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INTEGRATING ARTIFICIAL INTELLIGENCE WITH BIOLOGICAL DATA FOR PREVENTIVE PHARMACOTHERAPY: A SYSTEMATIC LITERATURE REVIEW

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ABSTRACT

Background

Chronic non-communicable diseases (NCDs) remain the leading causes of global morbidity and mortality, necessitating a transition from reactive treatment to proactive prevention strategies. The integration of artificial intelligence (AI) with biological data offers a promising approach to enhance preventive pharmacotherapy through improved risk prediction, early detection, and personalized treatment planning. Methods This study employed a systematic literature review following PRISMA guidelines. A comprehensive search was conducted across Scopus, PubMed, and Web of Science databases for articles published between 2020 and 2026. Eligible studies included peer-reviewed research examining AI or machine learning applications integrating biological data such as genomics, proteomics, biomarkers, and electronic health records in preventive pharmacotherapy contexts. A total of 47 studies were included for qualitative synthesis, with 42 studies contributing to quantitative analysis. Results. The findings indicate that AI-driven models consistently outperform conventional approaches, achieving accuracy above 90% and AUC-ROC values exceeding 0.96 in several applications. Machine learning and deep learning models, particularly hybrid and ensemble approaches, demonstrated superior performance in disease risk prediction, early detection, and treatment optimization. Integration of multi-omics and clinical data enhanced predictive capabilities and enabled precision prevention strategies across cardiovascular, metabolic, oncological, and renal disease domains. Conclusions. The integration of AI with biological data significantly improves the effectiveness of preventive pharmacotherapy and supports the transition toward precision prevention. However, challenges related to clinical validation, implementation, and data governance must be addressed to ensure successful translation into routine healthcare practice.

Keywords: Artificial Intelligence; Biological Data; Disease Prevention; Precision Medicine; Preventive Pharmacotherapy

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INTRODUCTION

Chronic non-communicable diseases (NCDs), including cardiovascular disease, diabetes, cancer, and chronic respiratory conditions, continue to dominate global morbidity and mortality, exerting escalating pressure on healthcare systems worldwide (1). The rising prevalence of metabolic disorders driven by urbanization, sedentary lifestyles, and demographic aging reflects a shared pathophysiological basis involving insulin resistance, chronic inflammation, and metabolic dysregulation (2). This convergence underscores a critical limitation of conventional reactive healthcare models, which predominantly address disease after onset, thereby necessitating a strategic transition toward predictive and preventive paradigms capable of identifying risk prior to clinical manifestation.

The urgency of this transition is amplified by population aging, a major determinant of cardiovascular risk, where disease incidence rises sharply with advancing age (3). Despite substantial progress in acute and interventional care, preventive strategies remain inconsistently implemented and insufficiently personalized. Preventive pharmacotherapy spanning primary and secondary prevention has evolved conceptually from categorical risk stratification toward a continuum-based framework, emphasizing individualized risk profiling (4,5). However, current approaches remain constrained by limited integration of multidimensional patient data, thereby restricting their capacity to deliver truly tailored interventions.

Although guideline-directed medical therapies (GDMT), including renin-angiotensin system inhibitors, SGLT2 inhibitors, mineralocorticoid receptor antagonists, and GLP-1 receptor agonists, have demonstrated substantial efficacy in reducing disease progression and cardiovascular outcomes, their translation into routine practice remains suboptimal (6,7). This persistent implementation gap highlights a fundamental disconnect between evidence generation and clinical application, particularly in heterogeneous and resource-constrained settings. Consequently, there is a pressing need for advanced decision-support frameworks capable of optimizing therapeutic selection and timing based on individual risk dynamics.

The rapid expansion of high-throughput omics technologies, coupled with the growing availability of electronic health records (EHRs), has generated unprecedented volumes of multidimensional biological and clinical data, offering transformative opportunities to elucidate disease mechanisms and refine risk prediction (8–11). In parallel, artificial intelligence (AI), particularly machine learning and deep learning, has emerged as a powerful analytical paradigm capable of integrating and interpreting complex, high-dimensional datasets beyond the capacity of conventional statistical methods (12–14). Nevertheless, despite these technological advances, a critical fragmentation persists between AI development, biological data utilization, and their practical integration into pharmaceutical care, limiting their translational and clinical impact (8,15).

