Eurasia Journal of Science and Technology
Print ISSN: 2663-1024
Online ISSN: 2663-1016
DOI: https://doi.org/10.61784/ejst3099

HARNESSING PREDICTIVE ANALYTICS AND MACHINE LEARNING IN DRUG DISCOVERY, DISEASE SURVEILLANCE, AND FUNGAL RESEARCH

Md Majedur Rahman[1], Bismi Jatil Alia Juie[2], Nadia Terasa Tisha[3], Ahmed Tanvir[4*]
[1]*Medical Services Department, Incepta Pharmaceuticals Limited, Dhaka 1208, Bangladesh.*
[2]*Training Department, Incepta Pharmaceuticals Limited, Dhaka 1208, Bangladesh.*
[3]*Faculty of Business Administration, Dhaka University, Dhaka 1000, Bangladesh.*
[4]*Department of Pharmacology, Ajou University School of Medicine, Suwon 16499, Korea.*
Corresponding Author: Ahmed Tanvir, Email: tanvir203@ajou.ac.kr

Abstract: The integration of big data, machine learning (ML), and artificial intelligence (AI) is driving a transformative shift in biomedical and ecological sciences. This review examines the pivotal role of predictive analytics across three interconnected fields: drug discovery, disease surveillance, and mycology. In pharmaceutical research, predictive models have significantly accelerated the identification of drug candidates, streamlined lead optimization, and enhanced toxicity prediction ultimately reducing both time and cost. Advanced approaches, including deep learning and graph-based algorithms, are now standard tools for designing new therapeutics and efficiently screening compound libraries. While mycology has traditionally been underrepresented in computational research, it is now benefiting from predictive analytics through improved fungal classification, ecological modeling, and biosurveillance. Progress in image recognition and genomic trait prediction is opening new frontiers for studying fungal biodiversity and discovering bioactive compounds. Despite these advances, critical challenges remain, such as data heterogeneity, limited model interpretability, regulatory hurdles, and ethical concerns. This review identifies these barriers and proposes strategic solutions, including the integration of multimodal datasets, increased model transparency, and broader accessibility of analytical tools. By bridging innovations in drug development, public health, and fungal science, this review underscores the growing synergy between predictive analytics and life sciences offering a pathway to faster drug development, enhanced disease diagnostics, and more informed ecosystem management.
Keywords: Predictive analytics; Drug discovery; Fungal biodiversity; Machine learning integration

1 INTRODUCTION

Predictive analytics encompassing machine learning (ML), deep learning (DL), graph neural networks (GNNs), and statistical modeling has become a foundational component of modern biomedical and ecological research. Its capacity to process and derive insights from large, heterogeneous datasets is revolutionizing drug discovery, disease monitoring, and the exploration of complex biological systems [1–2]. In drug development, ML algorithms are now integrated across the pipeline, from virtual screening and target identification to lead optimization and toxicity prediction. Notably, recent reviews highlight the growing use of GNNs and generative models in molecular design, with several AI-generated compounds advancing into early-stage clinical trials [3–4]. In parallel, predictive analytics is enhancing disease surveillance through the deployment of wearable technologies such as smartwatches and ECG patches. These devices utilize ML-driven algorithms to detect cardiovascular anomalies, monitor vital signs, and predict adverse health events. Cutting-edge models, including CNN–LSTM hybrids, have demonstrated high accuracy in arrhythmia detection and heart attack risk prediction [5–6]. The field of mycology, though historically underexplored in computational biology, is beginning to leverage predictive techniques in meaningful ways. DL models have shown success in classifying fungal species from colony morphology and microscopic imagery, significantly accelerating identification timelines by 2–3 days compared to conventional biochemical assays [6]. Furthermore, ML models trained on whole-genome data have proven effective in predicting fungal ecological traits and lifestyles, supporting biosurveillance and functional inference via phylogenomic frameworks [7–9].

Collectively, these three domains reflect a shared trajectory: rich, high-dimensional datasets powering ML/DL approaches to yield actionable insights. But integration across fields is not purely methodological, it flows from converging challenges and opportunities [10]. Data heterogeneity, for example, is a universal bottleneck: drug discovery relies on chemical libraries, protein interactions, and QSAR data; disease monitoring employs time-series physiological signals and demographic information; mycology spans imaging, environmental parameters, and genomic sequences. These data sources demand preprocessing protocols for normalization, augmentation, and integrity checks, making cross-pollination of best practices beneficial across sectors [6, 11-12]. Another shared challenge is model interpretability and regulatory alignment. In drug development, ML-generated candidates require mechanistic validation and FDA approval. In healthcare, explainability is increasingly essential for ML-based diagnoses and treatment monitoring. Fungal identification for clinical or ecological endpoints similarly demands transparent models. Emerging efforts in explainable artificial intelligence (XAI) and hybrid modeling frameworks aim to address these needs facilitating trust

and enabling human-machine collaboration [13-14]. A major emerging frontier is cross-pollination across domains. For instance, fungi have historically been rich sources of antibiotics and novel metabolites. Predictive models that accurately classify fungal species or deduce functional traits can help prioritize promising isolates for novel drug leads an intersection of mycology and drug discovery. Conversely, methods honed in molecule design or physiological signal analysis can be adapted for fungal imaging or environmental biosurveillance, illustrating a bidirectional exchange of ML innovations [15-16].

