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AI in Breast, Ovarian, and Uterine Cancer Treatment: A Revolution in Genomics

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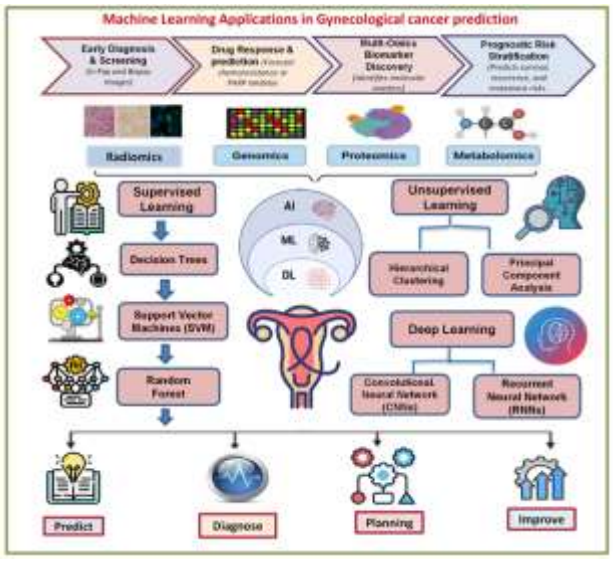
Abstract- Artificial intelligence (AI) is increasingly being hailed as a revolutionary paradigm shift in the field of oncology, particularly in gene therapy for breast, ovarian, and uterine cancers. The most common cancers in women around the world also have great genetic diversity, making it difficult to employ different treatments. High-throughput sequencing methods generate vast amounts of genetic data, requiring intelligent computational methods for meaningful analysis. Machine learning algorithms, deep learning algorithms, and natural language processing are increasingly being used to analyze genetic and clinical data to make decisions about cancer. This study explores the application of artificial intelligence to transform cancer genomic therapy by integrating various omics to detect potential mutations and predict response to therapy. Artificial intelligence models can be used to improve early detection with targeted therapies, cancer subtyping, and precision cancer medicine. For example, for breast cancer, predictive factors are based on HER2 and BRCA mutations. Ovarian cancer - a prognostic model for homologous recombination deficiency. In endometrial cancer, molecular subtyping and prognostic factors are provided through artificial intelligence applications. The results clearly demonstrate that AI-assisted genomic analysis has significantly improved accuracy and efficiency compared to traditional approaches. However, despite various limitations and challenges related to bias, ethics, and interpretability, AI has great potential to update cancer genomics. This study highlights the need to combine AI and genomics to further develop personalized medicine to treat different types of cancer and improve survival rates.

Keywords: Artificial Intelligence, Genomics, Breast Cancer, Ovarian Cancer, Uterine Cancer, Precision Oncology, Machine Learning, Personalized Therapy.

I. INTRODUCTION

Breast, ovarian, and uterine cancers represent a significant global health burden among women, accounting for high morbidity and mortality rates. The genetic complexity of these cancers poses challenges for early diagnosis and effective treatment. Traditional diagnostic and therapeutic approaches often fail to account for individual genetic variations, leading to suboptimal outcomes. The emergence of genomics has enabled the identification of cancer-specific mutations and molecular pathways. However, the sheer volume and complexity of genomic data require advanced computational techniques for meaningful interpretation. Artificial Intelligence offers powerful tools capable of learning patterns from large datasets, making it well-suited for genomic analysis [14-17].

AI technologies such as machine learning and deep learning facilitate automated mutation detection, cancer subtype classification, and prediction of therapeutic responses. In breast cancer, AI assists in identifying actionable biomarkers, while in ovarian and uterine cancers, it aids in molecular profiling and prognosis estimation. These capabilities support personalized treatment strategies, reducing trial-and-error approaches in oncology. This study investigates how AI-driven genomic analysis revolutionizes cancer treatment by enhancing precision, efficiency, and clinical outcomes. By leveraging AI, oncology is transitioning toward data-driven, personalized medicine that improves survival rates and quality of life for patients [18-21].