Integrating AI with biological data represents a pivotal step toward realizing precision prevention, enabling earlier disease detection, more accurate risk stratification, and optimized pharmacotherapeutic interventions aligned with individualized patient profiles (8,16). However, significant barriers including data heterogeneity, lack of clinical validation, and implementation challenges continue to impede this integration. Accordingly, this systematic literature review aims to critically evaluate the current landscape of AI-driven integration with biological data in preventive pharmacotherapy, identify methodological trends and applications, assess translational readiness, and delineate future directions to advance precision-driven disease prevention strategies.

MATERIALS AND METHODS

This systematic literature review was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines to ensure methodological rigor, transparency, and reproducibility. A review protocol was established a priori, defining clear criteria for study selection, data extraction, and quality assessment. A comprehensive literature search was performed across three major databases Scopus, PubMed, and Web of Science (WoS) to capture a broad spectrum of biomedical, pharmaceutical, and computational research. The search strategy utilized Boolean operators combining key terms related to artificial intelligence (“Artificial Intelligence,” “Machine Learning,” “Deep Learning”), biological data (“Genomics,” “Proteomics,” “Biomarkers,” “Electronic Health Records”), and preventive pharmacotherapy (“Disease Prevention,” “Precision Medicine,” “Drug Therapy”). Additional targeted searches and manual screening of reference lists were conducted to ensure completeness, with publications limited to the period 2020–2026.

Eligibility criteria were predefined to ensure relevance and quality. Included studies were peer-reviewed articles published in English within the last five years that examined AI or machine learning applications integrating biological data in preventive contexts, particularly those related to pharmacotherapy outcomes. Exclusion criteria encompassed non-peer-reviewed publications, studies lacking relevance to prevention or pharmacotherapy, research focused solely on diagnostic imaging without biological data integration, animal studies without clear translational implications, and duplicate records. The study selection process followed a three-stage PRISMA framework: identification, screening, and eligibility assessment. From an initial pool of 1,847 records, 1,423 unique articles were screened after duplicate removal, resulting in 436 full-text articles assessed for eligibility. Ultimately, 47 studies were included in the qualitative synthesis, with 42 contributing to quantitative analysis.

Data extraction was conducted using a standardized form capturing study characteristics, including authorship, publication year, study design, AI/ML methodologies, types of biological data, preventive application focus, outcome measures, and key findings. Two independent reviewers performed data extraction, with discrepancies resolved through consensus. Study quality was evaluated using the Critical Appraisal Skills Programme (CASP) checklist for observational studies and adapted Joanna Briggs Institute (JBI) criteria for computational studies. Given the heterogeneity of study designs and outcomes, data synthesis was performed using narrative synthesis complemented by thematic analysis, grouping studies based on AI methods, biological data types, preventive applications, and performance outcomes. Where feasible, quantitative pooling of performance metrics was conducted to generate summary estimates of AI effectiveness.

RESULT

The systematic search identified 1,847 potentially relevant records, with the final inclusion of 47 studies meeting all eligibility criteria. The selection process demonstrated strong adherence to PRISMA guidelines, with clear documentation of exclusion rationales at each stage. The primary reasons for full-text exclusion were: insufficient focus on preventive applications (178 studies); lack of relevance to pharmaceutical practice (124 studies); and inadequate methodological reporting (87 studies).

The included studies represented diverse geographical origins and institutional settings, with contributions from academic medical centers, research institutions, and collaborative networks across North America, Europe, Asia, and Oceania. Publication trends demonstrated substantial growth in research output, with the majority of included studies published between 2024 and 2026, reflecting increasing interest in AI-biological data integration for prevention. publication_trends.pngFigure 2. Publication trends demonstrating increasing research output in AI and biological data integration for preventive pharmacotherapy (2020-2026). Source: Analysis of included studies.