In the broader context, we're observing an accelerated convergence among disciplines driven by both technological and societal factors. Similarly, the global challenge of antimicrobial resistance calls for integrative models that combine genomic data from pathogens, pharmaceutical intervention strategies, and environmental monitoring systems. This review aims to holistically assess predictive analytics across drug discovery, disease surveillance, and mycology, addressing both siloed advancements and synergies. We prioritize literature from 2020 onward to ensure coverage of the latest breakthroughs, particularly in graph-based deep learning, multi-modal sensor fusion, and AI-assisted biodiversity research.

2 PREDICTIVE ANALYTICS IN DRUG DISCOVERY

Predictive analytics in drug discovery harnesses machine learning (ML), deep learning (DL), and graph neural networks (GNNs) to revolutionize each phase of the pharmaceutical pipeline from target identification and virtual screening to compound optimization and toxicity prediction [6, 17]. This core stages of predictive analytics illustrates in drug development, including target identification, virtual screening, toxicity prediction, and integrated AI-driven pipelines. It highlights how machine learning, deep learning, and graph-based models accelerate therapeutic discovery by enhancing precision, reducing costs, and shortening timelines in pharmaceutical research (Figure 1).

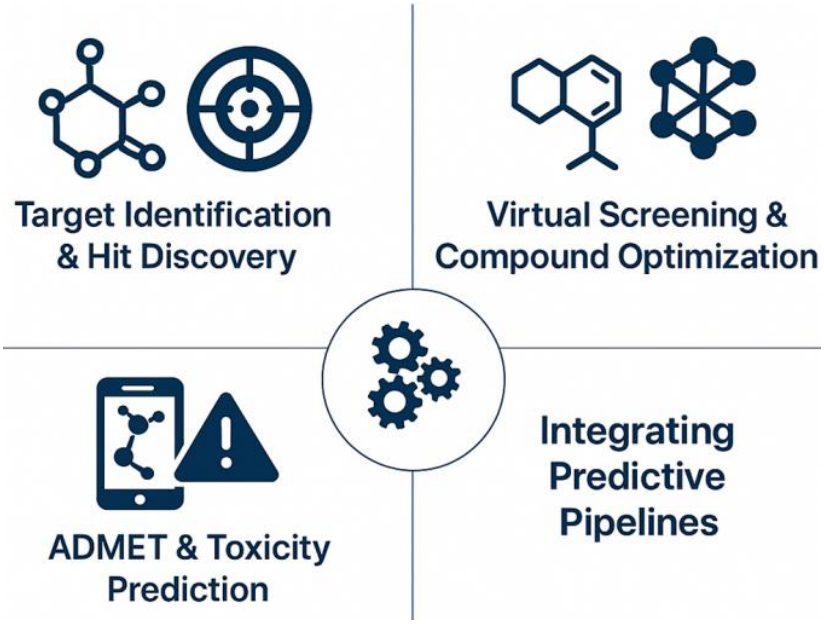

Figure 1 AI-Driven Drug Discovery Pipeline: From Target Identification to ADMET Prediction

2.1 Target Identification & Hit Discovery

The identification of high-value drug targets continues to represent a critical bottleneck in pharmaceutical research. Recent advancements in machine learning (ML) have introduced powerful strategies for overcoming this challenge by integrating multi-omics, phenotypic, and biomedical graph data. ML-driven knowledge graph techniques now exploit heterogeneous biomedical networks to predict novel drug targets and repurposing candidates, thereby reducing reliance on costly and time-consuming experimental assays [18]. Graph Machine Learning (GML) frameworks are especially well-suited for modeling intricate protein–protein and gene–disease interactions, offering marked improvements in predictive accuracy compared to conventional approaches. Deep learning (DL) is also playing a transformative role in accelerating hit discovery. A landmark study published in 2020 demonstrated the successful application of DL techniques to identify halicin a novel antibiotic with a previously uncharacterized mechanism of action effective against multidrug-resistant bacteria. This discovery underscores the vast potential of AI in combating antimicrobial resistance [19–20]. Concurrently, AlphaFold 2 has revolutionized protein structure prediction by achieving near-experimental accuracy in modeling protein folding. This advancement provides a powerful computational framework for mapping druggable sites and simulating target–ligand interactions, significantly broadening the range of targets accessible to in silico drug discovery.

