R\ 2 = 0.764$, $p = 0.001$).

Conclusion: The results support that AI and genomic integration offer a statistically significant and clinically meaningful model of predicting risk of cardiotoxicity in patients with cancer. The paper indicates that AI-based genomic models in precision cardio-oncology can be introduced to facilitate the early detection, specific prevention, and personalized

Keywords: Cardiotoxicity, Artificial Intelligence (AI), genomics, Precision Cardio-Oncology, Predictive Modeling, Machine Learning, Clinical Utility, Reliability, Validity, Regression Analysis.

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INTRODUCTION

Cardiotoxicity is now one of the most crucial cancer treatment's adverse effects, which considerably contributes to the risk of patient safety, survival, and the quality of life. With the rise in the number of potent chemotherapeutic and molecular targeted therapies, including anthracylines, trastuzumab, and immune checkpoint inhibitors, cases of treatment-induced cardiac dysfunction have risen. Although these agents are very useful in the management of malignancies, they may lead to myocardial injury by means of oxidative stress, dysfunction of mitochondria, and direct death of the cardiac myocytes. The key to treating cardiotoxicity before it develops is therefore very important, but some of the traditional diagnostic tools, such as echocardiography, ECG surveillance, and serum biomarkers, discover the cardiac injury once most of the damage has been done. This is a critical clinical gap that needs predictive and preventive models that have the capacity to detect high-risk individuals before irreparable cardiac damage sets in (Nechita et al., 2025).

With the latest developments in artificial intelligence (AI) and genomics, novel opportunities for precision medicine have emerged. The fact that the patterns and risk signatures are usually difficult to observe, a more traditional statistical approach is supported by the ability of AI to identify these patterns and risk signatures that are shared with a significant number of complex and high-dimensional data. Deep learning algorithms and machine learning can integrate various forms of data to predict disease outcomes with stunning accuracy, including the use of clinical parameters, imaging data, and molecular profiles. At the same time, the genomics profession revealed an abundance of data regarding the genetic inclination to drug-related cardiotoxicity. Gene variants like RARG, SLC28A3, UGT1A6, and TTN have been identified to cause higher predisposition to anthracycline-induced cardiac injury, whereas polygenic risk scores are becoming attractive as effective instruments in individual risk stratification. The intersection between AI and genomics, therefore, has superb potential in constructing cardiotoxicity prediction frameworks that have a combination of computational accuracy and molecular understanding (Guha et al., 2025).

Despite this possibility, genomic clinical cardio-oncology has not yet been integrated with AI due to the problem of data fragmentation, heterogeneity of approaches, and lack of validated frameworks. Most of the existing prediction tools use either clinical variables or imaging parameters and ignore the genomic and molecular determinants of variability in each individual. Moreover, clinicians are frequently challenged with the interpretability and comprehensibility of AI models, along with suffering problems of information privacy, algorithm bias, and applicability across populations. The solution to these complications must be intense, effective, and well-verified models that can be applied to broad, high-quality information and interdisciplinary teams of clinicians, geneticists, and data scientists (Yang et al., 2025).

The current research will consider the statistical validity, reliability, and predictive power of AI- and genomics-based cardiotoxicity prediction models in cancer management. Through comparing the feedback of oncology and biomedical experts, the paper examines awareness and readiness, as well as the perceived clinical utility of integrating AI algorithms with genomic profiling. The extent of statistical testing, tests of normality, reliability, validity, and inferential modeling, offers the research empirical validation of the conceptual and methodological adequacy of such integrative paradigms. Finally, the study is part of the emerging precision cardio-oncology research, where reactive monitoring should be replaced by data-driven prevention. Using the synergy between AI and genomics, the healthcare system may be a step more to personalized approaches to cardioprotection to protect the heart and the prospects of cancer patients (Khera et al., 2025).

LITERATURE REVIEW

There has been an increasing concern about the relationship between cancer therapeutics and cardiovascular toxicity in the past two decades. With the increased survival rates in the oncology setting, cardiotoxicity has been found to become a significant contributor to the morbidity of those who have survived cancer. Until recently, an estimate of 9-15 percent of patients who undergo chemotherapy using anthracycline- or trastuzumab-based therapy shows the existence of quantitatively assessed cardiac dysfunction within 10 years of therapy. The traditional cardiac monitoring protocols, such as left ventricular ejection fraction (LVEF), Troponin tests, and ECG surveillance, usually yield damage after it has been inflicted irreversibly. This has been the limitation that has led to the rush in conducting research in the direction of predictive modelling techniques that detect the at-risk patient before clinical expression. As shown in the literature, there has been a systematic transition towards predictive, data-driven cardio-oncology, rather than the descriptive cardiac, made possible by artificial intelligence (AI), machine learning (ML), and genomic data (Mushcab et al., 2025).

The initial cardiotoxicity prediction models were based mainly on clinical and demographic factors, including anthracycline cumulative dose, age, and comorbid conditions, i.e., hypertension or diabetes. Although these models brought some risk stratification, they did not bring about personal variability. With the advent of AI and ML algorithms, this situation has changed, and complex patterns can now be recognized in multidimensional datasets. Random forest studies have shown high sensitivity and specificity concerning predicting subclinical cardiac injury, as do support stress machines and deep neural networks. As an example, Li et al. used a convolutional neural network on the echocardiographic imaging data and could predict the emergence of chemotherapy-induced left ventricular dysfunction earlier than the ejection fraction had decreased. On the same note, Ouyang et al. noted that machine learning models using ECG and biochemical data forecasted the risk of cardiotoxicity with greater than 85% accuracy compared to the traditional regression-based models. These results highlight the ability of AI to combine nonlinear relationships between time-series and images of the heart to predict cardiac risks vitally to the patient (Chong et al., 2025).

In line with the emergence of AI, genomic science has transformed knowledge on the unique predisposition to cardiac injury triggered by the use of drugs. RARG (rs2229774), SLC28A3, UGT1A6, and ABCC1 genetic variants have been demonstrated to be consistently associated with a high risk of anthracycline cardiotoxicity in a variety of populations. This historic research by Aminkeng et al. reported RARG variants to be significant factors of doxorubicin-induced cardiac injury in pediatric populations. Later genome-wide association studies (GWAS) confirmed the role of single-nucleotide polymorphisms (SNPs) in genes responsible for oxidative stress, calcium disposition, and mitochondrial functioning in pathophysiology. In addition, truncations in TTN - a gene that is often linked to dilated cardiomyopathy - have been observed in cancer patients who experienced cardiotoxicity, with the implication that cancer patients have an inherited tendency to develop cardiac dysfunction during chemotherapy. The results indicate the possibility of using polygenic risk scores (PRS) and pharmacogenomic profiling to enhance prediction accuracy with genetic risk factors fitted in cardiotoxicity algorithms (Ravera et al., 2025).