Table 1. Characteristics of Included Studies

Characteristic	N (%)
Study Design	
Computational/Modeling	22 (47%)
Clinical Validation	14 (30%)
Observational/Retrospective	8 (17%)
Systematic Review	3 (6%)
Geographic Region	
North America	16 (34%)
Europe	12 (26%)
Asia	14 (30%)
Multi-regional	5 (10%)
Primary Disease Focus	
Cardiovascular Disease	18 (38%)
Diabetes/Metabolic	12 (26%)
Cancer	8 (17%)
Kidney Disease	5 (11%)
Other	4 (8%)

The included studies demonstrated a diverse range of artificial intelligence (AI) methodologies, with machine learning (ML) approaches

predominating across preventive pharmacotherapy applications. Traditional algorithms such as Random Forest, Support Vector Machines, and Gradient Boosting were utilized in approximately 32% of studies, showing strong performance in structured clinical data analysis (17). Deep learning architectures including Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), and Long Short-Term Memory (LSTM) models were applied in 28% of studies, particularly for processing sequential and high-dimensional data from electronic health records (EHRs) and imaging sources (18). Advanced approaches, including ensemble models and transformer-based architectures, demonstrated superior predictive performance, with accuracy exceeding 94% and AUC-ROC values reaching 0.92 in drug response prediction tasks (19,20). EHRs emerged as the most frequently utilized data source, often integrated with multi-omics datasets such as genomics, proteomics, and metabolomics to enhance predictive accuracy and capture complex disease mechanisms (9,21–23).

AI applications in preventive pharmacotherapy were primarily centered on disease risk prediction, with 42 studies focusing on predictive modeling for chronic disease onset. AI-driven models integrating clinical, genetic, and imaging data significantly outperformed traditional risk assessment approaches, particularly in cardiovascular and chronic kidney disease prediction, achieving accuracy values above 90% (17,18). These predictive frameworks enable early identification of high-risk individuals by analyzing large-scale, heterogeneous datasets, including EHRs, genetic profiles, lifestyle factors, and environmental exposures (24). In addition to risk prediction, AI-supported drug optimization strategies demonstrated substantial clinical value, encompassing personalized dosing, drug-drug interaction prediction, and treatment response forecasting. Hybrid models integrating pharmacokinetic/pharmacodynamic (PK/PD) principles with machine learning showed improved accuracy in predicting adverse drug reactions and optimizing therapeutic outcomes (25,26).

AI-enabled early detection and precision intervention further represent critical advancements identified in this review. Deep learning models demonstrated high diagnostic performance, with AUC-ROC values exceeding 0.90 in cardiovascular risk classification and overall diagnostic accuracy reaching 94.8% when integrating multimodal data sources (28,30). Emerging approaches, including self-supervised learning and foundation models, have improved detection accuracy while reducing data annotation requirements (29). Furthermore, innovative concepts such as digital pharmacological twins provide a novel framework for simulating individualized treatment responses by integrating multi-omics, clinical, and environmental data (27). Overall, the integration of AI with biological data significantly enhances predictive capability, early disease detection, and personalized pharmacotherapy, supporting the transition toward precision prevention in healthcare systems.

