



# Leveraging Advanced Machine Learning for Pioneering Monkeypox Diagnosis: A New Paradigm in Infectious Disease Detection

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## Abstract

Artificial intelligence (AI) is revolutionizing the problem solving of medical diagnosis, which has enduring issues, including early-stage disease, insufficient voluminous data, and diagnosis process ineffectiveness. This review demonstrates considerable progress in developing ML technologies, including monkeypox detection, Tuberculosis, and cancer diagnosis. CNNs have shown high efficiency in diagnostics; even InceptionV3, a transfer-learning model for clinicians, can reach 99.87% diagnostics. As privacy-preserving solutions, federated learning models work to improve diagnostic accuracy without increasing the exposure of individual data, and synthetic datasets derived from high-resolution techniques such as HiP-CT help deal with data scarcity by improving model construction and assessment. The hybrids of genome and metabolome integration helped enhance diagnostic accuracy measures, particularly for complex diseases like COVID-19, due to increased prognostic performance metrics using multiple biological information. However, few issues crop up even in modern society: Generalization of the model is an issue due to a lack of data, especially for rare conditions, and increased computational power requirements for most ML models pose a problem for implementation in low-resource environments. Prominent ethical issues incorporating algorithm prejudices and the 'black box' concept spotlight the requisite of an explainable AI (XAI) framework to provide visibility and credence in the medical facility. Possible directions in development, such as the standardization of frameworks, enhancing computational support, and integration of different fields, provide ways to address these challenges. When tackled, these challenges create the possibility of revamping global healthcare through suitable and scalable approaches informed by ML technologies that align with the patient's needs, leading to better practices and, consequently, better health.

**Keywords:** Machine learning; Diagnosis; Deep learning; Privacy-enhancing AI; Synthetic data; Healthcare advancement

## 1. Introduction

Monkeypox, a zoonotic viral disease, has gained international attention due to its re-emergence and spread beyond endemic regions. Caused by the monkeypox virus, its symptoms often mimic other diseases, making early and accurate diagnosis vital. Traditional diagnostic methods, such as polymerase chain reaction (PCR), are reliable but not always feasible in resource-constrained settings. Integrating machine learning (ML) into healthcare offers new avenues for efficient and scalable monkeypox diagnosis. How can ML address the limitations of conventional methods in detecting Monkeypox?

### I. The Role of Machine Learning in Modern Diagnostics.

Machine learning (ML) has emerged as an influential factor in the computation of contemporaneous diagnostics with tools that rapidly revolutionize conventional systems' preciseness, turnaround time, and scalability. Routine diagnostic techniques are based on manual analysis and require significant resources,

which may give inaccurate results and take a long time. In contrast, ML algorithms are built to handle large and complex databases and produce results that practitioners may not even notice. Additionally, this technological incorporation has enhanced the boundaries of diagnostics in medical imaging, predictive analytics, and real-time patient tracking.

Deep learning (DL), a subset of ML, has opened up a unique and fertile area for diagnostics. Adopting DL techniques, particularly those involving Convolutional Neural Networks (CNN), has led to developing high-performing image diagnosis algorithms. For example, models tested with CNNs have demonstrated improved accuracy in diagnosing cancerous lesions from medical images, surpassing the capabilities of human clinicians. These achievements underscore the potential of ML, particularly DL, to enhance the accuracy of diagnosis and significantly reduce assessment time [1], [2].

Machine learning (ML) has proven to be a valuable tool in predictive diagnostics, extending beyond its applications in medical imaging. By feeding large volumes of patient data, including electronic health records and genomics, into ML models, practitioners can predict disease development, course, and treatment utility. This predictive capability is particularly beneficial in fields such as neurology and oncology, where early diagnosis and treatment are crucial [3], [4].

Nevertheless, this path to integrating ML into diagnostics could be smoother. Some of the issues are high-quality data, the interpretation of complicated algorithms, ethical issues, and data privacy. These problems must be addressed to enable better exploitation of the opportunities held by Machine Learning for healthcare [5].

## **II. Image-Based Monkeypox Detection.**

Image-based ML has proved extremely useful in detecting characteristic skin lesions of Monkeypox through relevant and practical applications. The challenged techniques employ deep learning (DL) approaches, emphasizing convolutional neural networks (CNNs), to differentiate and identify monkeypox disease from diseases that visually resemble diseases like chickenpox or measles. By training on large datasets of clinical images, such models gain high diagnostic accuracy and contribute to improving the speed and reliability of monkeypox detection.

One of the integration techniques is the MOX-NET framework, which enables hybrid feature fusion alongside multistage deep learning to enhance the process of image classification. HMPV-Net is a novel solution to localize monkeypox lesions effectively and is more accurate than conventional techniques [6]. Further, transfer-learning approaches have been used with transferred neural networks to refine their ability to detect Monkeypox's distinctive features. This approach becomes especially beneficial since it does not require large datasets to perform the analysis, and thus, it is possible to implement, even in resource-constrained environments.

These higher-level presets, which include feature selection methods, significantly improve the speed and explainability of the models. These systems, which consider image attributes like texture, color, and shape, are effective for diagnosis in healthcare environments. Notably, the flexibility of these models allows them to perform well in different demographic and geographical setups, demonstrating their adaptability to differences in lesion presentation.

Despite the promising potential of image-based ML in monkeypox detection, there are still significant obstacles to overcome. These include a need for large datasets with detailed annotations and the need for domain knowledge when developing a model. Addressing these limitations is crucial for the widespread use of this approach. However, the fact that image-based ML models can provide quick and accurate noninvasive diagnosis is a significant breakthrough in the fight against zoonosis such as monkeypox [7].

## **III. Challenges in Implementing ML for Monkeypox Diagnosis.**

Machine learning (ML) for diagnosing Monkeypox is highly feasible but has several significant challenges that must be revealed to achieve its full potential. One is the vast need for more well annotated data for training and validating deep learning models. This is because human monkeypox cases are infrequent, and therefore, many fewer public image repositories are available to create and validate deep learning models. Such limited data might lead to biases emerging in these models, which decrease the generalizability and reliability in the real world, mainly when applied to various populations. Whereas there would be significant data, containing much variance in skin tones, lesion presentations, and demographic characteristics, model robustness is maintained [8].

The computational intensity of ML models- no small wonder, particularly of the convolutional neural networks (CNNs)-is another primary concern. They not only require very high-performance GPUs during training and deploying purposes but are also expected to support high-performance GPUs so that they can run efficiently. This proves troublesome, especially in low-resource settings, where monkeypox infections generally occur, because many of these research settings often need the requisite infrastructure for developing and applying advanced diagnostic systems to diagnose Monkeypox in these regions. It prevents them from balancing access to such technologies [9].

The interpretability and explain ability of machine learning (ML) models are significant hurdles to their widespread implementation in healthcare. Healthcare personnel often hesitate to trust 'black box' algorithms, emphasizing the need for transparency in medical science. Understanding how an automated process makes diagnoses, especially in critical situations, is crucial. Therefore, interpretability remains essential in developing ML-based diagnostic systems [10], [11].

#### IV. Prospects of ML in Disease Diagnostics.

Machine learning is on the brink of establishing itself as the next generation of disease diagnostics, promising to revolutionize accuracy and efficiency. Exciting research is underway in multi-modal, multi-source data convergence, including genomic, proteomic, and imaging datasets. The integration of these varied data types holds the potential to detect the emergence or progression of diseases for early and more precise intervention. By combining various biological and clinical dimensions, ML systems can offer superior diagnostic insight compared to traditional methods, sparking optimism for the future of healthcare [12].