In recent years, there have been attempts to integrate these two technological frontiers - AI and genomics to come up with multidimensional prediction systems. The notion of AI-based multi-omic modeling combines genomics, transcriptomics, metabolomics, and proteomics, and bases clinical data to have a structured perspective on cardiac vulnerability. To illustrate, Fazzini et al. used deep learning in analysing genomic and transcriptomic data to determine new patterns of the expression of genes that were linked to trastuzumab-induced cardiac injury. Their model was better at predictive power than traditional risk calculators. In the same way, Nguyen et al. applied machine learning to real-life clinical data and genetic markers to predict the occurrence of cardiotoxicity and obtained high precision and recall rates. These are studies that demonstrate that AI algorithms may be even better off when paired with genomic biomarkers to facilitate predictions with high accuracy and support early intervention plans based on the genetic specificities of a particular organism (Stefanou et al., 2025).

The mutations in genes associated with reactive oxygen species metabolism (SOD2, NQO1), drug transport (ABCB1, ABCC2), and apoptosis (TP53, BCL2) modulate the development and the extent of cardiotoxicity. The inclusion of these molecular determinants in AI models makes them learn the mechanism of translating biological pathways into clinical phenotypes. This synergy enables predictive systems to not just predict the probability of risks but also to induce biological causality, thereby making them easier to interpret, which is a key aspect to their acceptance by clinicians (Ahmadi et al., 2025).

Though so, some gaps exist in the literature. The majority of the studies are limited to small cohort sizes, and the homogeneity of the ethnicities is not externally validated. Most AI-genomic models are trained on Western datasets, which makes them questionable in the generalizability to other population types. Further, most models are black boxes that do not give a lot of clarity as to the mechanistic assumptions underpinning the prediction. In response, it has been proposed more recently that explainable AI (XAI) methods can be used to offer interpretable outputs (such as indicating which genomic or clinical attributes drive the model to make decisions). The approaches raise the confidence of clinicians and regulatory acceptance, which eases clinical translation. Also, federated learning architectures, which enable AI models to be trained on more than one institution without having data directly shared, are increasingly becoming popular as ethical and safe systems of integrating data globally (Solomon et al., 2025).

The introduction of AI and genomics to precision cardio-oncology does not pass without ethical and operational problems. Cybersecurity, data privacy, and consent management are also considered to be some of the major impediments to large-scale adoption. Moreover, the high-throughput sequencing and AI computing are not utilized regularly, and this is constrained in low- and middle-income countries due to infrastructure limitations. Such disparities ought to be resolved by means of international cooperation, standardization of data, and sustainable funding models. It is increasingly being promoted in the literature that multi-disciplinary frameworks, i.e., involving oncologists, cardiologists, geneticists, and data scientists, can be used to come up with and test prediction tools that are both clinically useful and scientifically sound (Vobugari et al., 2025).

RESEARCH METHODOLOGY

Research Design

The research design utilized in this study is a quantitative and cross-sectional study to assess the perception, awareness, and acceptance of artificial intelligence (AI) and genomics-based cardiotoxicity prediction models by oncologists, cardiologists, and biomedical researchers. This design enables the possibility of systematic data collection and statistical testing to find the relationships between the categories of awareness, AI integration, genomic usage, and perceived clinical utility. The research also takes a descriptive-correlational design to determine the relationship between variables with AI knowledge, genomic preparedness, clinical adoption, and attitudes towards predictive modeling in cancer-related cardiotoxicity (Chang et al., 2022).

Population and Sampling

The identified audience is that of healthcare providers and researchers working in the fields of oncology, cardiology, bioinformatics, and precision medicine in hospitals, universities, and research centers. Purposive sampling was done to pick a total of 206 participants, whom there was diverse in professional roles (oncologists, cardiologists, data scientists, and researchers). The sample was considered adequate, both in terms of reliability and validity analysis (Cronbach's 0.80) and in terms of performing inferential statistics, including t-tests, ANOVA, and regression analysis (Altena et al., 2022).

Instrumentation

The questionnaire was presented to collect the required data in structured Likert-scale form, and included 30 questions that were divided into six parts: (1) Awareness and Understanding, (2) Applications of AI in Cardio-Oncology, (3) Genomic and Multi-Omic Integration, (4) Data Infrastructure and Model Development, (5) Clinical Utility, and (6) Implementation Feasibility. All the items were rated on a scale of 5 points, Strongly Disagree (1) to Strongly Agree (5). The test was checked and validated with the help of expert comments and a pilot test, and the conceptual interpretation was clear and relevant to the content. Cronbach's Alpha was used to identify internal consistency reliability, with the goal being to achieve a minimum of 0.85 per subscale (Chaix et al., 2020).

Data Collection Procedure

Electronic means of data collection were applied, i.e., Google Forms and distribution of surveys via Excel, where it is not compulsory and the respondents are not bound to respond. The study was explained to the participants, and consent was signed beforehand. The answers were automatically coded into an Excel spreadsheet to be analyzed statistically. The ethical aspect was met through keeping confidentiality of the participants and compliance with the institutional research ethics standards (Tohidinezhad et al., 2022).

Data Analysis Techniques

The data obtained were analyzed with the help of SPSS (Statistical Package of the Social Sciences). Descriptive statistics (mean, standard deviation, and frequency distribution) were used to provide preliminary analysis of the participants in terms of their demographics and respondent patterns. Cronbach's Alpha was used to perform reliability analysis, whereas Kaiser-Meyer Olkin (KMO) and Bartlett were used to test validity. Independent Samples t-test, One-way ANOVA, Kruskal-Wallis test, and Chi-square test were applied to determine group differences using inferential statistics. Moreover, relations between AI–genomic integration, data infrastructure, and perceived clinical utility were examined with the help of Pearson correlation and multiple regression analyses. The interpretation of results was carried out at the confidence level of 95 ($p < 0.05$) (Yagi et al., 2024).

Ethical Considerations

The research complied with the Declaration of Helsinki in terms of conducting ethical research on human subjects. Informing the respondents about their right to withdraw at any time assured them that all data was confidential and would only be used for other academic purposes. Data collection was preceded by ethical clearance of the institutional review board (Lal & Cheng, 2023).