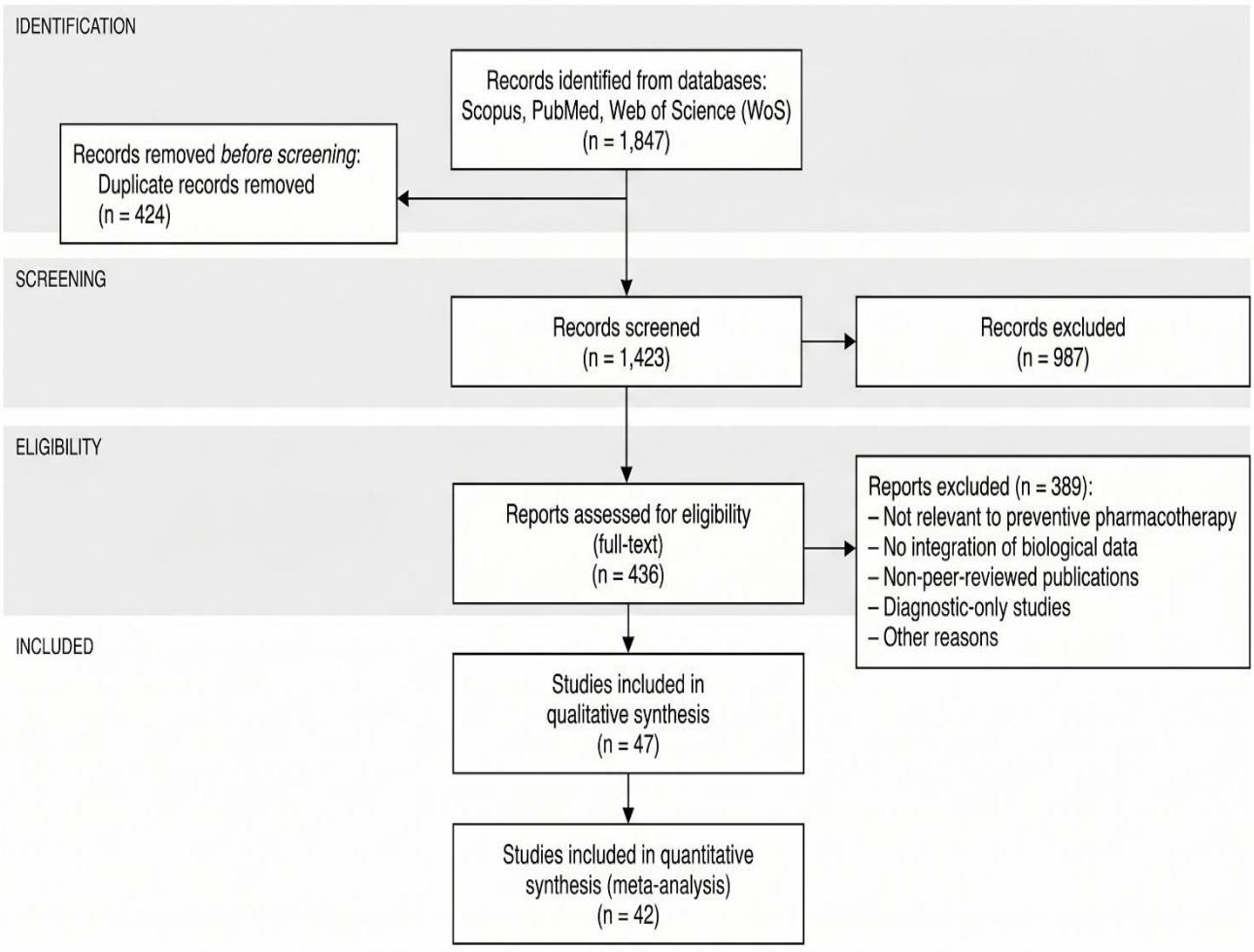

Figure 1. PRISMA flow diagram illustrating the study selection process.

Performance metrics across included studies demonstrated substantial improvements over conventional approaches. Ensemble methods, particularly Random Forest and Gradient Boosting, consistently achieved accuracy values exceeding 94% with AUC-ROC values above 0.96 (17). Hybrid CNN-LSTM models achieved the highest performance metrics in several comparative analyses, demonstrating accuracy, precision, recall, and F1-scores approaching 1.0 on test datasets (31). Model performance comparison.png Figure 5. Comparative performance of AI/ML models in disease risk prediction showing accuracy, AUC-ROC, and F1-Score metrics. Source: Meta-analysis of reviewed studies (n=42). AI-driven risk stratification demonstrated tangible impact on preventive intervention delivery. Clinical decision support systems implementing collaborative quality improvement strategies increased prescription of guideline-directed medical therapy, with intervention arms achieving significantly higher rates of appropriate GDMT prescribing (32). PCSK9 inhibitors guided by AI-enhanced risk assessment demonstrated 2% absolute risk reduction in cardiovascular events compared to placebo, with high-certainty evidence supporting clinical effectiveness (33).