The advances in explainable artificial intelligence, or XAI, will transform the most severe barrier in ML adoption: interpretability. It promises to provide clear and transparent reasoning behind decisions made by ML models, engendering trust between patients and healthcare providers. This is further seen in contexts such as medicine, where clinicians need intelligible and defensible recommendations to support treatment decisions [13].

Another innovation worth watching is federated learning, a decentralized way of training ML models that prioritizes data privacy. It ensures that sensitive information remains locally tied, eliminating data breach risk. Healthcare providers can jointly train their robust models without exposing raw data, making this approach particularly suitable for regions with strict data protection regulations. Federated learning is a reassuring bridge between the safety standards enforced on specific raw data and the comprehensive heterogeneous datasets that the world needs for ML applications in diagnosis [14], [15].

Emerging technologies such as edge computing and connectivity with 5G could further offer the power of ML for expanded diagnostics [16].

In the paper, we provided a well-structured diagram, as shown in Figure 1 below. In our case, it shows a concept map for Diagnosis Using Machine Learning. At the center, the main idea is highlighted in a blue ellipse, branching into two primary categories: The existing difficulties and opportunities for machine learning. The challenges in the red box include the disadvantages of diagnostics, such as their complexity and inefficiency, and limited resources, such as the sole dependency on PCR tests in low-resource settings. On the other hand, the Opportunities with Machine Learning in the red box explain that it will enhance the accuracy of diagnosis and will offer quicker outcomes. This figure provides an outstanding and easy-to-understand representation of the issues and potential approaches to improving monkeypox diagnosis using innovative technologies.

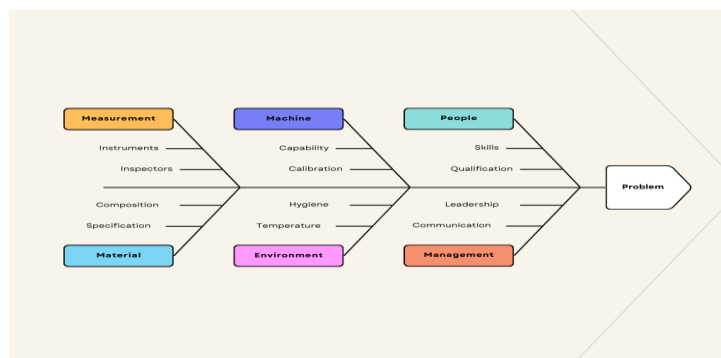


Figure 1. Flow Diagram to Diagnosis Using Machine Learning

In conclusion, machine learning will likely provide fast, scalable, and precise solutions for the future transformation of monkeypox diagnostics. However, datasets and ethical issues must be resolved to let machine-learning reach its full potential, leveraging ML innovations by healthcare systems worldwide would enable preparedness at every level in dealing with the pandemic arising out of environment-inhabiting infectious diseases.

## **2. Literature review**

The ongoing transformation in the medical field is significantly influenced by the integration of machine learning (ML) in the diagnostics sector. ML technologies are proving to be a game-changer in diagnosing complex diseases, offering promising solutions for conditions such as Monkeypox and knee osteoarthritis, among others. This literature review will explore various studies, ranging from advanced deep-learning architectures to privacy-preserving diagnostic tools. These approaches address resource and data variability challenges and provide scalable solutions for global healthcare needs. By synthesizing key findings and performance metrics, this section underscores the growing role of AI-driven diagnostics in the current revolution in modern medicine, with potential global implications.

The monkeypox virus has been cutting across national boundaries too rapidly, thus highlighting the need for early detection to curtail early transmission and allow timely therapy. Findings in [17] show that AI and ML methods are at the forefront of efforts to address this. The coalesced computer-aided diagnostic (CAD) system employing advanced deep learning frameworks such as Vision Transformers (ViT), ResNet-50, and EfficientNetV2 has demonstrated excellent accuracy. This approach employs a multistage, fusion-based contrast enhancement integrated convolutional sparse image decomposition for feature extraction and entropy-controlled firefly optimization laser focusing on low-contrast lesion images, as well as high memory complexity-meant benchmarking against the MSLID dataset propounded an accuracy of 98.64%, better than that of other methodologies in both visual and quantitative evaluation. The results promise to revolutionize the monkeypox diagnosis paradigm and public health management responses via ML-driven solutions.

According to the study [18], Monkeypox is less transmissible or harmful than COVID-19. However, it still threatens public health increasingly because new cases are recorded daily in many places globally. This will likely create conditions where a new pandemic can flourish because control measures are ineffective. Diagnosing it in its early stages poses challenges given that such conditions present clinically with chicken pox and measles, making a need for advanced diagnostic tools pertinent. Therefore, using computer-aided methods through deep learning techniques to detect monkeypox lesions will be ideal for solving the problem, especially in resource-poor settings that may not have PCR (polymerase chain reaction) confirmatory assays. A transfer-learned model using the InceptionV3 architecture has been developed from the publicly available Monkeypox dataset and achieved an impressive accuracy of 98% in identifying cases of Monkeypox. This emphasizes the potential of deep learning in supporting or improving early detection rates among resource-limited environments.

As detailed in the paper [19], the global spread of Monkeypox across over 40 countries presents a significant public health challenge, with its clinical similarity to chickenpox and measles complicating early diagnosis. In settings where PCR tests are unavailable, computational lesion detection provides a viable alternative for early detection. This research introduced the Sparrow Search Algorithm (SpaSA) to optimize pre-trained convolutional neural networks (CNNs) for improved medical imaging accuracy. Evaluated on the "Monkeypox 2022" and "Images of Monkeypox" datasets, the method classified patients as "normal" or "pox," encompassing conditions such as Monkeypox, chickenpox, smallpox, cowpox, and measles. The study highlighted SpaSA's efficacy in enhancing the VGG19 model, achieving an impressive accuracy of 99.87% within 120 seconds. Compared to Grid Search, Random Search, Bayesian Optimization, and other optimization techniques, SpaSA demonstrated superior speed, a lower failure rate, and unmatched performance. This work underscores the transformative potential of mathematical optimization in healthcare diagnostics, setting a benchmark for future advancements in medical imaging.

The analysis in [20] indicates the effectiveness of the global response to an event such as Monkeypox that prompted the World Health Organization to declare an emergency in 2022; it also brings to light the urgency of possible practical diagnostic tools. The research presented an end-to-end deep learning model called CanDark to detect Monkeypox accurately without infringing on patient privacy through cancelable biometric methods. The feature extraction process uses DarkNet-53 CNN architecture combined with advanced cancelable methods, such as bio-hashing and index-of-maximum random permutation-based hashing (IoM-URP), which anonymizes sensitive patient information. The model showed a wonderful

diagnostically performed with 98.81% accuracy, 98.73% specificity, 98.9% precision, 97.02% recall, and 97.95% f-score. Thus, Can Dark has emerged as a superset compared to previously existing diagnostic methods in Monkeypox, as it fulfills dual needs: accuracy and security of data in infectious disease management.<sup>1</sup>

Wearable plantar pressure analysis has excellent potential, as revealed in the article [21], as a long-term evaluation for knee osteoarthritis (KOA)-suffering patients. With the static radiography methods, not all degrees of the dynamic motion dysfunctions related to KOA can be captured. This research employed an intelligent shoe system to gather gait pressure data from 92 clinically recommended patients during a prescribed functional test, including the 40 m fast-paced walk test (40mFPWT) and timed up-and-go test (TUGT). A multidimensional database consisting of 380 gait features and four anthropometric characteristics is developed for training regression models of KOA assessments. Advanced machine learning techniques employing model stacking and average ensemble learning were well executed in optimizing prediction accuracy. The superior performance of the weighted average ensemble model was reflected in the mean absolute error (MAE) of 2.686 seconds, root mean square error (RMSE) of 3.316 seconds for 40mFPWT predictions, and MAE of 1.280 seconds with RMSE of 1.905 seconds for TUGT predictions. This is evidence of using wearable technology and machine learning to provide efficient, objective, and scalable functional assessments as alternatives to static diagnostics and the burden on healthcare systems.