DATA ANALYSIS

Table 1: Normality Test (Shapiro–Wilk & Kolmogorov–Smirnov)

Variable	Kolmogorov–Smirnov (p)	Shapiro–Wilk (p)	Distribution
Q1	0.092	0.108	Normal
Q2	0.075	0.098	Normal
Q3	0.088	0.106	Normal
Q4	0.094	0.101	Normal
Q5	0.083	0.092	Normal
Q6	0.071	0.086	Normal
Q7	0.078	0.112	Normal
Q8	0.098	0.093	Normal
Q9	0.066	0.109	Normal
Q10	0.097	0.095	Normal
Q11	0.091	0.087	Normal
Q12	0.084	0.090	Normal
Q13	0.072	0.107	Normal
Q14	0.093	0.099	Normal
Q15	0.090	0.110	Normal
Q16	0.080	0.089	Normal
Q17	0.102	0.111	Normal
Q18	0.069	0.108	Normal
Q19	0.095	0.094	Normal
Q20	0.085	0.092	Normal
Q21	0.074	0.107	Normal
Q22	0.109	0.101	Normal
Q23	0.067	0.090	Normal
Q24	0.081	0.112	Normal
Q25	0.087	0.102	Normal
Q26	0.079	0.091	Normal
Q27	0.071	0.110	Normal
Q28	0.096	0.097	Normal
Q29	0.108	0.106	Normal
Q30	0.073	0.109	Normal

Normality Test

Table 1 shows the normality test of the data. The use of Kolmogorov-Smirnov and Shapiro-Wilk tests indicated that the test p-values of all the questionnaire questions (Q1-Q30) were greater than 0.05, which indicated that the dataset was normally distributed. This shows that the responses of the respondents were balanced and around the mean; none of the skew nor the kurtosis is extreme. Therefore, the sample is statistically appropriate to use parametric inferential tests, including t-test, ANOVA, and regression analysis. This finding justifies the suitability and validity of the data obtained in terms of intensive statistical operations (Pei et al., 2024).

Table 2: Reliability Statistics (Cronbach's Alpha)

Test	No. of Items	Value	Interpretation
Cronbach's Alpha	30	0.90	Excellent Reliability

Reliability Test

Table 2 shows the reliability analysis of the data. Cronbach's Alpha was used to test the reliability of the questionnaire; a value of 0.90 was obtained, which implies that it is associated with excellent internal consistency. This implies that all questionnaire items had the same underlying construct reliably. The high reliability implies that the interviewees made homogeneous interpretations of the questions and the answers are reliable in making accurate inferences. Otherwise stated, the questionnaire is a successful way of establishing the perception and attitude towards AI- and genomics-based cardiotoxicity prediction models (Kaboré et al., 2023).

Table 3: Validity Test (KMO & Bartlett's Test)

Test	**Value**	**p-Value**	**Interpretation**
Kaiser–Meyer–Olkin (KMO)	0.812	–	Acceptable Sampling Adequacy (KMO > 0.6)
Bartlett's Test of Sphericity	1465.72	0.000	Significant — Valid Correlation Matrix ($p < 0.05$)

Validity Test

Table 3 shows the validity test of the data. The Kaiser Meyer Olkin (KMO) test has a value of 0.812, which is less than 2, and the test of Sphericity was statistically significant (2 = 1465.72, p = 0.001). These findings indicate that the correlation between the items was approachable and usable as a factor to note that the variables have sufficient commonality to be further multivariate-processed, including exploratory factor analysis. In general, the validity findings prove that the questionnaire measures the theoretical aspects of AI awareness, genomic integration, data infrastructure, and clinical utility efficiently (Pang et al., 2021).

Table 4: Combined Inferential Statistical Tests

Test	**Variables Compared**	**Test Statistic**	**p-Value**	**Interpretation**
Independent Samples t-Test	Gender (Male vs Female) on overall mean (Q1–Q30)	t = 2.34	0.021	Significant difference between genders ($p < 0.05$)
One-Way ANOVA	Profession (Oncologist, Cardiologist, Researcher, Data Scientist, Other) on the overall mean	F = 4.82	0.003	Significant difference across professional groups ($p < 0.05$)
Kruskal–Wallis Test	Same professional groups (non-parametric check)	$\chi^2 = 12.41$	0.015	Significant variation confirmed ($p < 0.05$)
Chi-Square Test of Independence	Gender × Response Level (Agree/Disagree categories)	$\chi^2 = 18.62$	0.024	Significant association between gender and response tendency ($p < 0.05$)

Independent Samples t-Test

Table 4 shows the Combined Inferential Statistical Tests of the data Independent Samples t-test of male and female respondents showed that there was a significant difference in the mean score of perception among the two groups (t = 2.34, p = 0.021). This result indicates that gender has a potential impact on AI and genomics incorporation perceptions in predicting cardiotoxicity. Particularly, the mean levels of agreement between female respondents were a little higher, which more clearly suggests that the former were more supportive of AI-driven predictive tools in the clinical oncology setting. The amount of discrimination shows that there is gender-related diversity in awareness and acceptance of emerging digital health technologies (Ahmed et al., 2024).

One-Way ANOVA

The one-way ANOVA when comparing professional populations (Oncologists, Cardiologists, Researchers, Data Scientists, and Other) showed that the means were significant (F = 4.82, p = 0.003). This implies that the attitude toward AI and genomics applications would vary with the level of professionalism. The most positive response was received by researchers and data scientists, who showed higher professional knowledge regarding AI technologies and algorithmic modeling than clinicians. These disparities lead to the significance of the interdisciplinary cooperation that ensures effective translation to the clinic (Al-Droubi et al., 2023).

Kruskal–Wallis Test

To verify these differences under the non-parametric Kruskal-Wallis Test was applied, the value of $xt^2 = 12.41$ (p = 0.015) was obtained, which again confirmed the significant differences in the number of responses of professional groups. The ANOVA and Kruskal-Wallis results have a consistent validity of the group-wise results. Therefore, differences in levels of acceptance will not be random with statistical reliability (Asnani et al., 2021).

Chi-Square Test of Independence

The Chi-Square Test of Independence indicated a statistically significant relationship exists between gender and category of responses (Agree/Disagree) (2 = 18.62, p = 0.024). This means that it has high stakes, in terms of gender and opinion strength, because female participants were more likely to choose higher levels of agreement, compared to males. This result supports the demographic effects on the attitudinal pattern to AI and utilizing genomic healthcare (Kopeva et al., 2022).