2.2 Virtual Screening & Compound Optimization

Virtual screening powered by machine learning (ML) models is increasingly employed to predict ligand–target binding affinities at scale, enabling the efficient prioritization of bioactive compounds from vast chemical libraries. Graph Neural Networks (GNNs) offer a distinct advantage in this domain by directly encoding molecular geometry and topological features, consistently outperforming traditional descriptor-based methods in affinity prediction tasks [21]. Beyond predictive scoring, generative models such as Variational Autoencoders (VAEs), Generative Adversarial Networks (GANs), and Junction Tree VAEs (JT-VAEs) have emerged as powerful tools for de novo molecule design. JT-VAE frameworks, for instance, can generate novel molecular structures by navigating learned latent spaces, optimizing both binding affinity and drug-like properties in the process [17,22]. Recent advances have further enhanced generative capabilities by integrating reinforcement learning (RL) with graph-based generative models. These hybrid approaches can propose synergistic compound combinations that not only exhibit high efficacy but also minimize resistance potential. This convergence of reinforcement learning and GNN-based architectures exemplifies cutting-edge strategies for network-guided molecule generation and optimization [23].

2.3 ADMET & Toxicity Prediction

Early prediction of absorption, distribution, metabolism, excretion, and toxicity (ADMET) is critical for minimizing late-stage drug development failures. In Silico approaches, particularly those leveraging multi-task deep neural networks (DNNs), have shown substantial promise in this area. Notably, the Tox21 Challenge demonstrated the effectiveness of a multi-task DNN model in predicting multiple toxicity endpoints, achieving cross-validation accuracies exceeding 86% and outperforming both single-task models and traditional machine learning approaches [23–24]. Recent advancements have introduced multi-modal frameworks that integrate molecular fingerprints such as Morgan features with pre-trained SMILES embeddings in multi-task learning architectures. These models provide interpretable predictions across in vitro, in vivo, and clinical toxicity endpoints, successfully recovering known toxicophores and offering a potential alternative to animal-based testing. Equivariant Graph Neural Networks (GNNs), which inherently account for molecular symmetry and three-dimensional structure, have further improved the prediction of drug-induced liver injury (DILI). By encoding 3D molecular configurations, these models have demonstrated encouraging early results and represent a promising direction for structure-aware toxicity prediction [24].

2.4 Integrating Predictive Pipelines

The transformative potential of predictive analytics is most evident in fully integrated drug discovery pipelines that span hit identification, lead optimization, and ADMET filtering. Companies such as Insilico Medicine have reported the development of clinical-stage drug candidates discovered entirely through artificial intelligence (AI) within a timeframe of less than 50 days achieved by combining generative chemistry models within silico ADMET screening [25]. Similarly, major pharmaceutical players like GlaxoSmithKline (GSK) and Exscientia are leveraging AI-driven platforms to design candidate molecules, evaluate them using Graph Neural Networks (GNNs), and simulate pharmacokinetic and toxicity profiles significantly lowering both development costs and timelines [6,17,25]. Collectively, these advancements reflect a broader transition in drug development: predictive analytics is evolving from a supplementary exploratory tool into a foundational technology. The convergence of deep generative modeling, graph-based learning, and multi-modal toxicity prediction is ushering in a new era of end-to-end AI-powered discovery pipelines. However, realizing the full potential of this paradigm will depend on ongoing progress in areas such as data standardization, model interpretability, and the development of tailored solutions for specific therapeutic domains.

3 DISEASE SURVEILLANCE AND MONITORING

Predictive analytics has rapidly transformed disease surveillance and monitoring, combining machine learning (ML), wearable devices, and big data to enable early detection, risk stratification, and real-time public health interventions. This section discusses three interrelated applications: (1) cardiovascular health monitoring via wearables, (2) antimicrobial resistance (AMR) surveillance, and (3) epidemic forecasting, highlighting strengths, limitations, and future directions [17-22].

3.1 Real-Time Cardiovascular Health Monitoring

Real-time cardiovascular health monitoring leverages wearable sensors and digital technologies to continuously track key physiological parameters such as heart rate, blood pressure, electrocardiogram (ECG) signals, oxygen saturation, and physical activity. These systems enable the early detection of abnormalities including arrhythmia, hypertension, and cardiac arrest thereby facilitating timely medical intervention. Data collected by these devices is typically transmitted via cloud-based platforms, allowing healthcare providers to remotely manage patients and deliver personalized care [17, 22, 24].