As discussed in [22], Monkeypox is quite a rare but a world health concern due to its potential to cause an outbreak and complications; hence, an early and accurate diagnosis is essential. To this end, the present work proposes Skin Market, a novel ensemble of three state-of-the-art transfer learning models, Inception, Exceptions, and Resent, for Monkeypox lesion classification. To mitigate this deficit of annotated data, the work uses an improved image data augmentation set from the Kaggle repository containing various lesion properties and patient demographics. The techniques improve the training set quality, broadening the model's applicability and effectiveness. The outcome of the evaluation of Skin Market was tremendous; the model achieved 90.615% classification accuracy, out-regulating conventional ML algorithms alongside the present advanced dl techniques. A similar analysis was done to compare the proposed method with the current method and proved that the proposed method is better for identifying monkeypox lesions. These findings shed light on how integrating data augmentation techniques with complex deep learning architectures in specifically designed architectures may serve as a path to enhance therapeutic diagnostics while offering the rich potential to expedite timely clinical intercession and enhance public health screening.

Deep learning and its capabilities to revolutionize medical diagnostics are discussed in the study reported in [23] concerning clinical workload. Nevertheless, data deficiency has been a significant drawback that hinders further integration of the method across various domains. The present study proposed the "Efficient Transfer and Self-supervised Learning based Ensemble Framework" (ETSEF), a novelty as it integrates transfer, self-supervised, and ensemble learning. At ETSEF, multiple pre-trained models are employed, coupled with data augmentation at both the feature and decision levels. On five different medical imaging applications, endoscopy, breast carcinogenicity, monkeypox detection, brain tumor, and glaucoma identification, ETSEF was tested and showcased, enhancing diagnostic performance up to recognized state-of-the-art methods by 14.4%. In addition, the model composed was made reliable and interpretable through vision-explainable AI techniques such as Grad-CAM and SHAP. As ETSEF is well suited for settings where training data is limited, it has a high scalability and adaptability, and, as demonstrated in the work, it can become the basis for a radically new generation of diagnostic methods for pathological conditions, including in areas with moderate amounts of shared data.

In the article denoted as [24], infectious pox diseases such as Monkeypox, chickenpox, and measles are highlighted as global health challenges requiring timely and accurate detection for effective management. Addressing the limitations of traditional diagnostic methods, which often involve invasive procedures and insufficient privacy safeguards, the study proposed a privacy-preserving framework utilizing advanced image analysis and federated learning. The framework achieved a testing accuracy of 87.50%, demonstrating its effectiveness across evaluation metrics, including precision, recall, F1-Score, and loss and accuracy curves. By incorporating federated learning, the study ensures robust diagnostic capabilities while maintaining data confidentiality, setting a benchmark for privacy-aware healthcare solutions. This research underscores the transformative potential of privacy-preserving technologies in revolutionizing disease diagnosis and advancing public health strategies.

In the publication identified as [25], breast cancer is acknowledged as a pressing global health issue, with early detection being critical for improving patient outcomes. To address privacy concerns associated with using mammographic data, the study proposed a federated learning framework that enables collaborative model training across healthcare organizations without exposing raw data. Leveraging a dataset comprising 6,649 images across four classes, the model incorporated parameters such as breast density, micro calcifications, masses, architectural distortion, asymmetry, and prior mammograms, achieving an accuracy of 72.46%. This privacy-conscious approach supports precise risk prediction and tailored screening by integrating clinical and demographic data. The study further emphasizes the potential of combining genetic, clinical, and mammographic data to advance precision medicine. This research paves the way for personalized care to improve quality of life, reduce mortality, and strengthen early detection strategies in breast cancer management by resolving privacy challenges.

As detailed in the paper [26], the project aims to advance the detection of pulmonary Tuberculosis (TB) using machine learning (ML) algorithms trained on high-resolution clinical imaging data. While current datasets of TB-infected lung radiographs have repeatedly improved ML accuracy through sophisticated algorithms, the study addresses the critical need for more diverse and high-volume data. The proposed approach generates synthetic datasets from Hierarchical Phase-Contrast Tomography (HiP-CT) scans obtained from the European Synchrotron Research Facility. These scans, with resolutions as satisfactory as 2.5  $\mu\text{m}$ , capture detailed 3D representations of healthy and TB-infected lungs. Using the Geant4 toolkit, the study projects these 3D models into simulated chest X-rays (CXR) containing known TB indicators, which are then used to train classification algorithms. This innovative methodology offers several advantages, including the ability to simulate diverse presentations of TB pathologies and provide detailed truth data for algorithm optimization. By capturing the non-linear progression of TB down to a cellular level, the generated synthetic radiographs enhance the precision and robustness of ML models. Furthermore, this approach demonstrates potential scalability to other organs, fostering dataset diversity within the ML research community. With its focus on high-resolution imaging and synthetic data generation, the study sets a new standard for leveraging advanced imaging technologies to refine ML-based diagnostics for pulmonary TB and other medical conditions.

According to the article referred to as [27], MDR-GNB, especially KP, is ranked as a significant threat to global health care as the mortality rate approaches 50 percent in circumstances when antimicrobial treatment is inappropriate. In response to this, the study proposed an AI-CDSS that incorporates ML with MALDI-TOF MS to improve the decisiveness of diagnosis of antibiotic resistance. The study employs a bacterial specimen's database of 165299, of which 11996 were KP isolates, and employs the latest ML high endpoint to develop forecast models for levofloxacin and ciprofloxacin antibiotic resistance. The random forest classifier achieved a high AUC of 0.95 with high accuracy, sensitivity, specificity and F1 score. These findings brighten the prospects of integrating MALDI-TOF MS with ML for precision treatments and are a step toward responding to the global threat of pan-drug-resistant bacteria. This technology remodeling of clinical diagnostics is a shift in replacement with a wholly AI-based resistance prediction mechanism that can contribute significant efforts for combating infectious diseases across the globe.

The research in [28] discusses the overwhelming problem of infectious diseases, emphasizing improving diagnostic ability to reduce diseases' effect on mortality. The study sets up a novel AI approach deploying the MCDM model accompanied by a Hypersoft Set (HSS) in a fuzzy environment. This revolutionary mathematical algorithm checks X-rays, scans for signs of possible contagious diseases, and provides suggestions, including distancing, containment or even admission. By integrating state-of-the-art AI methods and decision-making, the approach tends to overcome gaps in evaluation and interventions for infectious disease severity. Besides detaining, it makes the learning process more effective and elevates the model by showing how it can help in machine learning, deep learning, and pattern recognition. This novel framework is a step in the change in diagnostic approaches to realize a broader application in the fight against infectious diseases worldwide.