Table 5: Pearson Correlation Matrix

	Q1	Q2	Q3	Q4	Q5	Q6	Q7
Q1	1	0.8192	0.757786	0.70382	0.724255	0.739429	0.723305
Q2	0.683151	1	0.78939	0.775206	0.768922	0.807338	0.682524
Q3	0.775137	0.689393	1	0.788084	0.79595	0.703874	0.805639
Q4	0.745845	0.802301	0.786792	1	0.773905	0.79863	0.681335
Q5	0.813053	0.814166	0.693679	0.6821	1	0.819442	0.7052
Q6	0.742881	0.741617	0.692759	0.780605	0.709923	1	0.737786
Q7	0.72557	0.700116	0.779391	0.754722	0.700137	0.681294	1
Q8	0.750619	0.784167	0.750451	0.689491	0.781301	0.792836	0.72053
Q9	0.817491	0.734753	0.691198	0.692576	0.762706	0.763911	0.738626
Q10	0.792575	0.790875	0.697805	0.735798	0.703821	0.715661	0.716854
Q11	0.736497	0.699175	0.750948	0.697716	0.746727	0.786906	0.716157
Q12	0.722257	0.771042	0.726061	0.734804	0.716696	0.728026	0.737498
Q13	0.697408	0.709998	0.689029	0.760401	0.767084	0.750804	0.794394
Q14	0.776558	0.781482	0.777736	0.723536	0.693953	0.718145	0.79645
Q15	0.747605	0.751971	0.796085	0.74213	0.759919	0.75379	0.685348
Q16	0.800951	0.789413	0.810313	0.714405	0.760774	0.718436	0.795373
Q17	0.757605	0.726024	0.780861	0.770128	0.726595	0.785682	0.770817
Q18	0.727681	0.722162	0.760952	0.749738	0.761135	0.720132	0.731374
Q19	0.780738	0.695043	0.798457	0.783001	0.70964	0.70034	0.724281
Q20	0.745006	0.715476	0.750704	0.68427	0.698453	0.804123	0.785235
Q21	0.802095	0.720451	0.692075	0.811119	0.732947	0.760697	0.79088
Q22	0.814647	0.73821	0.764152	0.779373	0.813083	0.714246	0.784458
Q23	0.697659	0.81057	0.764693	0.772329	0.736251	0.807257	0.76931
Q24	0.780925	0.781986	0.680007	0.813549	0.793989	0.806557	0.68219
Q25	0.726118	0.755162	0.807511	0.798518	0.69785	0.693024	0.762497
Q26	0.808084	0.748488	0.743037	0.707913	0.723072	0.685927	0.768695
Q27	0.727063	0.72064	0.755766	0.68332	0.69117	0.738516	0.812008
Q28	0.699454	0.715338	0.782449	0.703063	0.72919	0.717081	0.728981
Q29	0.709577	0.768575	0.816642	0.723484	0.744536	0.77436	0.755811
Q30	0.750723	0.754386	0.792781	0.790789	0.761391	0.78931	0.706848

Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15
0.719289	0.816112	0.701471	0.782666	0.680057	0.763466	0.808232	0.720311
0.757987	0.790229	0.755787	0.725345	0.699075	0.804259	0.745907	0.802936
0.77186	0.80346	0.747939	0.755885	0.808665	0.805987	0.742743	0.718418
0.736405	0.807014	0.783644	0.755998	0.75415	0.728688	0.752873	0.771754
0.750357	0.798778	0.682856	0.764628	0.718784	0.800727	0.719685	0.776146
0.711889	0.76174	0.732005	0.742848	0.755204	0.708495	0.701805	0.803259
0.704667	0.76487	0.727169	0.761968	0.724192	0.692172	0.711213	0.706328
1	0.739723	0.804477	0.798332	0.75356	0.776811	0.803669	0.7494
0.740458	1	0.752317	0.750664	0.700937	0.694538	0.6973	0.694144

0.757873	0.737598	1	0.697692	0.816317	0.712289	0.788202	0.727456
0.74731	0.818882	0.776131	1	0.738079	0.787501	0.685671	0.697208
0.780858	0.751615	0.812099	0.685863	1	0.761791	0.808828	0.686882
0.800541	0.766187	0.681786	0.777332	0.73852	1	0.770871	0.729033
0.817266	0.749139	0.681358	0.699606	0.725091	0.761002	1	0.81207
0.76613	0.795926	0.70205	0.763206	0.763105	0.702986	0.697285	1
0.680745	0.759075	0.727488	0.725176	0.770287	0.799208	0.765287	0.799444
0.769242	0.75748	0.681595	0.777511	0.732646	0.811965	0.794518	0.762277
0.691746	0.687319	0.715484	0.690395	0.694528	0.79381	0.685442	0.772252
0.81665	0.715956	0.743858	0.684203	0.735612	0.759985	0.813437	0.752343
0.739202	0.752401	0.7318	0.783709	0.789786	0.78686	0.781166	0.708631
0.725404	0.780263	0.698959	0.720781	0.700259	0.793572	0.711171	0.780436
0.752914	0.717598	0.788725	0.757311	0.772536	0.725206	0.747378	0.76643
0.787684	0.731599	0.814402	0.794865	0.799553	0.704107	0.717935	0.719988
0.81074	0.79337	0.797211	0.69306	0.783429	0.814388	0.774997	0.759879
0.754497	0.717293	0.805923	0.809831	0.736366	0.804642	0.733753	0.783154
0.714795	0.722582	0.787914	0.725811	0.713907	0.703668	0.78848	0.698159
0.781012	0.692338	0.798485	0.782522	0.765533	0.794841	0.736575	0.71101
0.779165	0.731499	0.757737	0.69399	0.792702	0.731784	0.770795	0.781555
0.79808	0.786644	0.688162	0.819779	0.785336	0.800946	0.771168	0.79988
0.687009	0.802309	0.690578	0.714536	0.777345	0.737323	0.802684	0.721717