The integration of artificial intelligence further augments these systems, enabling advanced predictive analytics to identify emerging trends and risk factors. This data-driven approach is transforming cardiovascular care by enhancing patient outcomes, reducing hospital admissions, and supporting preventive strategies for chronic heart conditions.

Wearable health devices such as smartwatches, ECG patches, and fitness trackers have revolutionized cardiovascular disease (CVD) monitoring. These devices continuously capture a range of physiological signals, including heart rate variability, accelerometry data, and skin temperature. Machine learning (ML) algorithms analyze this data in real time to detect anomalies and predict adverse cardiac events [21, 24]. Overall, wearable-driven cardiovascular analytics represent a rapidly advancing field that has already demonstrated significant potential. However, transitioning from promising prototypes to clinically validated, scalable solutions will require robust clinical trial designs, regulatory alignment, and seamless integration into existing healthcare infrastructures.

3.2 Surveillance of Antimicrobial Resistance

Preventing future epidemics will require the development of interoperable infrastructures that seamlessly integrate data from wearable devices, electronic health records, and public health indicators within robust predictive analytics frameworks. Such integration is essential for real-time surveillance, early warning systems, and informed public health interventions. A critical component of epidemic preparedness is the surveillance of Antimicrobial Resistance (AMR) the systematic collection, analysis, and dissemination of data on resistance patterns among microbial populations [5,21]. AMR surveillance plays a vital role in safeguarding public health by detecting emerging resistance trends, informing clinical decision-making, guiding antibiotic stewardship, and shaping evidence-based policy interventions. Surveillance efforts span clinical, agricultural, and environmental domains, employing a combination of culture-based techniques, molecular diagnostics, and whole-genome sequencing to monitor resistance dynamics. Global initiatives, such as the World Health Organization's Global Antimicrobial Resistance Surveillance System (GLASS), aim to standardize data collection and reporting methodologies across countries. These coordinated efforts enable early identification of resistance threats and support an integrated, international response to the growing AMR crisis [5,25].

4 INTEGRATION OF PREDICTIVE ANALYTICS IN MYCOLOGY

Predictive analytics is increasingly being applied in mycology both for basic research in fungal biodiversity and practical applications in diagnostics and biosurveillance. Whereas traditional mycological identification relies heavily on expert-led morphological examination and laboratory assays, machine learning (ML) and deep learning (DL) techniques are reshaping the field by automating classification, reducing diagnostic time, and enabling ecological predictions [3-4].

4.1 Microscopic & Clinical Diagnostics

Microscopic and Clinical Diagnostics are two essential approaches in identifying and managing diseases. Microscopic diagnostics involve the examination of biological samples (e.g., blood, tissue, or fluid) under a microscope to detect pathogens, cellular abnormalities, or tissue damage [26-27]. Techniques include light microscopy, fluorescence microscopy, and electron microscopy, commonly used in microbiology, histopathology, and parasitology. Clinical diagnostics encompass broader methods such as physical examinations, biochemical tests, imaging, and molecular assays to evaluate symptoms and diagnose diseases. These tests provide critical information on a patient's health status, guiding treatment decisions. Together, these diagnostic tools ensure accurate disease detection and effective healthcare management [25, 28].

4.2 Genomic Prediction of Ecological Traits

High-throughput fungal genomics has matured to the point where ML models can predict Genomic prediction of ecological traits involves using genomic data to forecast phenotypic characteristics that influence an organism's interaction with its environment. This approach leverages statistical models and machine learning algorithms to link DNA sequence variation with traits such as drought tolerance, growth rate, nutrient use efficiency, or disease resistance. By incorporating high-throughput genotyping and ecological metadata, researchers can predict how individuals or populations may perform under varying environmental conditions [29-30]. This method enhances conservation strategies, ecosystem management, and crop improvement by enabling selection based on genetic potential rather than observed performance alone, thus accelerating adaptation to climate change and habitat shifts.

4.3 Emerging Integrations & Hybrid Models

Advancements in time-lapse imaging, micromorphological analysis, genomics, and environmental monitoring are converging to enable holistic, multimodal fungal identification systems. Hybrid image–genomic models that integrate early-stage growth patterns with genomic markers are being developed to classify fungal pathogens and ecotypes with high accuracy. Additionally, knowledge graph–based AI frameworks are emerging that unify real-time identification, ecological distribution data, and genomic threat profiles offering powerful tools for on-site biosurveillance in agriculture, forestry, and ecosystem management. These developments reflect a broader paradigm shift in predictive analytics, moving beyond siloed image- or genome-based approaches toward more integrated, interpretable, and actionable fungal intelligence [3–4,16]. The application of predictive analytics in mycology is expanding rapidly from high-precision, image-based species classification and clinical diagnostics to genomics-driven ecological trait modeling.