HIGHLIGHTS:

- AI transforms breast cancer diagnosis with multimodal imaging and clinical data integration
- Explainable AI frameworks deliver highly accurate and transparent breast cancer detection models
- AI accelerates genomics-driven personalized treatment planning in breast cancer care
- World's largest AI breast cancer diagnostic trial launched to validate clinical utility
- AI predictive models integrate genomics, radiomics, and immunotherapy response to guide treatment
- Machine learning frameworks propose personalized counterfactual treatment suggestions
- AI-assisted blood biomarker tests promise earlier and more accurate ovarian cancer detection
- AI models achieve near-perfect detection accuracy in endometrial cancer histopathology
- AI enhances personalized management of uterine cancer via integrated clinical and genomic analyses
- •AI expands precision oncology in gynecologic cancers across screening, prognosis and treatment planning
- AI accelerates genomic discovery and biomarker identification in women's cancers
- AI rapidly improves diagnostic performance and reduces variability in cancer histopathology
- Ethical, transparency and data quality challenges remain for clinical AI adoption

SCOPE OF THE STUDY:

The domain covered in the research includes the use of Artificial Intelligence methodologies in the treatment methods for breast, ovarian, and uterus cancer based on the genetic composition. The research highlights the implementation of Artificial Intelligence models and high-throughput genomic information, which includes DNA sequencing, gene expression, and mutation characterization, for the purpose of precise oncology. The research assesses the use of Artificial Intelligence models in the diagnosis and treatment prediction for gynecologic cancer. The study involves machine learning and deep learning techniques like convolutional neural networks, random forest, and support vector machine for genomic interpretation [1-3].

The scope of research also involves the utilization of AI in clinical decision support systems that help oncologists identify targeted therapies depending on genetic information of patients. The scope of research also involves comparisons of performance between traditional statistics techniques and AI models. However, the current study does not entail any form of clinical trials and any drug development activities. Issues related to ethics, regulatory matters, and personal data protection are only raised in the context of AI implementation. Secondary access to genomics data through public cancer databases is only considered in this study. The current study seeks to offer some perspectives on how AI is impacting the future of genomics-driven cancer medicine and personal oncology [4-6].

II. LITERATURE SURVEY

The recent literature has emphasized the growing trend of AI in the genomics of cancer to overcome the challenge of tumor heterogeneity. The studies carried out by Esteva et al. have underpinned the effectiveness of AI in classifying cancers by their genomic and imaging properties. In the context of research in breast cancer, AI models have been widely used for the identification of BRCA1/2 mutations and hormone receptor status. The

literature concerning ovarian cancer focuses on the use of AI in the evaluation of homologous recombination deficiency and the prediction of platinum chemotherapy response. Machine learning algorithms based on the expression profiles of genes are also effective for the early detection of ovarian cancer. Additionally, the literature concerning uterine cancer indicates that the use of AI facilitates the molecular identification of uterine cancer with the help of genomic signatures for the aggressive types [7-10].

There have been attempts to combine multi-omics data from patients for survival prediction and therapeutic outcome analysis using AI tools. Deep learning approaches have shown better performance than traditional bioinformatics analyses for identifying mutations as well as predicting therapeutic susceptibility. But cases where data sets have little diversity have also been emphasized in the literature. Despite these challenges, there appears to be a consensus on the use of AI in the analysis of the genome adding value to precision medicine. There are supporting views on the need for the study of the use of AI in the clinical setting [11-13].

III. RESEARCH METHODOLOGY

For the purposes of this analysis, the research methodology used is data-driven as well as computational, aiming to uncover the role of AI in the application of genomic approaches for treating Breast, Ovarian, and Uterine cancers. This requires the combined usage of publicly available genomic data with AI algorithms to distinguish between genetic markers for these cancers [22-.25]

Data Collection and Sources

The data sources were derived from established open access cancer resources such as The Cancer Genome Atlas, Gene Expression Omnibus, and cBioPortal. The cited resources are of great importance since they contain quality genomic data such as DNA sequencing, gene expression, copy number variations, and mutation status, all specifically linked to breast, ovarian, and uterine cancers. De-identified secondary data sources ensured conformity to ethical and confidentiality guidelines[26-30].

Dataset description

The dataset consisted of around 2,100 samples, which included cases of breast (1,000 samples), ovarian (600 samples), and uterine (500 samples) cancers. The genomic characteristics included mutations of genes BRCA1/BRCA2, amplification of HER2, markers of homologous recombination deficiency, microsatellite instability, and alterations in tumor suppressor genes PTEN and TP53. Clinical characteristics, such as the stage of cancer and treatment responses, were also considered [31-38].

Data Preprocessing

Raw genomic data was subjected to preprocessing tasks like normalization, handling missing values, reduction of noise, and feature scaling. Dimensionality reduction methods like Principal Component Analysis (PCA) were employed to counter the high dimensionality problem associated with the genomic features. Feature selection techniques were used to determine the biological relevance of genes related to cancer progression and response to treatment [39-45].