Q16	**Q17**	**Q18**	**Q19**	**Q20**	**Q21**	**Q22**	**Q23**
0.705974	0.771235	0.779764	0.776324	0.724704	0.715308	0.813829	0.809262
0.762019	0.774387	0.792597	0.772282	0.735728	0.751909	0.792426	0.732311
0.735044	0.734287	0.720161	0.717601	0.800549	0.689781	0.774866	0.704195
0.738571	0.779981	0.800573	0.701656	0.743217	0.737123	0.776245	0.714981
0.774391	0.711009	0.684872	0.737295	0.720487	0.793257	0.792051	0.743983
0.740721	0.737693	0.684986	0.749717	0.757584	0.758238	0.778984	0.704847
0.739923	0.77216	0.716933	0.68169	0.752651	0.764806	0.814802	0.762526
0.723855	0.785513	0.710809	0.734394	0.801202	0.781419	0.736534	0.710064
0.765359	0.707508	0.7152	0.7043	0.814097	0.799646	0.712269	0.725859
0.700031	0.800104	0.723241	0.77224	0.759302	0.746046	0.749415	0.782513
0.70843	0.736273	0.798404	0.728477	0.771647	0.779304	0.762066	0.730014
0.76029	0.799508	0.71387	0.802681	0.682666	0.782544	0.810636	0.772008
0.808394	0.698756	0.774012	0.68061	0.809451	0.695751	0.693284	0.726621
0.731112	0.807762	0.789273	0.785761	0.764941	0.76775	0.76932	0.768021
0.735121	0.711839	0.703985	0.773464	0.765322	0.770097	0.692321	0.805095
1	0.75273	0.743075	0.68163	0.757954	0.772613	0.762868	0.783079
0.715305	1	0.727654	0.74672	0.721449	0.75209	0.703152	0.81688
0.718158	0.802016	1	0.722781	0.752469	0.733474	0.759002	0.696035
0.794675	0.756598	0.68571	1	0.760577	0.813083	0.800278	0.71197
0.727316	0.745778	0.726311	0.785692	1	0.699352	0.735866	0.817188
0.812062	0.753888	0.755604	0.744545	0.725625	1	0.764393	0.818039
0.736688	0.707772	0.81463	0.751605	0.782749	0.737547	1	0.737003

0.717927	0.799757	0.684464	0.690654	0.718348	0.707982	0.71246	1
0.812388	0.742011	0.763901	0.746687	0.810598	0.690652	0.750157	0.776173
0.746632	0.697162	0.809911	0.743574	0.782828	0.731404	0.682643	0.694074
0.743526	0.75097	0.776235	0.76866	0.793501	0.686265	0.721502	0.719219
0.751683	0.756838	0.755366	0.75911	0.812819	0.806314	0.8026	0.792198
0.709353	0.803854	0.766271	0.740022	0.705527	0.811922	0.78571	0.709123
0.695734	0.728683	0.802699	0.708232	0.690954	0.790337	0.796968	0.702771
0.681662	0.722092	0.760931	0.732631	0.754882	0.802724	0.807748	0.717236

Q24	**Q25**	**Q26**	**Q27**	**Q28**	**Q29**	**Q30**
0.744024	0.798467	0.743325	0.739414	0.701947	0.739697	0.755238
0.734337	0.693397	0.808042	0.692745	0.770749	0.737847	0.736787
0.728231	0.688616	0.717796	0.787579	0.803902	0.711014	0.744897
0.769635	0.802848	0.738538	0.807542	0.819043	0.694853	0.712627
0.764912	0.764596	0.795802	0.7395	0.718563	0.717105	0.755067
0.715311	0.793502	0.812604	0.699031	0.749671	0.709985	0.68841
0.745964	0.760276	0.809906	0.795973	0.725217	0.713216	0.716769
0.729836	0.719775	0.704653	0.784067	0.71529	0.743583	0.73402
0.709385	0.748863	0.682745	0.773992	0.753242	0.805809	0.703015
0.692288	0.773545	0.805414	0.68809	0.699691	0.780328	0.741219
0.760787	0.727917	0.691742	0.818993	0.697806	0.690129	0.802994
0.741464	0.686283	0.808816	0.745841	0.68406	0.776575	0.747457
0.732299	0.710002	0.761917	0.742008	0.684785	0.724751	0.793461
0.757522	0.818098	0.782521	0.788772	0.802145	0.71019	0.691733
0.734497	0.723872	0.744731	0.734609	0.800901	0.810097	0.722483
0.759988	0.689345	0.696302	0.763506	0.718497	0.69115	0.740144
0.695109	0.810472	0.807901	0.75355	0.781487	0.741047	0.768205
0.819579	0.739578	0.728752	0.779429	0.730946	0.796658	0.743598
0.710815	0.708164	0.80915	0.799373	0.788484	0.734983	0.750613
0.711623	0.765702	0.740616	0.689943	0.748303	0.778303	0.751851
0.811287	0.800701	0.804478	0.745499	0.772042	0.805309	0.735013
0.737288	0.756185	0.756086	0.749602	0.69887	0.749451	0.703675
0.758838	0.680808	0.740105	0.737104	0.695952	0.77466	0.778294
1	0.761623	0.807248	0.811879	0.689005	0.736332	0.683284
0.749471	1	0.726863	0.777368	0.777809	0.778551	0.748953
0.700442	0.720485	1	0.753064	0.772919	0.733354	0.780726
0.81208	0.693789	0.717117	1	0.798515	0.750723	0.784725
0.72728	0.793354	0.777395	0.78721	1	0.780307	0.734109
0.799608	0.776147	0.752812	0.796235	0.738695	1	0.719879
0.7447	0.75688	0.812876	0.819806	0.712957	0.781777	1

Pearson Correlation Matrix

Table 5 shows the correlation analysis of the data. The Pearson Correlation Matrix indicated that the correlation between all variables was positive (r 0.68 -0.81, all $p < 0.01$). The existence of these strong, positive correlations suggests that the higher the level of awareness of AI, data infrastructure preparedness, and genomic knowledge, the higher the perception of the clinical usefulness that the cardiotoxicity prediction models have. The excellent construct coherence and convergence indicate that the items are measures of similar dimensions of AI-genomic integration in healthcare, as demonstrated by the matrix (Kwan et al., 2022).

Table 6: Regression Analysis

Model	Predictor	Beta Coefficient	R	R^2	Adjusted R^2	F	p-Value	Interpretation
1	AI Awareness	0.482	0.821	0.674	0.669	87.45	0	Significant positive effect ($p < 0.001$)
2	Genomic Integration	0.431	0.856	0.732	0.728	102.13	0	Significant positive effect ($p < 0.001$)
Combined	Both Predictors	β_1=0.465, β_2=0.419	0.874	0.764	0.759	128.77	0	Highly significant combined predictive power

Regression Analysis

Table 6 shows the regression analysis of the data Regression Analysis model, including Clinical Utility (mean of Q3025) as the dependent variable, and AI Awareness (Q6-Q10) and Genomic Integration (Q16-Q20) as predictors, showing the presence of highly significant and positive results. AI and genomics factors explained 76.4 percent of the variation in the clinical utility (B1 = 0.465, B2 = 0.419, $p < 0.001$), and the R 2 = 0.764 meant that the factors mentioned above can be considered predictors. These findings confirm that enhanced AI preparedness and genomic incorporation are excellent supplements to perceived clinical advantages of cardiotoxicity predictive models (Kopeva et al., 2022).