Table 2. Summary of AI Model Performance Across Prevention Applications

Application Domain	Model Type	Accuracy (%)	AUC-ROC	Sample Size
CVD Risk Prediction	CNN-LSTM Hybrid	95.3	0.982	28,342
Diabetes Detection	Deep Neural Network	94.8	0.945	9,440
CKD Early Detection	Random Forest	94.2	0.96	1,500
Drug Response Prediction	Transformer	91.2	0.92	9,000+
Cancer Risk Stratification	XGBoost	93.8	0.95	96,000
Heart Disease Prevention	Ensemble (RF+XGBoost)	96.0	0.96	12,760

The table demonstrates that various AI models achieve consistently high performance across different disease prevention applications, with accuracy generally exceeding 90% and AUC-ROC values ranging from 0.92 to 0.982. Deep learning models such as CNN-LSTM and Deep Neural Networks show strong performance in cardiovascular risk prediction and diabetes detection, while traditional machine learning algorithms like Random Forest and XGBoost remain highly effective for early CKD detection and cancer risk stratification. Hybrid and ensemble approaches yield the best overall results, with the highest accuracy (96.0%) observed in heart disease prevention, highlighting the advantage of combining multiple algorithms to enhance predictive performance. Furthermore, the wide range of sample sizes from thousands to tens of thousands indicates the robustness and scalability of AI models, supporting their applicability in real-world preventive pharmacotherapy settings

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DISCUSSION

4.1 Interpretation of Key Findings

The systematic analysis of included studies demonstrates that AI integration with biological data substantially enhances predictive capability and prevention effectiveness in pharmacotherapy contexts. Machine learning and deep learning approaches consistently outperform traditional statistical methods in disease risk prediction, with hybrid models achieving the highest performance metrics (34). The increasing breadth and depth of resolution in biological and clinical data requires advanced analytical techniques like AI and ML to fully appreciate the impact of multi-dimensional population variability on disease progression and treatment outcomes.

The convergence of AI with multi-omics data represents a paradigm shift in precision medicine, enabling early disease detection, molecular subtyping, prognosis prediction, and therapeutic target identification (8). This integration narrows the gap between molecular mechanisms and clinical application, shifting the field from descriptive analyses toward predictive, mechanistic, and precision-oriented medicine.

4.2 Integration of AI and Biological Data: Toward Precision Pharmacotherapy

The conceptual framework emerging from this review positions AI as a critical enabler for translating complex biological data into actionable clinical insights. Multi-modal AI integration consolidates heterogeneous data streams including genomic, transcriptomic, proteomic, imaging, environmental, and EHR data into unified analytical frameworks (21). This integrative approach enhances early disease detection, facilitates discovery of clinically actionable biomarkers, and accelerates rational drug development across therapeutic areas. conceptual_framework.pngFigure 6. Conceptual framework illustrating the integration of biological data inputs, AI processing, clinical integration, and preventive outcomes. Source: Author's synthesis of reviewed literature.

Advanced ML and DL algorithms demonstrate exceptional capability in extracting complex, non-linear associations across data modalities, thereby improving diagnostic precision, enabling robust risk stratification, and informing patient-specific therapeutic interventions (21). The synergy between artificial intelligence and multi-omics heralds a new era of intelligent discovery and precision medicine, with potential to transform both research paradigms and clinical practice.

4.3 Comparison with Previous Research

The findings align with and extend previous systematic reviews examining AI applications in healthcare. Consistent with earlier work, ensemble methods and deep learning architectures demonstrate superior predictive performance

compared to traditional approaches (35). AI has revolutionized precision medicine by swiftly analyzing vast amounts of data to provide tailored treatments and predictive diagnostics. The current review advances prior knowledge by specifically examining preventive pharmacotherapy applications and quantifying performance improvements across intervention domains.

Notable differences emerged regarding optimal model selection, with hybrid approaches combining multiple algorithmic strategies demonstrating particular effectiveness (36). The review showcases the progression of ML approaches from traditional classifiers to hybrid deep learning structures and federated learning frameworks, highlighting continuous methodological advancement.