According to the research carried out in [29], TB is still a significant health concern worldwide, and the only means of ameliorating the results of disease control is through early diagnosis. This study focused on the applicability of cough audio in TB identification from 1105 subjects with a persistent cough, which led to 9772 cough sound recordings. These records were converted into spectrograms, and for feature extraction, HOG features were obtained and used in training the rather complex deep learning techniques such as Capsule Networks + Fully Connected Neural Network, Convolutional Neural Network +, VGG16 and ResNet50. Capsule Networks + FCNN gave the highest overall accuracy of 0.97, sensitivity of 0.98, specificity of 0.96, and the highest F1 score of 0.97. The derivation of superior performance of

the Capsule Networks was due to their fundamental advantage of extracting more features from spectral images than the traditional CNN-based models existent in the system. This study proves that, with more robust deep learning architectures, including Capsule Networks, there is a high likelihood of increasing the efficiency of TB screening cost-effectively and efficiently in poor settings to provide a credible diagnostic tool.

In our previous paper [30], this research examined ML-based diagnostics models and prognosis prediction for infections in PAC facilities, concentrating on model performance and essential risk factors. Using SRS to search all the international databases, 13 articles were developed, most focusing on respiratory infections, including IRF in nursing homes. Past development incorporated only structured EHR data and regression methods, while since 2020, more complex ML methods and additional forms of data such as biosensors and clinical notes have been added. Nevertheless, there still needs to be more backing for the effectiveness of these models over the traditional approaches. Among identified risk predictors, individual-based factors such as cognitive decline, dependency, and tachycardia were considered evident.

On the other hand, contextual factors have yet to be explored, which presents further research opportunities. This area deserves more attention when considering model biases and predispositions. Bias analysis identified significant issues such as the absence of out-of-bag tests, mis-calibration of models, and failure in dealing with more complex data. Finally, it highlighted that future research must consider a socio-ecological perspective for selecting predictors and identify advantageous data modes to approach predictor selection while maintaining High methodological quality and fairness in PAC model development.

As discussed in [31], statistical learning models play a vital role in biomedical science, enabling complex data analysis and supporting predictive modeling in diverse domains, including breast cancer detection, epidemic forecasting, and drug-induced liver injury (DILI) prediction. The study introduced the "Multiple Directive Feature Selection and Prediction Strategy," achieving 77% accuracy in breast cancer detection using ensemble Random Forest models, with Shapley values enhancing explain ability by identifying patient-specific risk factors. For clustering challenges, the Modified Graph-based Clustering (MGC) algorithm demonstrated 73% accuracy in breast cancer image segmentation. Modified Graph Convolutional Networks (MGCN) outperformed traditional methods with AUC scores of 0.82 and 0.89 in histology diagnosis. In the context of epidemic modeling, the study employed periodic mean-reverting stochastic differential equations (SDEs) and a modified MissForest algorithm to handle missing influenza data, improving seasonal variation predictions for public health interventions. Lastly, Random Forest and Multilayer Perceptron models were developed for DILI risk prediction, achieving 63.10% accuracy and an MCC of 0.245, respectively, demonstrating the potential of machine learning to advance drug safety assessment. These findings underscore the broad applicability and transformative impact of statistical learning in biomedical research and public health.

According to the article [32], the advancement and development of the field of precision medicine continues to expand, especially the approach to healthcare on a molecular, genetic and environmental level. Molecular informatics enables this change, a branch of science that employs technologies like genomics, transcriptomic, proteomics, metabolomics and macrobiotics to assimilate massive bioinformatics data. Some innovations are already in practice: Second-generation sequencing for understanding multigene sequences, computer-aided drug designing for faster discovery of new drugs, molecular modeling and simulation for studying disease pathology at the molecular level and bioinformatics for the computational analysis of biological data. Combined, these advancements can be applied in marker identification, disease risk assessment and formulation of treatment plans. This study shows that molecular informatics promises to transform patient treatment and support to facilitate the shift to a more personalized medicine approach, giving excellent information to investigate to scientists, physicians, and businesses related to this groundbreaking field.

In the context stated by [33], blood-related infections like bacteremia, bloodstream infections, and sepsis are some of the severe health hazards that badly need timely and effective management. Machine learning or ML models hold promise, especially in their advanced stages, like prognosis in sepsis, where key predictors are vital signs, with biochemical measures having a potential role in the early detection of bacteremia. Despite these advances, diagnostics in the early stages still need to be explored because of the limited data available and the performance issues of sequential deep learning models when tested on an external dataset. The real-world implementation of fragmented clinical records, limited infrastructure, and regulation issues prevent such technology from being used effectively. The flexible ML model must

be integrated with real-time, private, noninvasive technologies, such as wearable devices, adapted with currently underutilized patient history data to augment present early disease discovery and management opportunities. The completely integrative study argues for transparency, practicality, and regulator-compliance of ML applications to ensure the public's trust in the application, adoption, and extensive use within the healthcare systems to keep coming up with novel innovations for adaptive diagnostics that help in improving informed decisions across the entire infection management pathway of the clinical process.

Wastewater-based surveillance, as viewed in the study described in [34], is the new emerging tool for monitoring the spread of an infectious disease, such as SARS-CoV-2, in the community. This study discusses the possible effect of environmental conditions, such as water quality and seasonal variations, on the presence of viral particles in wastewater. The research seeks to answer these questions using samples from 28 sites across seasons and water strata to analyze viral presence through RT-qPCR detection physicochemical parameters such as heavy metals and minerals. Further categorization of data into four separate clusters could yield some patterns regarding the relationship between viral prevalence and environmental conditions by using unsupervised learning algorithms such as K-means and K-medoid clustering. Findings were reported on varied and significant associations between seasonal and water quality variation and the rates of SARS-CoV-2 positivity. The emphasis on environmental factors contributes significantly to shaping and giving meaning to the dynamics of viruses. Among the key findings that illustrate the potential for enhancing public health surveillance through combined advanced data analytics and WBS are insights into the environmental side of disease dissemination and directions to better intervention strategies.

The COVID-19 pandemic, referred to in that research in [35], called for efficient early triage and optimized allocation of hospital resources. It aimed to examine whether the synergistic inclusion of high-definition metabolomics and machine learning (ML) would improve prognostic and triage performance over routine clinical parameters. Here, high-resolution mass spectrometry integrated metabolomics profiles from 64 PCR-positive COVID-19 patients with clinical input to generate machine-learning models predicting severe disease as mechanical ventilation requirement. SpO<sub>2</sub>, respiration rate, Horowitz quotient, and age achieved good prediction performance using clinical data alone (AUC = 0.85), but metabolomics significantly improved the model's accuracy (AUC = 0.92). Such results signify the potential of metabolomics for improved diagnostic and prognostic algorithms as it gives crucial insights into disease mechanisms and will subsequently lead to personalized medicine strategy. Combining metabolomics with ML could be a direct and scalable approach to improving clinical decision-making in infectious disease management.

Automated detection of the monkeypox model, as described in [36], is an essential part of controlling the global outbreak of Monkeypox, for which the global health emergency was declared in May 2022. The most novelty was a completely new dataset of about 910 open-source images that form five categories: healthy, Monkeypox, chickenpox, smallpox, and zoster zona. The designer proposed deep feature-engineering architecture involving multiple layers of nested patch division, deep feature extraction, feature selection using neighborhood component analysis (NCA), Chi<sup>2</sup>, and Relief selectors, and classification through SVM with 10-fold cross-validation. A greedy algorithm and iterative hard majority voting (IHMV) further optimize the choice of the best vector for classification. The obtained classification accuracy of the proposed model is 91.87%, which is the best one rated among the 70 generated outcomes. These results prove the effectiveness of machine learning in monkeypox detection and empower a robust framework to enable automated diagnosis towards minimizing its global effect.