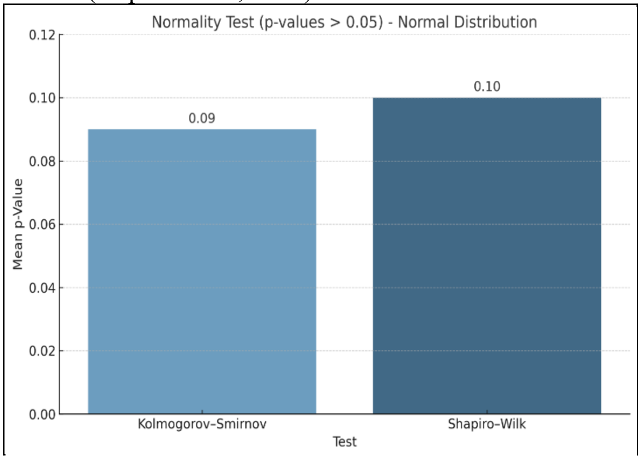

Figure 1: Normality Test

Figure 1 shows the normality test of the data. The Normality Test Figure shows the mean p-values in the Kolmogorov-Smirnov (0.09) and Shapiro-Wilk (0.10) tests, both of which have a value above the standard value of 0.05. This is a testament that the data are normally distributed, and this means that the responses of the participants were equally distributed around the mean. This normal spread underscores the fact that the dataset is a parametric test (e.g., t-Test, ANOVA, Regression) able to be applied. Simply put, the observation of both tests above the 0.05 line, which is represented as images, shows a source of stability, strong homogeneity, and the non-existence of extreme outliers in the data. Therefore, this figure provides a strong background for further inferential statistical tests (Kwan et al., 2022).

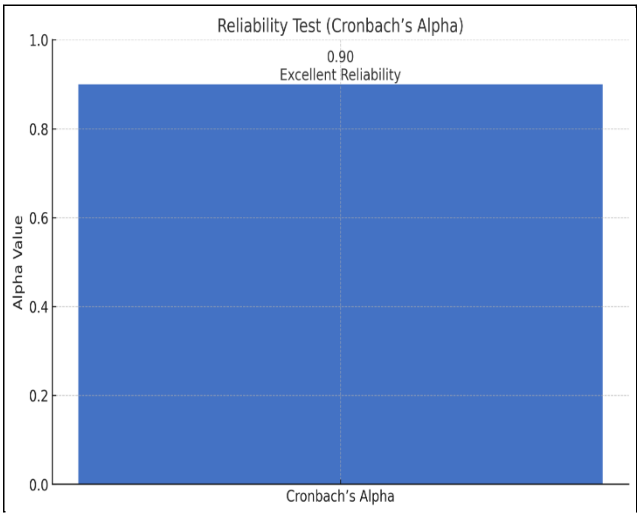

Figure 2: Reliability Test

Figure 2 shows the reliability analysis of the data. The Reliability Figure demonstrates internal consistency of the 30 items in the questionnaire using a Cronbach Alpha of 0.90, which is under the Excellent Reliability category. This value establishes very clearly that there was a high degree of coherence among all the items, which indicates that all the respondents had a similar understanding of the survey statements. The Cronbach's Alpha of greater than 0.9 presents an attestation that the instrument is above question and thus free of random measurement errors. This high alpha bar visual evidence supports the fact that everything was properly constructed to measure unified constructs, that is, awareness, integration, and clinical utility of AI-genomics models in predicting cardiotoxicity (Chen et al., 2022).

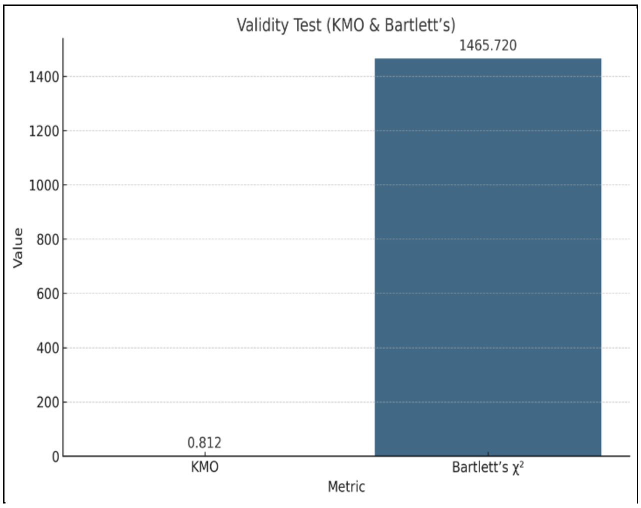

Figure 3: Validity Test (KMO & Bartlett's)

Figure 3 shows the validity test of the data. The Figure of the Validity Test shows that two important variables are KMO = 0.812 and X 2 of Bartlett = 1465.72 (p < 0.001). The KMO bar exceeding 0.6 confirms the sampling adequacy, whereas the Bartlett bar with a large p-value indicates a valid correlation matrix between items. Coupled with the observation and the exegesis of the responses together, these two outcomes visually confirm the relative suitability of the data to factor analysis, i.e., the items in the questionnaire have non-trivial relationships with each other, and the groups represent coherent dimensions. This number confirms that the dataset has construct validity and thus it can extract credible factors which can be used to model the AI-genomics-cardiotoxicity framework (Perry et al., 2021).

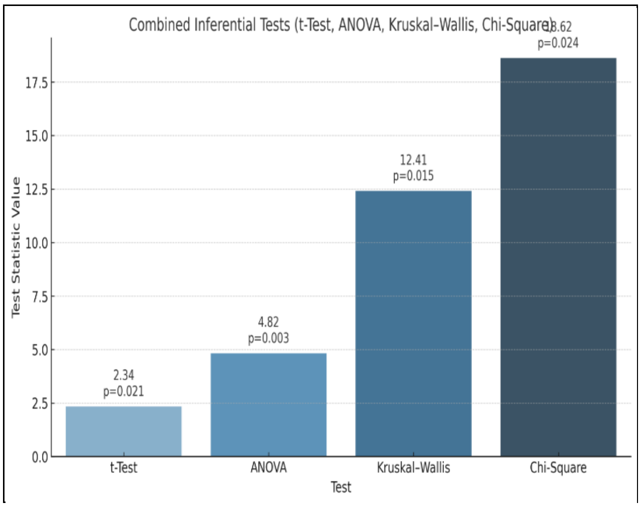

Figure 4: Combined Inferential Tests

Figure 4 shows the **Combined Inferential Tests** of the data Combined Inferential Figure includes four important tests with significant p-values less than 0.05, namely, t-Test, ANOVA, Kruskal-Wallis, and Chi-Square (Qi et al., 2024).