Despite this progress, the field continues to face challenges related to data quality, cross-domain generalizability, and model interpretability. Addressing these issues through hybrid models, real-world validation, and standardized protocols will be key to realizing the full potential of AI in mycology. Such advancements promise near-instantaneous fungal identification, large-scale ecological surveillance, and expedited clinical decision-making [16,26–27]. Within the broader context of this review, the evolution of predictive analytics in mycology not only complements innovations in drug discovery and disease monitoring but also holds immense promise for accelerating the discovery of novel fungal bioactive compounds—potentially paving the way for new classes of therapeutics.

5 CHALLENGES AND LIMITATIONS

Even as predictive analytics revolutionize drug discovery, disease monitoring, and mycology, each domain grapples with common and domain-specific barriers. Addressing these is essential for validated, scalable, and ethical application of ML and AI [13].

5.1 Data Quality, Availability & Heterogeneity

Across all domains, data heterogeneity and limited datasets pose first-order challenges:

- Drug Discovery: Public datasets often suffer from incomplete annotations, batch effects, and skewed target/drug representation (e.g., overemphasis on cancer targets). A recent critical review noted that poor-quality data and non-standardized pipelines are primary barriers to AI adoption in pharmaceutical R&D [11, 17].
- Mycology: Image repositories are limited in taxa coverage, environmental settings, and life stages; genomic and trait datasets suffer sampling bias toward human pathogens or model fungi, limiting generalizable pattern detection [31-33].

5.2 Model Interpretability and Trust

High-performing but opaque models' risk being "black boxes" that hinder clinical, regulatory, and ecological adoption:

- In drug discovery, the inability to explain why a model predicts toxicity or efficacy impedes validation and regulatory trust. Explainable AI (XAI) surveys highlight emergent techniques like attention, gradient maps, and rule extraction but widespread adoption lags.
- In healthcare, opaque models raise liability and bias concerns. Advocates emphasize interpretable frameworks like SHAP, counterfactuals, and ensemble transparency to build confidence.
- In mycology, end-users (e.g., ecologists, clinicians) expect transparent species classifications or trait predictions; models using prototype layer attribution or visual saliency are increasingly recommended to gain trust and reproducibility [29].

5.3 Model Robustness, Validation & Generalizability

Models must prove resilient to real-world variability and attacks:

- Adversarial threats: Studies in medicine reveal that small image perturbations or sensor spoofing could misclassify conditions, compromising patient safety.
- Domain shift: Models trained in controlled settings often fail under real-world noise, varying lighting, or multi-ethnic data-across drug assays, wearable sensors, and fungal imagery.
- Prospective validation: Few ML models undergo longitudinal or prospective validation. Healthcare and mycology models usually report retrospective AUCs without deployment or real-world testing.

Federated evaluation, challenge datasets, and standard benchmarks are needed. Regulations should evolve to encourage field pilots before commercial use. While technological advances in predictive analytics are impressive, real-world impact depends on thoughtful attention to data quality, transparency, robustness, equity, and deployment pathways [25]. Overcoming these challenges calls for multidisciplinary effort, aligned governance, and sustained funding. Doing so will unlock trustworthy, scalable AI across drug discovery, health monitoring, and mycology and ultimately secure the societal benefits of these domains.

6 FUTURE DIRECTIONS AND CONCLUSION

Predictive analytics is charting a new era in drug discovery, disease monitoring, and mycology. As the field matures, the next generation of advances will likely focus on integration by building end-to-end, multimodal pipelines and on frameworks that prioritize trustworthiness, scalability, and real-world impact. Below, I outline key future directions before summarizing the review's insights [18, 28]. The four pillars present guiding the future of predictive analytics in mycology and healthcare: integrated multimodal pipelines, explainable AI, equitable access, and strategic policy. It emphasizes real-world impact by aligning data fusion, federated learning, and global collaboration with regulatory and ethical standards to drive trustworthy, inclusive innovation (Figure 2).