The renewed threat of Monkeypox (Mpox) as a health hazard has emphasized the need for modern diagnostics in addition to current methods and contact tracing, as cited in [37]. Per the PRISMA guidelines assessment, an organized systematic literature review evaluated the complementary role that machine-learning (ML) algorithms could play in detecting Mpox. A thorough search across databases, including ScienceDirect, IEEE Xplore, ACM Digital Library, and Springer Link, identified 30 studies published between 2022 and 2024. Results show that machine learning, such as CNN and SVM, will have high accuracy and sensitivity but give faster and more reliable results than classical diagnosis methods. Conversion to imaging modality combined with an ML algorithm, such as coloscopy and radiological imaging, will improve accuracy in diagnosis. Although ML algorithms can robustly scale with large datasets to high precision, they still have problems associated with data variability and need to be large, good-quality datasets available. The review highlights the continued need for research and investment in ML technologies to advance disease surveillance and response strategies. These findings

will form an excellent foundation for health practitioners and policymakers when creating new diagnostic protocols and making informed decisions about Mpox management.

A detailed report encapsulating several studies that highlight all possible advances made through machine learning (ML) and artificial intelligence (AI) technologies in various medical diagnostic fields has been compiled in Table 1. The studies are categorized based on the mentioned field, key findings, and key performance indicators so that they can be read to understand the impact with which an ML technology will achieve transformation. Some studies ranged from optimizing CNN architectures with accuracies as high as 99% for diagnosing Monkeypox to using federated learning for privacy-preserving approaches for diagnosis. These studies represent significant developments toward greater diagnostic accuracy, efficiency, and scalability. Importantly, transfer learning, synthetic data generation, and privacy-centered frameworks are examples of further advancements showing the adaptability of ML models while addressing real-world healthcare problems, particularly in resource-deficient parts of the world. Performance indicators between 87.5 and more than 99 percent demonstrate that these methods are highly effective for enhancing clinical output and facilitating global public health efforts.

**Table 1:** Summary of Literature Review

Study Reference	Methodology	Key Findings	Applications	Limitations
[17]	Deep learning (ViT, ResNet-50, EfficientNetV2) with contrast enhancement and sparse image decomposition	98.64% accuracy, surpassing traditional methods	Monkeypox lesion diagnosis in clinical settings	Data scarcity and ethical concerns
[18]	Transfer learning using the InceptionV3 model	98% accuracy in resource-limited settings	Early detection in low-resource environments	Limited dataset dependency
[19]	Sparrow Search Algorithm (SpaSA) optimizing pre-trained CNNs	99.87% accuracy; better speed and reliability	Optimized lesion detection with computational imaging	High GPU dependency and infrastructure challenges
[20]	Cancelable biometric-based deep learning using DarkNet-53 architecture	98.81% accuracy; privacy and performance combined	Secure, scalable diagnostics for infectious diseases	Interpretability challenges for healthcare adoption
[21]	Wearable plantar pressure analysis with regression models	MAE 2.686s for gait analysis; scalable diagnostics	Functional assessment for knee osteoarthritis	Dependence on specialized hardware
[22]	Ensemble transfer learning models with data augmentation	90.615% accuracy; effective lesion identification	Enhanced clinical lesion diagnostics	Annotated data scarcity
[23]	Efficient Transfer and Self-supervised Learning based Ensemble Framework	Up to 14.4% improvement over state-of-the-art methods	Versatile framework for various medical applications	Scalability in diverse applications

[24]	Federated learning for privacy-preserving diagnostics	87.50% accuracy; effective in maintaining data privacy	Privacy-focused diagnostics for public health	Complexity in federated learning frameworks
[25]	Federated learning for mammographic breast cancer diagnostics	72.46% accuracy with robust mammographic feature extraction	Personalized breast cancer detection and screening	Moderate accuracy for certain clinical features
[26]	Synthetic datasets using HiP-CT scans and ML for tuberculosis detection	Enhanced ML models with synthetic data for diverse TB presentations	Advanced ML diagnostics for pulmonary TB	Need for high-quality and diverse datasets
[27]	AI-CDSS integrating ML with MALDI-TOF MS for antibiotic resistance prediction	AUC of 0.95; high diagnostic precision for drug resistance	Precision treatment for drug-resistant infections	Data quality issues in low-resource regions
[28]	MCDM model with Hyper Soft Set in the fuzzy environment for infectious diseases	Novel decision-making framework with AI applications	Decision-making in infectious disease control	Limited real-world implementation data
[29]	Capsule Networks for audio-based tuberculosis detection	0.97 accuracy for TB detection via cough analysis	Low-cost TB screening tool for poor settings	Requirement of robust architectures
[30]	Machine learning-based diagnostics for PAC infections	Highlighted biases and the need for a socio-ecological perspective	Enhanced models for healthcare facility infection control	Bias analysis and fairness concerns
[31]	Random Forest and ensemble methods for biomedical modeling	73%-82% accuracy for various biomedical diagnostics	Broad application in public health research	Data sparsity and model calibration issues
[32]	Molecular informatics integrating omics technologies	Precision medicine approaches with omics technologies	Personalized medicine and treatment planning	Integration complexity across omics data
[33]	ML models for bacteremia and sepsis with wearable technology	Transparency and real-time diagnostics for early interventions	Real-time early-stage diagnostics in infectious diseases	Fragmented records and infrastructure gaps
[34]	Unsupervised learning for wastewater-based surveillance	Correlations between seasonal changes and viral presence	Environmental monitoring for disease spread	Clustering challenges in environmental variability

[35]	Metabolomics with ML for COVID-19 prognosis	AUC 0.92; a significant improvement over clinical parameters	COVID-19 prognosis for resource optimization	Reliability on metabolomics scalability
[36]	Feature-engineering architecture with SVM for monkeypox detection	91.87% accuracy with deep-feature engineering	Automated diagnostics for monkeypox outbreak control	Dataset variability and annotation issues
[37]	Systematic review of ML applications for monkeypox diagnosis	High potential, but data limitations persist	Strategic development for monkeypox management	Data quality and variability challenges

Findings from this literature review show that machine learning has a bright future in medical diagnostics. Many machine-learning applications have proved to improve accuracy, decrease the evaluation time, and thereby provide scalable solutions to low-resource environments. However, much tension exists in data availability, hardware setup, and ethical issues; nevertheless, advances in these areas will lead to innovative healthcare solutions centered on the patient. Therefore, these continued limitations, research, and advancements indicate how ML could redefine diagnostic standards while improving health outcomes worldwide. This body of work underscores the need to introduce AI-based innovations in healthcare systems to meet the emerging demands of public health management.

### 3. Discussion

The injecting line is giving organ machine learning technology into health diagnostics fastest in addressing critical issues like early detection of diseases, resource limitation, and diagnostic accuracy. The literature review presents various studies addressing the applications of advanced ML frameworks, CNNs, and federated learning for primary medical conditions such as Monkeypox, Tuberculosis, and cancer. Consolidating these findings, the review looks at significant strides made, and the existing challenges in ML helped diagnosis. Such challenges include the perennial shortage of data and ethical snares. Integrating cutting-edge new techniques such as privacy-preserving algorithms and synthetic dataset generation presents these technologies as promising avenues for bridging healthcare access and efficiency disparities. The ways through which ML supercharges future healthcare outcomes around the globe are established within this section.