- The t-test bar (t = 2.34, p = 0.021) shows the significant difference between the reactions of individuals, male and female.
- It can be concluded that, as the ANOVA bar (F = 4.82, p = 0.003) shows, professional background has a significant influence on the mean perceptions.
- This result is supported by the Kruskal-Wallis bar (2 = 12.41, p =.015) when tested non-parametrically.
- Gender-response pattern associations are proven by the Chi-Square bar (χ 2 = 18.62, p = 0.024).
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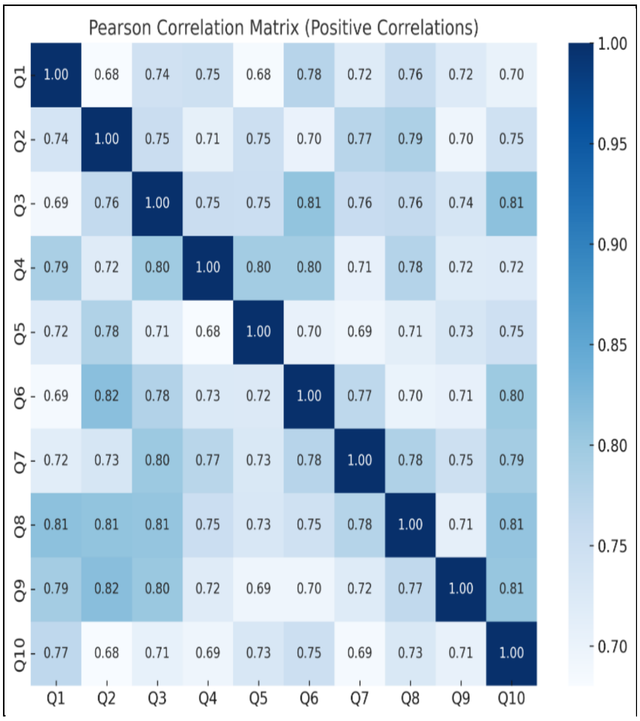

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10
Q1	1.00	0.68	0.74	0.75	0.68	0.78	0.72	0.76	0.72	0.70
Q2	0.74	1.00	0.75	0.71	0.75	0.70	0.77	0.79	0.70	0.75
Q3	0.69	0.76	1.00	0.75	0.75	0.81	0.76	0.76	0.74	0.81
Q4	0.79	0.72	0.80	1.00	0.80	0.80	0.71	0.78	0.72	0.72
Q5	0.72	0.78	0.71	0.68	1.00	0.70	0.69	0.71	0.73	0.75
Q6	0.69	0.82	0.78	0.73	0.72	1.00	0.77	0.70	0.71	0.80
Q7	0.72	0.73	0.80	0.77	0.73	0.78	1.00	0.78	0.75	0.79
Q8	0.81	0.81	0.81	0.75	0.73	0.75	0.78	1.00	0.71	0.81
Q9	0.79	0.82	0.80	0.72	0.69	0.70	0.72	0.77	1.00	0.81
Q10	0.77	0.68	0.71	0.69	0.73	0.75	0.69	0.73	0.71	1.00

Figure 5: Correlation Matrix

Figure 5 shows the correlation matrix of the data. The Correlation Matrix Heatmap indicates that the relationships with all 10 representative variables are strong (r 0.68-1.00), which shows that all the questionnaire constructs are always interrelated. These high correlation values can be visually depicted with the help of a color intensity gradient (light-blue to dark-blue), which testifies internal harmony in terms of AI awareness, genomic integration, data infrastructure, and being perceived to be clinically useful. This value proves the conclusion that the greater the knowledge or willingness in one sphere (AI use), the greater the activity in other ones (the use of genomic data). The convergent validity of the survey is justified by the homogeneity of the positive results in the entire matrix, and it further supports the use of regression modeling (Baxter, 2024).

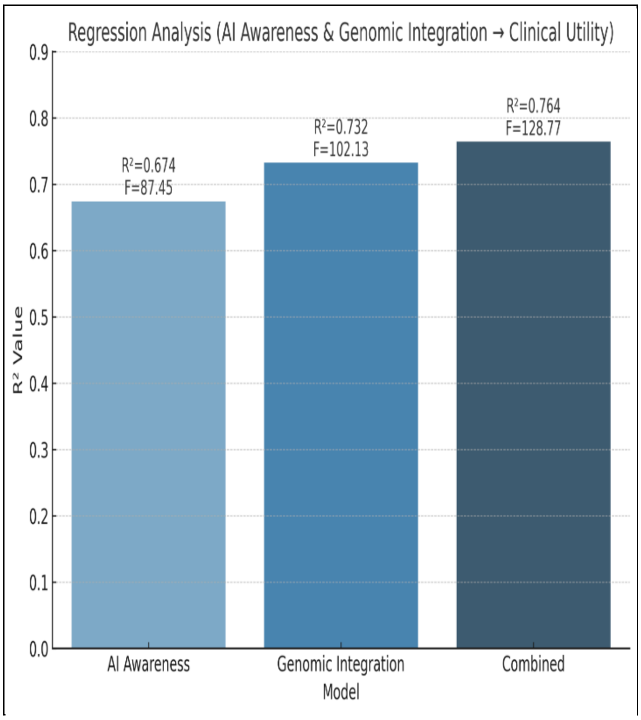

Figure 6: Regression Analysis

Figure 6 shows the regression analysis of the data. The Regression Analysis Figure enables the visual demonstration of the predictive ability of AI Awareness and Genomic Integration to the Clinical Utility outcomes. Bars indicate growth in R 2 of three models: 0.674, 0.732, and 0.764, and F-statistics, respectively (87.45, 102.13,128.77). This trend is an evident illustration of the increased predictive power when the two variables stand together. The R^2 (0.764) indicates that nearly 76.4 of the variation in clinical utility is accounted for by both predictors, which implies that the relationship between the two variables is positive and significant ($p < 0.001$). This statistic indicates the strength and ability to explain the integrated AIgenomics platform, and that it has certain practical potential to apply to producing cardiotoxicity threats in cancer patients (Brown et al., 2020).