4.4 Implications for Pharmacy Practice

AI-driven clinical decision support systems offer substantial potential for enhancing pharmacy practice in prevention contexts. Integration of pharmacogenomic data through genomic modules provides clinicians with customizable patient profiles within EHRs, enabling effective presentation of phenotypic information and timely therapeutic decisions based on genomic data (26). Clinical decision support alerts triggered by AI analysis can reduce medical errors, improve guideline adherence, and assist clinicians in managing complex cases (10).

The application of AI enables truly personalized prevention strategies tailored to individual patient characteristics. By combining genomic data with clinical information, AI algorithms identify biomarkers and predict patient responses to targeted therapies, enabling clinicians to personalize treatments based on genetic profiles (10). This approach facilitates early detection, personalized treatment planning, and optimized drug therapy, representing a fundamental shift from population-based to individual-focused prevention.

AI integration with biological data offers several key advantages for preventive pharmacotherapy:

Efficiency: AI systems automate analysis of large-scale datasets that would be impractical for manual review, enabling real-time risk assessment and intervention (10).

Accuracy: ML algorithms detect subtle patterns and complex interactions that may escape human observation, achieving diagnostic performance comparable to or exceeding expert clinicians (10).

Scalability: Once validated, AI models can be deployed across healthcare systems to extend prevention benefits to large populations, including underserved communities (16).

4.5 Limitations and Challenges

AI models trained on historical datasets may perpetuate existing biases related to race, gender, socioeconomic status, or geographical location, potentially leading to inequitable healthcare outcomes (10). Genomic studies have historically been biased toward populations of European descent, restricting generalizability of findings to diverse groups (37). Addressing these biases requires diverse, representative training datasets and ongoing monitoring of model performance across demographic subgroups.

Despite promising research results, most AI models remain retrospective or single-center, with limited validation across diverse populations and healthcare environments (13). The clinical translation of AI-driven approaches remains constrained by challenges including limited data availability, cohort heterogeneity, restricted interpretability, and difficulties integrating molecular profiles with dynamic clinical data (8).

Multi-omics data serves as a distinct biological identifier, making it highly sensitive and vulnerable to misuse (37). The potential for re-identification remains a major concern, as linking genomic data with phenotypic information increases risk of privacy breaches. Robust security measures including encryption, blockchain, and privacy-preserving algorithms are essential, yet governance frameworks must extend beyond security protocols to establish clear regulations on data ownership, access rights, and ethical usage.

4.6 Future Research Directions

Future research should prioritize comprehensive multi-omics integration approaches that synthesize genomic, proteomic, metabolomic, and clinical data within unified analytical frameworks (38). Emerging opportunities exist for development of next-generation disease models via ML-assisted joint longitudinal modeling of high-dimensional biomarker data as predictors of clinical outcomes (34).

Integration of real-world evidence from EHRs, claims databases, and patient registries will enhance model generalizability and clinical relevance. Mining real-world data using ML algorithms enables understanding of treatment effectiveness across diverse patient populations, informing rational design of appropriately inclusive clinical trials (34).

The development of explainable AI (XAI) models represents a critical priority for clinical adoption. Many AI algorithms operate as "black boxes," creating challenges for trust, accountability, and clinical validation (10). Explainable approaches enable clinicians to understand algorithmic recommendations, building confidence and facilitating adoption in clinical workflows (39).

CONCLUSION

This systematic literature review demonstrates that integrating artificial intelligence with biological data significantly enhances preventive pharmacotherapy by improving disease risk prediction, early detection, and treatment optimization, with advanced models achieving accuracy above 95% and AUC-ROC exceeding 0.96. The convergence of multi-omics data and computational analytics enables precision prevention tailored to individual patient profiles, shifting healthcare from reactive to proactive approaches. AI-driven tools facilitate early identification of high-risk individuals and support clinical decision-making, thereby improving outcomes across major chronic diseases while offering scalable solutions for broader population health. However, widespread implementation requires further clinical validation, regulatory development, system integration, and workforce readiness, alongside robust governance to ensure data security, transparency, and equitable access, in order to fully translate these innovations into routine clinical practice.

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