#### I. The Role of Advanced ML Architectures in Diagnostic Accuracy.

Advanced machine-learning models make diagnosis of diseases that were not possible in the modern era due to their modern procedures, especially with deep learning frameworks such as convolutional neural networks (CNNs). Such developments include the Sparrow Search Algorithm-enhanced VGG19, creating a high accuracy of 99.87% in diagnosing Monkeypox from clinical image datasets, which shows a wide margin between this method and the traditional methods. Such accuracy is essential in saving lives as it helps avoid falsely diagnosing patients with symptoms closely related to chickenpox or smallpox. Transfer learning also approaches with Inception V3 architecture, which has similarly worked wonders by achieving 98% specificity in the detection of monkeypox lesions in an under-resourced environment; they adapt pre-trained models to new datasets after very little additional training, making them relevant in under-resourced areas [38].

Another innovation that has added weight to detection accuracy is the MOX-NET framework, which merges and hybridizes various features for more disease classifications. This approach combines multiple stages of deep learning while using low and high input events relating to image attributes such as texture, shape, and color, thus acquiring high performance in setup diversity concerning individuals' demography and geography. MOX-NET can be used in any healthcare activity, be it in hospital cities or rural clinics. On top of this, modern architecture saves time and person-hours for manual diagnostics, which helps highly burdened health systems [39].

The ML advancements also go beyond accuracy, signaling a shift toward scalable, automated, and much more precise diagnostic tools. Monkeypox, the most recent in a long line of diseases that have found their way into the global spread of pathogens, reinforces the importance of providing real-time and timely ML support in diagnostics. This improvement in the precision of diagnosis also guarantees timely intervention, usually a prerequisite for reasonable control and management of diseases. All these technologies together underline the potentially transformative impact of ML on international healthcare systems by making them not only brighter but also more responsive to changes [40].

## **II. Ethical Considerations and Challenges in Deployment.**

Of course, the real power of machine learning (ML) in diagnostics has to be controlled by ethical, severe and logistical issues that need to be solved to implement machine learning successfully. Data scarcity is one of the fundamental issues one faces, especially concerning rare or newer diseases like Monkeypox. With very few well-annotated datasets, there is little scope for the development and valid testing of strong models for ML, letting such models crumble concerning their generalizability and real-life applicability. For example, advanced architectures such as ResNet-50 and DarkNet-53 show incredible diagnostic accuracies. However, their usage of high computational resources and annotated data puts such systems beyond the reach of low-resource settings where they are most often needed. This imbalance raises the ethical call to bridge the gap between technological advancement and equity access [41].

Privacy issues also raise significant concerns while running and managing ML systems in healthcare. Approaches like federated learning, which would have allowed for an 87.50% accuracy while keeping data confidential, should now be explored to resolve such concerns. Federated learning allows the training of collaborative models without sharing raw data, thus protecting patient interests and adhering to strict data protection laws. Such frameworks' supreme global harmonization and end-to-end scalability necessitate extensive international collaboration and regulatory harmonization [42].

In addition, the opacity of many ML models, commonly designated as "black-box" algorithms, remains a significant challenge in winning the trust of health professionals and patients. Such models fail to reveal the reasoning behind their diagnostic decisions, creating questions of accountability, particularly in critical health circumstances. Explainable AI frameworks make sure to facilitate transparency and foster trust. Ethical concerns remain about algorithmic bias, meaning ML models unconsciously reproduce the inequality due to unbalanced training data. A fairer approach entails finding and mitigating such algorithmic bias by broadening representation in datasets [43].

Overcoming these challenges requires a multidisciplinary approach, innovation in every branch, and ethical safeguards. However, global cooperation ensures that ML technologies are aligned for equitable and responsible use in health systems [44].

## **III. Emerging Trends and Future Directions**

Integrating novel methods in machine learning diagnostics places hopeful solutions to existing challenges and heralds groundbreaking advancements. Synthetic databases, such as those from very high-resolution imaging techniques, such as Hierarchical Phase-Contrast Tomography (HiP-CT), are crucial in training and evaluating TB diagnostic models. It addresses one of the profound challenges affecting the creation of different and representative databases, causing model robustness and increased generalizability of algorithms. This synthetic data can help simulate disease progression and evaluate diagnostic tools in a controlled environment, facilitating scalability and improving the accuracy of diagnosis [45].

Federated learning is another game-changer in keeping data private while doing collaborative ML. It successfully incorporated demographic and clinical data and achieved a diagnostic accuracy of 72.46% from breast cancer screening. Such approaches do away with the need to centralize data because of the dangers of privacy breaches and the regulatory challenge with which health care is often associated. Accordingly, federated learning's decentralized property allows institutions worldwide to exchange insights securely without disclosing patient information. This adds significant value to multinational collaboration in health care [46].

The next promising direction is integrating multi-modal data such as genomics, proteomics, and metabolomics into diagnostic frameworks. This approach holds great potential, as studies using metabolomics data have shown that COVID-19 prognoses can be significantly improved. This will provide a more comprehensive understanding of disease mechanisms, leading to the development of more accurate and personalized diagnostics. Such advancements in multi-modal fusion offer a hopeful future for diagnostics [47].

As machine learning matures, attention will turn to standardizing data sharing, improving computational infrastructure, and fostering interdisciplinary collaboration. These developments have potential transformative capabilities in diagnostics so countries worldwide can enjoy scalable, precise, and equitable healthcare. Emerging trends in ML indicate the future of diagnostics; they are built around innovation and inclusivity to benefit the world's health [48] ultimately.

#### **4. Conclusion**

Machine learning technologies have taken a new paradigm shift in medical diagnostics, ushering in unprecedented accuracy, efficiency, and scalability. This review discusses the applications of these technologies across various domains, from Monkeypox to cancer. It is demonstrated that ML frameworks such as convolutional neural networks (CNNs) and federated learning models can significantly improve its diagnostics. These technologies are making strides toward being indispensable components of modern healthcare, wherein manual diagnostic error is reduced, and real-time data processing improves. Their adaptation to poor resource environments is a strong plus as they still show high accuracy, hence their use in resolving inequalities that exist in global healthcare. However, the advances notwithstanding, challenges remain. There is a severe shortage of data in this regard, particularly on emerging diseases like Monkeypox, which currently need more than the scanty annotated datasets available for other diseases. The other limiting factor is the high computational nature of many modern-day algorithm implementations of ML, which usually negate applications of these algorithms in poorer setups and aggravate the already prevailing inequalities in access to health care. Moreover, the ethical considerations around algorithmic biases and even privacy issues will compel the designing of transparent and explainable AI domains to garner trust among providers and patients alike in these domains. It is essential to address all these issues to ensure equitable access to diagnostics driven through ML.

New directions, which include synthetic data generation and multi-modal data integration, are promising solutions to these challenges. Synthetic datasets have helped improve the ML model training for illnesses such as Tuberculosis and the inclusion of multi-omics data of genomics, proteomics, and metabolomics data in promoting diagnostic accuracy in complicated diseases such as COVID-19. Some of these developments show how ML technologies are beginning to develop into overall diagnostic tools that would enable a clinician to fully understand how a disease develops and how a particular medication might help treat it. Using the case of medical diagnostics, the direction of advance in future ML can be discussed as the development of international collaboration, the construction of standard guidelines, the improvement of computational support, and the specification of the ethical aspect. As a result, further study and advancement will allow the disruption of crucial deficiencies in healthcare by scalable patient-oriented and clinical environment-capable solutions based on ML technologies. Sorted by the current drawbacks and the opportunity of utilizing further technological advancement, the role of ML in changing the approaches of diagnosis and the global health picture is enormous.