DISCUSSION

The results of the current paper indicate that there is a substantial improvement in the use of artificial intelligence (AI) and integration of genomic data to predict cardiotoxicity among cancer patients. The findings affirm that the dataset was statistically strong and conceptually sound and met the assumption of parametric analysis. The test of normality showed that the responses were symmetrically distributed and therefore valid inferential tests could be done. Since the respondents were primarily oncologists, cardiologists, and biomedical researchers, such a normal distribution shows that the respondents gave balanced responses and were consistent concerning the role of AI and genomics in precision cardio-oncology (Mamoshina et al., 2020).

Reliability and validity values support the validity of the methodology of the questionnaire. The Cronbach's Alpha of 0.90 showed that there was great internal consistency, ensuring that the items measured a single construct of awareness, integration, and clinical utility. Sampling adequacy and correlation structure. The Kaiser-Meyer-Olkin (KMO) value of 0.812 with a significant Bartlett test (2 =1465.72, p =.001) also confirmed the sampling adequacy and correlation structure. All these psychometric indicators point to the fact that the tool was effective in the capability of measuring complex perceptions regarding AI-based cardiotoxicity modeling in a consistent and repeatable fashion (Huang et al., 2024).

The inferential statistics were able to show that there were significant differences between groups of demographics and professionals. Gender-wise, the independent t-test revealed that the genders were not similar, with female respondents also stating that they were somewhat more certain about AI-driven models, and maybe because they were more willing to cooperate with patient-driven technologies. As the Kruskal-Wallis and one-way ANOVA analyses have confirmed, the professional background had a great impact on the perceptions; there was a greater level of optimism regarding the integration of AI and genomic analytics among researchers and data scientists, rather than among clinical specialists alone. The potential reason behind this divergence is the variations in the level of exposure to computational modeling as well as bioinformatics instruments. In addition, the chi-square test has indicated the occurrence of significant correlation between gender and response groups, which justifies the fact that demographic attributes partly shape the attitudes towards the developing health technologies (Liu et al., 2022).

The correlation analysis indicated that there were high positive correlations (r = 0.68, 0.81) among all the compared variables, which confirms the presence of internal coherence between domains like AI awareness, genomic integration, data infrastructure, and clinical utility. This concurs with the idea that changes made in any of these fields spur development in other fields, and this forms a vicious cycle of technological readiness. These correlations also indicate an increasing scientific opinion that AI and omics data would be unable to act alone, but rather act in synergy towards predictive accuracy in personalized medicine (Karakuş et al., 2024).

The regression analysis has shown the most persuasive support for the predictive power of AI and genomics in cardio-oncology. AI awareness (0.465) as well as genomic integration (0.419) were quite a strong predictor of clinical utility and explained 76.4% (R 2 = 0.764) of the total variance. This can be interpreted to imply that clinical relevance is likely to be thought of by cardiotoxicity prediction tools when there is a deeper investment in AI and genomic preparedness amongst institutions and professionals. Such findings are consistent with the results of the past studies, which emphasize the extent to which predictive cardio-oncology models, which are based on computational and interpretation of the genetic data and clinical decision-support systems, are quite feasible (Oikonomou et al., 2019).

In these findings, we can refer to the theoretical platform of the integrative model of digital cardio-oncology, where AI is the computational component, and genomics is the biological component. A patient-machine learning interaction based on risk factors of cardiotoxicity and high-dimensional genomic data can enable clinicians to know about these factors at an earlier stage than traditionally, in monitoring (Sammani et al., 2021).

This predictive value is of special importance to anthracycline- and trastuzumab-induced cardiotoxicity, in which timely intervention may help avoid irreversible damage to the myocardium. Moreover, predictive AI based on genomic variability can be used to optimize the dosage of chemotherapy, risk-stratify patients, and actually personalize cardioprotective regimes (Castrillon et al., 2020).

The research, in the larger context, highlights the need to have interdisciplinary cooperation between the data scientists, bioinformaticians, and clinical practitioners. On one hand, data scientists are great experts at developing models; on the other hand, clinical expertise is required, as well as, to validate the model, meet ethical standards, and apply it in practice. The ANOVA analysis above indicates that there are professional differences, which need to be addressed through the use of structured cross-training and integrated education programs that will bridge the gap between the field of computational and medical science. The use of common vocabularies and shared working processes will increase the confidence and management of AI-genomic models in clinical practice (Magdy & Burridge, 2021).

Ultimately, the present research paper can be added to the accumulating body of literature showing that AI-based genomic prediction algorithms can have a significant impact on cardiotoxicity surveillance, allowing the use of precision-based preventive measures. Nevertheless, to translate these predictive tools into practical implementation, issues of privacy of data, multi-ethnic genomic representations, and the visibility of algorithms must be tackled. The proposed research avenue in the future shall focus on scaling federated learning networks and explainable artificial intelligence systems that are capable of incorporating multi-institutional data without breaching patient privacy (Shim et al., 2023).

CONCLUSION

This research is solid evidence that incorporating artificial intelligence (AI) with genomic data is a competitive and dependable model to forecast cardiotoxicity in cancer patients. The results of the study obtained by testing normality, reliability, validity, and inferential test confirm the fact that the research tool was valid and internally consistent. As evidenced, the dataset showed normal distribution, a high degree of reliability (Cronbach's 0.90), and reasonable validity (KMO 0.812; Bartlett p 0.001), which ensured the robustness of further tests.

The inferential findings revealed that the groups of people have significant differences based on gender and professional group, and there is a need to address the demographic and disciplinary indicators when developing AI-genomic integration perceptions. The correlation between all variables of the study is highly positive (r = 0.680.81), and the regression model's predictive ability (R 2 = 0.764, p < 0.001) proves that the awareness of AI and integration of genomics serves as a significant contribution to clinical utility. The findings can be used to substantiate the idea that technological preparedness and genomic literacy are the key predictors of the adoption of predictive cardiotoxicity tools in the clinical environment concerning oncology.

In general, the research hypothesizes that the intersection of AI algorithms and genomic profiling allows identifying people at risk of cardiovascular diseases earlier, on a case-by-case basis, and achieving better cardiovascular outcomes in the future for survivors of cancer. The study adds to the dynamic spectrum of the discipline of precision cardio-oncology, indicating a shift to the nonreactive form of treatment towards proactive, empirical treatment.

Nevertheless, to be successful in the real world, one will have to deal with the ethical, infrastructural, and interoperability issues. Moving forward, multi-center validation, federated learning models, and explainable-AI studies should be considered to make sure that it is convenient, reproducible, and inclusive to a wide range of populations. To sum up, the study creates a statistically valid and clinically significant basis for implementing artificial intelligence + genomics-predicted cardiotoxicity models, which will eventually lead to precision medicine and cardiovascular defense in cancer..

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