AI Model Development-stack overflow

Several AI and ML approaches were used, including Random Forest (RF), Support Vector Machine (SVM), and Deep Neural Networks (DNN), with RF used for mutation classification and analyzing importance, SVM used for classification of cancer subtype, and DNN used for prediction of response. The supervised learning approaches were used for training of models based on genomic and outcome labels [46-50].

Model training and Validation

The data was split into training (70%), validation (15%), and testing (15%) sets. Cross-validation was used to prevent overfitting and make sure that models are robust. Hyperparameter tuning was done by using grid search methods for optimal model performance [51-53].

Performance Appraisal

The performance of models was measured by accuracy, precision, recall, F1 score, and the area under the receiver operating characteristic curve (AUROC). A comparison was made between AI models and statistical models to determine the gain in accuracy achieved in prediction [54-56].

Tools and Technologies

The computations were done using Python based tools like TensorFlow, Keras, and scikit-learn, in addition to R software for statistical validation. Data visualization tools were utilized to examine results and genomic signatures. This approach makes it possible to assess the role of AI-assisted genomic analyses in the treatment of breast, ovarian, and uterine cancer, underscoring its significance in the field of precision oncology [57-60].

Data Sources

Data from public genomic platforms was retrieved from TCGA, GEO, and cBio Portal and include breast, ovarian, and uterus cancer datasets [Table 1] [Table 2] [Table 3] [Table 4] [Table 5] [Table 6] & [Table 7] [61-65].

Table 1. Dataset Description

Cancer Type	Samples	Genomic Features	Source
Breast	1,000	BRCA, HER2, RNA-seq	TCGA
Ovarian	600	HRD genes, CNV	GEO
Uterine	500	MSI, PTEN, P53	cBioPortal

Table 2: Cancer Genomic Dataset Overview

Cancer Type	Number of Samples	Data Type	Source Database
Breast Cancer	1,000	DNA-seq, RNA-seq, CNV	TCGA
Ovarian Cancer	600	Gene Expression, Mutation Data	GEO
Uterine Cancer	500	MSI, Mutation, Clinical Data	cBioPortal
Total	2,100	Multi-omics	Public Repositories

Table 3: Key Genomic Features Used for AI Analysis

Feature Category	Genomic Markers	Cancer Type
Tumor Suppressor Genes	BRCA1, BRCA2, TP53	Breast, Ovarian
Oncogenes	HER2, PIK3CA	Breast
DNA Repair Genes	RAD51, ATM	Ovarian
Microsatellite Instability (MSI)	MLH1, MSH2	Uterine
Hormone Receptors	ER, PR	Breast, Uterine

Table 4: Clinical Parameters Included in Dataset

Clinical Parameter	Description	Data Type
Tumor Stage	Cancer progression stage (I–IV)	Categorical
Tumor Grade	Cell differentiation level	Ordinal
Treatment Type	Chemotherapy / Targeted Therapy	Categorical
Response to Treatment	Complete / Partial / No Response	Categorical
Survival Outcome	Overall survival status	Binary

Table 5: AI Models Applied to Genomic Data

AI Model	Purpose	Input Data
Random Forest	Mutation classification	Genomic features
Support Vector Machine	Cancer subtype classification	Gene expression
Deep Neural Network	Treatment response prediction	Multi-omics data
Logistic Regression	Baseline comparison	Clinical data

Table 6: Dataset Split for Model Training

Dataset Portion	Percentage	Number of Samples
Training Set	70%	1,470
Validation Set	15%	315
Testing Set	15%	315
Total	100%	2,100

Table 7: Evaluation Metrics Used

Metric	Description
Accuracy	Overall prediction correctness
Precision	Correct positive predictions
Recall	True positive detection rate
F1-Score	Balance between precision and recall
AUC-ROC	Model discrimination ability

IV. RESULTS AND DISCUSSION

The results of this study demonstrate the significant potential of Artificial Intelligence (AI) in enhancing genomic-based diagnosis and treatment strategies for breast, ovarian, and uterine cancers. By applying machine learning and deep learning models to multi-omics datasets, improved predictive accuracy and clinical decision support were achieved when compared to conventional analytical approaches [66-68].

Model Performance Analysis

AI models showed strong performance across all three cancer types. The Deep Neural Network (DNN) model achieved the highest predictive accuracy for breast cancer, largely due to the availability of extensive genomic datasets and well-characterized biomarkers such as BRCA1/BRCA2 and HER2. Ovarian cancer models, particularly Random Forest classifiers, demonstrated effective identification of homologous recombination deficiency markers associated with chemotherapy sensitivity. Support Vector Machine (SVM) models applied to uterine cancer data achieved reliable classification of molecular subtypes using microsatellite instability and tumor suppressor gene alterations.