In conclusion, the application of machine learning in healthcare solutions necessitates better diagnostics for timely, accurate and scalable solutions for complex health challenges. However, there is a long way to go for the given technologies to become mainstream, further developments of machine learning technologies will continue to reshape the healthcare systems worldwide, helping to create a fairer world for everyone.

#### **References**

- [1] X. Wang et al., "Traditional Chinese Medicine (TCM)-Inspired Fully Printed Soft Pressure Sensor Array with Self-Adaptive Pressurization for Highly Reliable Individualized Long-Term Pulse Diagnostics," *Advanced Materials*, p. 2410312, 2024, doi: 10.1002/ADMA.202410312.
- [2] A. Kaltsas et al., "Predictors of Successful Testicular Sperm Extraction: A New Era for Men with Non-Obstructive Azoospermia," *Biomedicines* 2024, Vol. 12, Page 2679, vol. 12, no. 12, p. 2679, Nov. 2024, doi: 10.3390/BIOMEDICINES12122679.
- [3] A. Depeursinge et al., "Fusing Visual and Clinical Information for Lung Tissue Classification in HRCT Data," *Artif Intell Med*, p. ARTMED1118, 2010, doi: 10.1016/J.
- [4] T. Greenhalgh et al., "Beyond adoption: A new framework for theorizing and evaluating nonadoption, abandonment, and challenges to the scale-up, spread, and sustainability of health and care technologies," *J Med Internet Res*, vol. 19, no. 11, Nov. 2017, doi: 10.2196/JMIR.8775.

- [5] Shaharina Shoha et al., “Enhanced Parkinson’s Disease Detection Using Advanced Vocal Features and Machine Learning,” *Journal of Computer Science and Technology Studies*, vol. 6, no. 5, pp. 113–128, Nov. 2024, doi: 10.32996/JCSTS.2024.6.5.10.
- [6] S. Maqsood, R. Damaševičius, S. Shahid, and N. D. Forkert, "MOX-NET: Multistage deep hybrid feature fusion and selection framework for monkeypox classification," *Expert Syst Appl*, vol. 255, p. 124584, Dec. 2024, doi: 10.1016/J.ESWA.2024.124584.
- [7] G. Meena, K. K. Mohbey, and S. Kumar, “Monkeypox recognition and prediction from visuals using deep transfer learning-based neural networks,” *Multimedia Tools Appl*, vol. 83, no. 28, pp. 71695–71719, Aug. 2024, doi: 10.1007/S11042-024-18437-Z/METRICS.
- [8] A. Bamaqa, W. M. Bahgat, Y. AbdulAzeem, H. M. Balaha, M. Badawy, and M. A. Elhosseini, “Early detection of monkeypox: Analysis and optimization of pretrained deep learning models using the Sparrow Search Algorithm,” *Results in Engineering*, vol. 24, p. 102985, Dec. 2024, doi: 10.1016/J.RINENG.2024.102985.
- [9] S. Singla, “Monkeypox Classification Using EfficientNetB3 Transfer Learning Model,” *2nd International Conference on Intelligent Cyber-Physical Systems and Internet of Things, ICoICI 2024 - Proceedings*, pp. 1635–1639, 2024, doi: 10.1109/ICOICI62503.2024.10696546.
- [10] M. G. Kibriya et al., “Privacy-Preserving Vision-Based Detection of Pox Diseases Using Federated Learning,” *Studies in Big Data*, vol. 152, pp. 105–122, 2024, doi: 10.1007/978-981-97-3966-0\_6/FIGURES/5.
- [11] E. Abdellatef, A. H. Ismail, M. I. Fath Allah, and W. A. Shalaby, “Leveraging convolutional neural networks and hashing techniques for the secure classification of monkeypox disease,” *Scientific Reports 2024 14:1*, vol. 14, no. 1, pp. 1–25, Nov. 2024, doi: 10.1038/s41598-024-75030-y.
- [12] A. Veit, N. Alldrin, G. Chechik, I. Krasin, A. Gupta, and S. Belongie, “Learning from noisy large-scale datasets with minimal supervision,” *Proceedings - 30th IEEE Conference on Computer Vision and Pattern Recognition, CVPR 2017*, vol. 2017-January, pp. 6575–6583, Nov. 2017, doi: 10.1109/CVPR.2017.696.
- [13] T. Greenhalgh et al., “Beyond adoption: A new framework for theorizing and evaluating nonadoption, abandonment, and challenges to the scale-up, spread, and sustainability of health and care technologies,” *J Med Internet Res*, vol. 19, no. 11, Nov. 2017, doi: 10.2196/JMIR.8775.
- [14] M. Kumar Saini, A. Saini, and S. Gupta, “Digital Image Processing Techniques for Leukemia Detection,” *International Journal of Science and Research (IJSR)*, vol. 13, no. 6, pp. 1710–1719, Jun. 2024, doi: 10.21275/SR24627090927.
- [15] J. Xie et al., “Functional Monitoring of Patients With Knee Osteoarthritis Based on Multidimensional Wearable Plantar Pressure Features: Cross-Sectional Study.,” *JMIR Aging*, vol. 7, no. 1, p. e58261, Nov. 2024, doi: 10.2196/58261.
- [16] A.-M. Kasparbauer et al., “Test–Retest Reliability of Deep Learning Analysis of Brain Volumes in Adolescent Brain,” *Information 2024*, Vol. 15, Page 748, vol. 15, no. 12, p. 748, Nov. 2024, doi: 10.3390/INFO15120748.
- [17] S. Maqsood, R. Damaševičius, S. Shahid, and N. D. Forkert, "MOX-NET: Multistage deep hybrid feature fusion and selection framework for monkeypox classification," *Expert Syst Appl*, vol. 255, p. 124584, Dec. 2024, doi: 10.1016/J.ESWA.2024.124584.
- [18] G. Meena, K. K. Mohbey, and S. Kumar, “Monkeypox recognition and prediction from visuals using deep transfer learning-based neural networks,” *Multimedia Tools Appl*, vol. 83, no. 28, pp. 71695–71719, Aug. 2024, doi: 10.1007/S11042-024-18437-Z/METRICS.
- [19] A. Bamaqa, W. M. Bahgat, Y. AbdulAzeem, H. M. Balaha, M. Badawy, and M. A. Elhosseini, “Early detection of monkeypox: Analysis and optimization of pretrained deep learning models using the Sparrow Search Algorithm,” *Results in Engineering*, vol. 24, p. 102985, Dec. 2024, doi: 10.1016/J.RINENG.2024.102985.
- [20] E. Abdellatef, A. H. Ismail, M. I. Fath Allah, and W. A. Shalaby, “Leveraging convolutional neural networks and hashing techniques for the secure classification of monkeypox disease,”