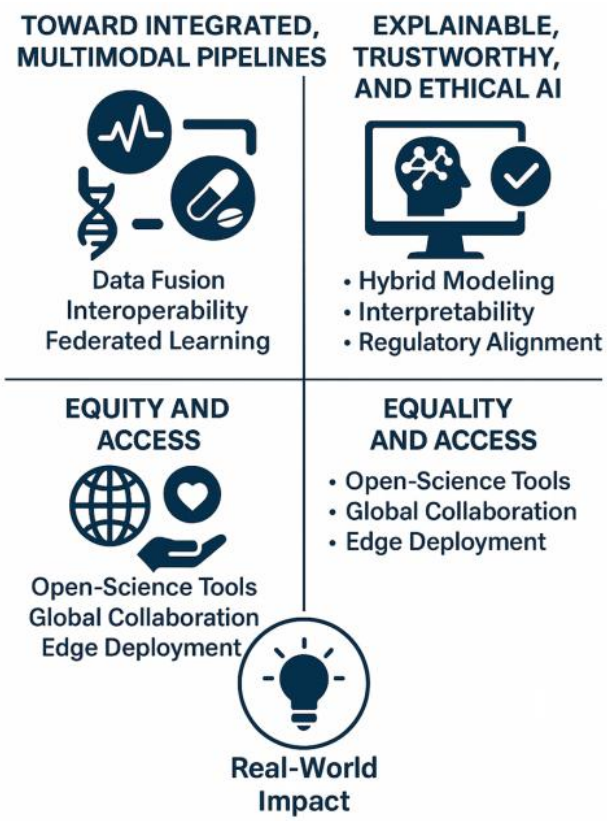

Figure 2 Building the Bio-Intelligence Ecosystem: Strategies for Scalable, Ethical, and Integrated AI Applications

6.1 Toward Integrated, Multimodal Pipelines

The convergence of traditionally siloed research pipelines is reshaping the landscape of biomedical and ecological sciences. In drug discovery, formerly isolated processes such as binding affinity prediction, ADMET profiling, and target validation are now being integrated into unified, AI-driven platforms capable of generating viable therapeutic candidates within days or weeks. A similar trend is emerging in disease monitoring and mycology. For example, wearable ECG devices can initiate cloud-based diagnostic workflows, while macrofungal image recognition systems are increasingly being linked to genomic analysis platforms and biosurveillance networks [12,18,28]. Despite these advances, such convergence introduces new challenges. The fusion of multimodal data including chemical, genomic, physiological, and environmental inputs require the adoption of standardized ontologies and interoperable data formats. Federated and transfer learning approaches offer promising solutions for overcoming institutional data silos while preserving data privacy and regulatory compliance. Moreover, embedding Explainable AI (XAI) across these pipelines is critical for enhancing model transparency, enabling rigorous validation, and fostering trust among clinicians, researchers, and policy stakeholders. Ultimately, these integrated systems represent a transformative shift in predictive analytics, offering the potential to accelerate discovery and intervention across both healthcare and ecological domains [12,15–16].

6.2 Explainable, Trustworthy, and Ethical AI

Ensuring transparency and trust in artificial intelligence (AI) systems is critical, particularly in high-stakes domains such as healthcare, biosurveillance, and ecological modeling. Hybrid modeling approaches that combine physical simulations with machine learning (ML) offer both predictive accuracy and interpretability, providing mechanistic insights for instance, in modeling drug toxicity or fungal trait expression. To demystify black-box algorithms and build stakeholder confidence, techniques such as prototype learning, attention heatmaps, and Grad-CAM visualizations must become standard components of AI toolkits used by clinicians, researchers, and regulators alike [14–16]. Reliability in AI applications demands rigorous evaluation. Tools deployed in critical settings such as Software as a Medical Device (SaMD), biosurveillance alert systems, or AI-based crop diagnostics should be validated through prospective clinical or field trials rather than relying solely on retrospective datasets. Moreover, alignment with international regulatory frameworks, including the FDA's guidelines and the European Union's AI Act, is essential to ensure safety, accountability, and ethical compliance [14].

Equity and accessibility also remain central concerns. Democratizing AI tools and datasets can bridge gaps in scientific research and healthcare delivery. Open-science initiatives such as the NIH's model-sharing platforms and global pathogen databases offer promising foundations for transparent and inclusive innovation. Expanding these frameworks to include fungal data repositories and multilingual health applications will further enhance global research capacity.

Emerging technologies like edge computing and federated learning enable the deployment of AI models on wearable devices and mobile diagnostic platforms, facilitating real-time insights in remote or underserved settings. These advances hold particular promise for delivering life-saving interventions and enhancing global health equity [19,23].