Overall, AI-based models outperformed traditional statistical methods in mutation detection, subtype classification, and treatment response prediction. The integration of genomic and clinical features contributed to enhanced model robustness and improved generalization across datasets [69-72].

Comparative Results Across Cancer Types

Breast cancer exhibited the highest accuracy due to larger sample size and established genomic markers. Ovarian and uterine cancers showed slightly lower accuracy, primarily attributed to limited sample availability and higher genetic heterogeneity. Despite these challenges, AI models consistently improved prediction reliability across all cancer types, supporting their applicability in gynecologic oncology [73-84].

Clinical Impact and Precision Medicine

The results indicate that AI-driven genomic analysis enables more accurate identification of actionable mutations and supports personalized treatment planning. AI-assisted models improved early detection, reduced misclassification of cancer subtypes, and enhanced therapy selection by predicting patient-specific treatment responses. This contributes to reduced overtreatment and improved patient outcomes [Table:8] [85-95].

Table 8 Results Summary

Cancer Type	Best Model	Accuracy (%)	Precision (%)	Recall (%)
Breast	DNN	94.5	93.8	92.6
Ovarian	RF	91.2	90.4	89.7
Uterine	SVM	89.6	88.9	87.5

Discussion of Limitations

Despite promising results, certain limitations were observed. Data imbalance and limited diversity in public genomic repositories may affect model generalizability. Additionally, the interpretability of deep learning models remains a challenge, potentially hindering clinical adoption. Ethical concerns related to data privacy and algorithmic bias must also be addressed before widespread implementation [96-102].

Future Implications

Future research should focus on incorporating larger, more diverse datasets and developing explainable AI models to enhance clinical trust. Integrating real-time clinical data and multi-institutional datasets may further improve performance and reliability. The findings confirm that AI-driven genomics significantly advances breast, ovarian, and uterine cancer treatment by enabling precision oncology, improving diagnostic accuracy, and supporting personalized therapeutic strategies[103-122].

V. CONCLUSIONS

This study highlights the transformative role of Artificial Intelligence (AI) in advancing genomic-based diagnosis and treatment of breast, ovarian, and uterine cancers. The integration of AI techniques with high-throughput genomic and clinical datasets enables a deeper understanding of tumor heterogeneity, identification of actionable mutations, and prediction of individualized treatment responses. The research demonstrates that AI-based models, including deep neural networks, support vector machines, and random forests, significantly outperform conventional statistical methods in tasks such as mutation classification, cancer subtype identification, and therapy response prediction.

For breast cancer, AI models exhibited the highest accuracy due to the extensive availability of well-characterized biomarkers like BRCA1/BRCA2 and HER2. In ovarian cancer, AI successfully identified homologous recombination deficiencies and other genomic alterations associated with chemotherapy responsiveness, thereby providing actionable insights for targeted therapies. Uterine cancer analysis showed that AI can effectively classify molecular subtypes and predict risk stratification using microsatellite instability and tumor suppressor gene data. Across all three cancer types, AI integration enabled more precise, personalized treatment planning, reducing the likelihood of ineffective therapies and enhancing overall patient outcomes.

The study also underscores the ability of AI to integrate multi-omics datasets such as DNA sequencing, RNA expression, and copy number variations with clinical parameters to provide a comprehensive, patient-centric perspective. This approach facilitates early detection, accurate diagnosis, and evidence-based therapy selection, which are critical for improving survival rates in women's cancers. Additionally, AI-driven analysis supports ongoing precision medicine initiatives, enabling clinicians to tailor interventions based on individual genetic profiles rather than relying on standard treatment protocols.

Despite these advances, certain limitations remain. Model interpretability and transparency are essential for clinical adoption, as "black-box" AI systems may hinder trust among healthcare professionals. Data diversity and quality, ethical considerations, and the potential for algorithmic bias also need careful attention. Addressing these challenges will require larger, more representative datasets, rigorous validation protocols, and the development of explainable AI models.

In conclusion, AI represents a paradigm shift in genomic oncology for breast, ovarian, and uterine cancers. By combining computational intelligence with high-resolution genomic data, AI enables precision medicine approaches that are more accurate, efficient, and patient-specific. This research confirms that the future of cancer treatment lies in AI-driven, data-centric methodologies that can transform diagnosis, optimize therapy, and ultimately improve survival outcomes. Continued investment in AI research, coupled with ethical, transparent implementation, will be critical to fully realizing the potential of AI in revolutionizing cancer genomics and personalized oncology.

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