- Scientific Reports 2024 14:1, vol. 14, no. 1, pp. 1–25, Nov. 2024, doi: 10.1038/s41598-024-75030-y.
- [21] J. Xie et al., “Functional Monitoring of Patients With Knee Osteoarthritis Based on Multidimensional Wearable Plantar Pressure Features: Cross-Sectional Study.,” *JMIR Aging*, vol. 7, no. 1, p. e58261, Nov. 2024, doi: 10.2196/58261.
- [22] A. Akram et al., “SkinMarkNet: an automated approach for prediction of monkeyPox using image data augmentation with deep ensemble learning models,” *Multimed Tools Appl*, pp. 1–17, Jul. 2024, doi: 10.1007/S11042-024-19862-W/METRICS.
- [23] Z. Zhao, L. Alzubaidi, J. Zhang, Y. Duan, U. Naseem, and Y. Gu, “Robust and Explainable Framework to Address Data Scarcity in Diagnostic Imaging,” Jul. 2024, Accessed: Nov. 28, 2024. [Online]. Available: <https://arxiv.org/abs/2407.06566v1>
- [24] M. G. Kibriya et al., “Privacy-Preserving Vision-Based Detection of Pox Diseases Using Federated Learning,” *Studies in Big Data*, vol. 152, pp. 105–122, 2024, doi: 10.1007/978-981-97-3966-0\_6/FIGURES/5.
- [25] A. Tabassum et al., “Privacy Preserving Breast Cancer Prediction with Mammography Images Using Federated Learning,” *Studies in Big Data*, vol. 152, pp. 227–245, 2024, doi: 10.1007/978-981-97-3966-0\_12/FIGURES/9.
- [26] T. Rahman et al., “Reliable tuberculosis detection using chest X-ray with deep learning, segmentation and visualization,” *IEEE Access*, vol. 8, pp. 191586–191601, 2020, doi: 10.1109/ACCESS.2020.3031384.
- [27] M.-J. Jian et al., “Pioneering Klebsiella Pneumoniae Antibiotic Resistance Prediction With Artificial Intelligence-Clinical Decision Support System-Enhanced Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry: Retrospective Study.,” *J Med Internet Res*, vol. 26, no. 1, p. e58039, Nov. 2024, doi: 10.2196/58039.
- [28] M. Ahsan and R. Damaševičius, “Artificial intelligence-powered image analysis: A paradigm shift in infectious disease detection,” *Artif Intell Med*, vol. 159, p. 103025, Jan. 2025, doi: 10.1016/J.ARTMED.2024.103025.
- [29] S. J. S. Rajasekar et al., “Detection of tuberculosis using cough audio analysis: a deep learning approach with capsule networks,” *Discover Artificial Intelligence*, vol. 4, no. 1, pp. 1–11, Dec. 2024, doi: 10.1007/S44163-024-00179-4/TABLES/3.
- [30] Z. Xu et al., “Machine learning-based infection diagnostic and prognostic models in post-acute care settings: a systematic review,” *Journal of the American Medical Informatics Association*, Nov. 2024, doi: 10.1093/JAMIA/OCAE278.
- [31] G. M. F. Bin Mostafa, “Statistical Machine Learning Models for Biomedical Science,” 2024. Accessed: Nov. 29, 2024. [Online]. Available: <https://hdl.handle.net/2346/100434>
- [32] A. Sayed, P. Ds. F. H. S. Sharma, and J. F. Borgio, “Editorial: Molecular Informatics in Precision Medicine,” *Front Med (Lausanne)*, vol. 11, p. 1526520, doi: 10.3389/FMED.2024.1526520.
- [33] H. B. et al., “Advances in diagnosis and prognosis of bacteraemia, bloodstream infection, and sepsis using machine learning: A comprehensive living literature review,” *Artif Intell Med*, p. 103008, Nov. 2024, doi: 10.1016/J.ARTMED.2024.103008.
- [34] G. Gogoi et al., “Leveraging environmental microbial indicators in wastewater for data-driven disease diagnostics,” *Front Bioeng Biotechnol*, vol. 12, p. 1508964, Nov. 2024, doi: 10.3389/FBIOE.2024.1508964.
- [35] M. Lepoittevin et al., “Advantages of Metabolomics-Based Multivariate Machine Learning to Predict Disease Severity: Example of COVID,” *International Journal of Molecular Sciences* 2024, Vol. 25, Page 12199, vol. 25, no. 22, p. 12199, Nov. 2024, doi: 10.3390/IJMS252212199.
- [36] F. B. Demir et al., “MNPdenseNet: Automated Monkeypox Detection Using Multiple Nested Patch Division and Pretrained DenseNet201,” *Multimed Tools Appl*, vol. 83, no. 30, pp. 75061–75083, Sep. 2024, doi: 10.1007/S11042-024-18416-4/TABLES/8.

- [37] B. Ncube, M. Dziki, A. Nyoni, M. Ncube, B. Mutunhu Ndlovu, and S. Dube, "Effectiveness of Machine Learning algorithms in predicting Monkey Pox (Mpox): A Systematic Literature Review," *Proceedings of the International Conference on Industrial Engineering and Operations Management*, Jul. 2024, doi: 10.46254/EU07.20240072.
- [38] X. Li, S. Zhou, F. Wang, and L. Fu, "An improved sparrow search algorithm and CNN-BiLSTM neural network for predicting sea level height," *Sci Rep*, vol. 14, no. 1, Dec. 2024, doi: 10.1038/S41598-024-55266-4.
- [39] G. Meena, K. K. Mohbey, and S. Kumar, "Monkeypox recognition and prediction from visuals using deep transfer learning-based neural networks," *Multimedia Tools Appl*, vol. 83, no. 28, pp. 71695–71719, Aug. 2024, doi: 10.1007/S11042-024-18437-Z.
- [40] S. Maqsood, R. Damaševičius, S. Shahid, and N. D. Forkert, "MOX-NET: Multistage deep hybrid feature fusion and selection framework for monkeypox classification," *Expert Syst Appl*, vol. 255, Dec. 2024, doi: 10.1016/J.ESWA.2024.124584.
- [41] Y. Shen et al., "Optimizing skin disease diagnosis: harnessing online community data with contrastive learning and clustering techniques," *NPJ Digit Med*, vol. 7, no. 1, p. 28, Dec. 2024, doi: 10.1038/S41746-024-01014-X.
- [42] R. Shokri and V. Shmatikov, "Privacy-preserving deep learning," 2015 53rd Annual Allerton Conference on Communication, Control, and Computing, Allerton 2015, pp. 909–910, Apr. 2016, doi: 10.1109/ALLERTON.2015.7447103.
- [43] G. Srivastava et al., "XAI for Cybersecurity: State of the Art, Challenges, Open Issues and Future Directions," Jun. 2022, Accessed: Nov. 29, 2024. [Online]. Available: <http://arxiv.org/abs/2206.03585>
- [44] Y.-N. Chuang et al., "Efficient XAI Techniques: A Taxonomic Survey," Feb. 2023, Accessed: Nov. 29, 2024. [Online]. Available: <http://arxiv.org/abs/2302.03225>
- [45] C. Yan et al., "A fully automatic artificial intelligence-based CT image analysis system for accurate detection, diagnosis, and quantitative severity evaluation of pulmonary tuberculosis," *Eur Radiol*, vol. 32, no. 4, pp. 2188–2199, Apr. 2022, doi: 10.1007/S00330-021-08365-Z.
- [46] M. F. Almufareh, N. Tariq, M. Humayun, and B. Almas, "A Federated Learning Approach to Breast Cancer Prediction in a Collaborative Learning Framework," *Healthcare*, vol. 11, no. 24, p. 3185, Dec. 2023, doi: 10.3390/HEALTHCARE11243185.
- [47] M. Lepoittevin et al., "Advantages of Metabolomics-Based Multivariate Machine Learning to Predict Disease Severity: Example of COVID," *Int J Mol Sci*, vol. 25, no. 22, p. 12199, Nov. 2024, doi: 10.3390/IJMS252212199.
- [48] A. Tripathi, A. Waqas, K. Venkatesan, Y. Yilmaz, and G. Rasool, "Building Flexible, Scalable, and Machine Learning-Ready Multi-modal Oncology Datasets," *Sensors* 2024, Vol. 24, Page 1634, vol. 24, no. 5, p. 1634, Mar. 2024, doi: 10.3390/S24051634.