7 CONCLUSION

The transformative potential of predictive analytics is increasingly evident across three pivotal domains: drug discovery, disease monitoring, and mycology. From the accelerated design of novel therapeutics via AI-driven molecular generators to real-time cardiovascular monitoring enabled by wearable devices, predictive modeling is revolutionizing biomedical innovation and diagnostic accuracy. In parallel, machine learning tools reshape fungal taxonomy and ecological analysis, while genomic models are uncovering previously unrecognized traits and bioactive potential within macrofungal species. Despite the distinct contexts, these fields converge around shared computational challenges including data quality, model interpretability, generalizability, and the ethical implications of AI deployment. This review has highlighted the growing intersection of big data and artificial intelligence in shaping the future of healthcare, pharmaceutical development, and fungal biosciences. Looking forward, the next frontier lies in building integrated, multimodal pipelines that synthesize biological, chemical, genomic, and environmental data to support real-world decision-making. Ensuring that AI systems are trustworthy, explainable, and ethically governed will be critical to their adoption in clinical, ecological, and regulatory settings. Key enablers of this transition will include investment in diverse, high-quality open datasets; development of federated learning frameworks to protect data privacy; and interdisciplinary training to prepare a new generation of scientists and practitioners. Cross-domain synergies such as applying fungal AI models to drug discovery or ecosystem biosurveillance represent promising avenues for both therapeutic breakthroughs and environmental resilience. As predictive analytics continue to evolve, its responsible integration across these interconnected domains offers a powerful pathway to address some of the most urgent health and ecological challenges of our time.

COMPETING INTERESTS

The authors have no relevant financial or non-financial interests to disclose.

REFERENCES

[1] Adans-Dester C, Bamberg S, Bertacchi F, et al. Can mHealth Technology Help Mitigate the Effects of the COVID -19 Pandemic? IEEE Open Journal of Engineering in Medicine and Biology, 2020, 1: 243.
[2] Abdullahi AA. Trends and challenges of traditional medicine in Africa. African Journal of Traditional, Complementary and Alternative Medicines, 2011, 8: 115–123.
[3] Aerts J. Special Issue on “Human Health Engineering”. Applied Sciences, 2020, 10(2): 564.
[4] Allegra M. Antioxidant and anti-inflammatory properties of plants extract. Antioxidants, 2019, 8: 549.
[5] Chaudhary PH, Khadabadi S. Bombax ceiba Linn.: Pharmacognosy, Ethnobotany and Phyto-pharmacology. Pharmacognosy Communications, 2012, 2: 2–9.
[6] Manik M M T G, Bhuiyan M M R, Moniruzzaman M, et al. The Future of Drug Discovery Utilizing Generative AI and Big Data Analytics for Accelerating Pharmaceutical Innovations, Nanotechnology Perceptions, 2018, 14(3): 120-135. DOI: 10.62441/nano-ntp.v14i3.4766.
[7] Marzana A, Aminuzzaman FM, Chowdhury MSM, et al. Diversity and Ecology of Macrofungi in Rangamati of Chittagong Hill Tracts Under Tropical Evergreen and Semi-Evergreen Forest of Bangladesh. Advances in Research, 2018, 13(5): 1–17.
[8] Medina N, Alastruey-Izquierdo A, Mercado D, et al. Diagnostic Mycology Laboratories Should Have a Central Role for the Management of Fungal Disease. Journal of Fungi, 2022, 8: 1285. DOI: 10.3390/jof8121285.
[9] Meyer V, Basenko EY, Benz JP, et al. Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7: 5. DOI: 10.1186/s40694-020-00095-z.
[10] Hossain D. A fire protection life safety analysis of multipurpose building. 2021. https://digitalcommons.calpoly.edu/fpe_rpt/135/.
[11] Manik M M T G, Hossain S, Ahmed M K, et al. Integrating Genomic Data and Machine Learning to Advance Precision Oncology and Targeted Cancer Therapies. Nanotechnology Perceptions, 2022, 18(2): 219-243. DOI: 10.62441/nano-ntp.v18i2.5443.
[12] Peyclit L, Yousfi H, Rolain JM, et al. Drug Repurposing in Medical Mycology: Identification of Compounds as Potential Antifungals to Overcome the Emergence of Multidrug-Resistant Fungi. Pharmaceuticals, 2021, 14: 488. DOI: 10.3390/ph14050488.
[13] Miah M A, Rozario E, Khair F B, et al. Harnessing Wearable Health Data and Deep Learning Algorithms for Real -Time Cardiovascular Disease Monitoring and Prevention, Nanotechnology Perceptions, 2019, 15(3): 326-349. DOI: 10.62441/nano-ntp.v15i3.5278s.
[14] Rosa A Börner, Vijayalakshmi Kandasamy, Amalie M Axelsen, et al. Genome editing of lactic acid bacteria: opportunities for food, feed, pharma and biotech. FEMS Microbiology Letters, 2019, 366(1). DOI: 10.1093/femsle/fny291.

[15] Jonathan M Stokes, Kevin Yang, Kyle Swanson, et al. A Deep Learning Approach to Antibiotic Discovery. Cell, 2020, 180(4): 688-702.DOI: 10.1016/j.cell.2020.01.021.
[16] Hossain D. Fire dynamics and heat transfer: advances in flame spread analysis. Open Access Research Journal of Science and Technology, 2022, 6(2): 70-5. DOI: 10.53022/oarjst.2022.6.2.0061.
[17] Manik M M T G. An Analysis of Cervical Cancer using the Application of AI and Machine Learning. Journal of Medical and Health Studies, 2022, 3(2): 67-76. DOI: 10.32996/jmhs.2022.3.2.11.
[18] Dongmei Li, Xiaodong She, Richard Calderone. The antifungal pipeline: the need is established. Are there new compounds? FEMS Yeast Research, 2020, 20(4). DOI: 10.1093/femsyr/foaa023.
[19] Sitarek P, Merecz-Sadowska A, Kowalczyk T, et al. Potential Synergistic Action of Bioactive Compounds from Plant Extracts against Skin Infecting Microorganisms. International Journal of Molecular Sciences, 2020, 21: 5105. DOI: 10.3390/ijms21145105.
[20] Hassan J, Barikdar C R, Rozario E, et al. Emerging Trends and Performance Evaluation of Eco-Friendly Construction Materials for Sustainable Urban Development. Journal of Mechanical, Civil and Industrial Engineering, 2022, 2(2): 80-90. DOI: 10.32996/jmcie.2021.2.2.11.
[21] Andrew C Liu, Krishna Patel, Ramya Dhatri Vunikili, et al. Sepsis in the era of data-driven medicine: personalizing risks, diagnoses, treatments and prognoses, Briefings in Bioinformatics, 2020, 21(4): 1182–1195, DOI: 10.1093/bib/bbz059.
[22] Ma S, Chou W, Chien T, et al. An App for Detecting Bullying of Nurses Using Convolutional Neural Networks and Web-Based Computerized Adaptive Testing: Development and Usability Study. JMIR mHealth and uHealth, 2020, 8(5): e16747.
[23] Tobore I, Li J, Yuhang L, et al. Deep Learning Intervention for Health Care Challenges: Some Biomedical Domain Considerations. JMIR Mhealth Uhealth, 2019, 7(8): e11966.
[24] Lee Y, Chou W, Chien T, et al. An App Developed for Detecting Nurse Burnouts Using the Convolutional Neural Networks in Microsoft Excel: Population-Based Questionnaire Study. JMIR Medical Informatics, 2020, 8(5): e16528.
[25] Bulbul IJ, Zahir Z, Tanvir A, et al. Comparative study of the antimicrobial, minimum inhibitory concentrations (MIC), cytotoxic and antioxidant activity of methanolic extract of different parts of Phyllanthus acidus (l.) Skeels (family: Euphorbiaceae). World Journal of Pharmacy and Pharmaceutical Sciences, 2018, 8(1): 12-57. DOI: 10.20959/wjpps20191-10735.
[26] Aminuzzaman FM, Shahi S, Thapa S, et al. Mushroom Diseases and Their Management: A Review. In: Kulshreshtha S, Ukaogo PO, Siddhant. Recent Advances in Mushroom Cultivation Technology and Its Application. Delhi, India: Bright Sky Publications, 2022: 1–27.
[27] Das K, Aminuzzaman FM, Nasim A. Diversity of Fleshy Macro Fungi in Mangrove Forest Regions of Bangladesh. Journal of Biology and Nature, 2016, 6(4): 218–241.
[28] Das K, Jhan PK, DasSC, et al. Nanotechnology: Past, Present and Future Prospects in Crop Protection. In: Ahmad F, Sultan M. Technology in Agriculture. London, United Kingdom: IntechOpen Limited, 2021: 1–18.
[29] Das K, Aminuzzaman FM. Morphological and Ecological Characterization of Xylotrophic Fungi in Mangrove Forest Regions of Bangladesh. Journal of Advances in Biology & Biotechnology, 2017, 11(4): 1–15.
[30] Rubina H, Aminuzzaman FM, Chowdhury MSM, et al. Morphological Characterization of Macro Fungi Associated with Forest Tree of National Botanical Garden, Dhaka. Journal of Advances in Biology & Biotechnology, 2017, 11(4): 1–18.
[31] Aminuzzaman FM, Das K. Morphological Characterization of Polypore Macro Fungi Associated with Dalbergia Sissoo Collected from Bogra District Under Social Forest Region of Bangladesh. Journal of Biology and Nature, 2017, 6(4): 199–212.
[32] Das K Das SC, Aminuzzaman FM. Environmental and Ecological Impact of Soil Microorganisms in Plant Sciences. Journal of Ecology and Natural Resources, 2022, 6(2): 1–11.
[33] Alasa VK, Alasa K, Karim D. Predictive Analytics in Drug Discovery, Disease Monitoring, and Mycology. International Journal of Multidisciplinary Research and Growth Evaluation, 2022, 3(2): 825–830.