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REVIEW **Open Access**

Artificial intelligence in the battle against epidemics: A review of techniques, developments, performance constraints, and solutions with a focus on lassa fever

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Abstract

In recent years, artificial intelligence (AI) has gained recognition as a transformative tool, aiding in the prediction of disease patterns, outbreak control, and the efficient distribution of medical resources. This review explores the extensive contributions of AI in epidemic response, with particular emphasis on its application to Lassa fever. The review begins by analyzing the disease's epidemiology and transmission patterns, laying the groundwork for understanding AI-driven approaches. Key AI technologies such as machine learning, deep learning, and natural language processing are examined for their impact on surveillance, diagnostics, and treatment innovation. Successful implementations include predictive models for outbreak identification and enhanced vaccine research. However, the integration of AI in epidemic contexts continues to face challenges, including insufficient epidemiological data, high computational requirements, and difficulty incorporating AI within existing healthcare infrastructures. These issues are particularly pronounced in the management of Lassa fever, where data limitations and disease variability add layers of complexity. Existing reviews fail to adequately address the latest AI advances in this domain, particularly in relation to implementation challenges, global trends, and emerging concerns. This gap is addressed by offering a comprehensive overview of AI-driven techniques, ongoing developments, and practical solutions tailored to Lassa fever control and prevention. Ultimately, this review champions an inclusive AI framework that improves preparedness and adaptability in the response to epidemics. By extrapolating insights from Lassa fever, it provides a strategic guide for stakeholders, scientists, healthcare professionals, and policymakers, seeking to take advantage of AI to strengthen public health resilience and epidemic management.

Keywords Artificial Intelligence, AI, Lassa, Machine Learning, ML, Deep Learning, NLP, Health, Sensor, Fever, Epidemic, Pandemic, Public Health

1 Introduction

Population growth in Africa is expected to rise significantly between 2015 and 2050 [1], and with it, the threat of communicable diseases like Lassa fever, Ebola, and other viral hemorrhagic fevers is expected to grow. Although efforts and funding have been directed toward controlling these diseases, much still remains to be done. Many public health systems continue to face inefficiencies, which can lead to more lives being lost and diseases spreading faster.

Specifically, Lassa fever is a serious hemorrhagic illness caused by a ribonucleic acid (RNA) virus from the *Arenaviridae* family. It is a zoonotic disease, meaning it is transmitted from animals to humans, mostly through contact with rodents such as *Mastomys natalensis* (multimammate rats). Infection often occurs when people are exposed to urine or feces from these rodents, especially through contaminated food, broken skin, or dirty surfaces. The disease can also spread from person to person through contact with infected blood, urine, or other body fluids. While hospital-acquired infections and infections among healthcare workers are not common, they can happen when proper infection control measures are not followed [2–4].

Frequent outbreaks of Lassa fever have been reported in West African countries such as Nigeria, Ghana, Benin, Mali, Liberia, Guinea, and Sierra Leone [5, 6]. The disease continues to place a heavy burden on these populations, with high rates of illness and death. According to the World Health Organization (WHO), between 100,000 and 300,000 cases occur each year, resulting in around 5000 deaths [2]. In Nigeria alone, by the end of 2024, 214 deaths were recorded among 10,098 suspected cases, with 1309 confirmed. The case fatality rate (CFR) was 16.3% in 2024, compared to 17.9% in 2023 [3, 7].

The incubation period for Lassa fever is between 6 and 21 days. In its early stages, the disease often looks like other common fevers, which makes it hard to diagnose. Symptoms may include fever ($\geq 38^\circ$C), muscle pain, sore throat, nausea, vomiting, and discomfort in the chest or abdomen [3]. These symptoms can range from mild to very severe, including bleeding and organ failure. Because of this wide range of symptoms, diagnosis can be difficult without a strong level of clinical suspicion, especially in people who live in or have recently returned from affected areas [6, 8, 9]. Laboratory confirmation is usually done through reverse transcription polymerase chain reaction (RT-PCR) testing to detect the virus's RNA in a blood sample, following standard case definitions.

Furthermore, the immune response to Lassa virus infection is complex, involving both cellular and humoral components, yet protective immunity remains only partially understood, contributing to recurrent outbreaks and reinfections in endemic regions. While neutralizing antibodies are detectable in some patients, robust T-cell responses appear more critical for viral clearance and long-term protection [10, 11]. This uncertainty complicates the identification of reliable correlates of immunity. The Lassa virus is also a genetically diverse arenavirus with multiple distinct lineages circulating across West Africa, particularly in Nigeria, Sierra Leone, Liberia, and Guinea. This extensive genetic variability complicates the development of broadly protective therapeutics and vaccines, as antigenic drift can reduce neutralization efficacy and diagnostic precision. Consequently, vaccine development efforts, including vector-based platforms, DNA vaccines, and recombinant proteins are ongoing, yet no licensed vaccine currently exists, largely due to antigenic variability and limited understanding of protective immune mechanisms [12].

Another major challenge in controlling Lassa fever is the lack of strong disease surveillance and early detection systems. Without early warning, it becomes harder to control outbreaks, and response efforts are delayed. These delays often result in more suffering and more deaths. In many places, the process of reporting cases through the integrated disease surveillance and response (IDSR) system takes too long, which makes timely intervention difficult [13].

To this effect, artificial intelligence (AI) is now being seen as a powerful tool in public health. It allows machines to simulate human thinking, understand language, recognize patterns, make decisions, and learn from experience [14, 15]. AI includes technologies such as machine learning (ML), neural networks, natural language processing (NLP), robotics, and expert systems. Its strength lies in its ability to analyze large datasets quickly and produce useful insights, which can greatly improve how we prepare for and respond to epidemics [16–18]. When AI is used in the fight against Lassa fever, it offers a chance to reduce the disease's impact, save lives, and protect communities.

As AI and pandemic research continue to evolve, it is important that recent developments are reviewed and understood. Many existing studies do not provide a complete overview of how AI is being used, the innovations being introduced, and the limitations being faced. This article addresses that gap by offering a detailed review of how AI is applied in managing Lassa fever. The focus is placed on machine learning models, recent technological advances, practical challenges, and possible solutions. By exploring the role of AI in this area, this article aims to highlight the current state of the field and suggest areas for future research. Thus, the main contributions of this review are summarized as follows:

1. A detailed review of AI methods used in Lassa fever management is provided. This includes key areas such as machine learning, current innovations, implementation challenges, and strategies for dealing with ongoing and future issues. The latest trends and potential research directions are also discussed.
2. The integration of AI technologies in Lassa fever response efforts is explored, with a focus on how they are being used to lower disease transmission and improve outbreak control.
3. The key limitations of current AI approaches are discussed, particularly in terms of scalability, efficiency, and how well they meet user needs in public health settings.

The structure of this article is as follows: Section 2 reviews related reviews and distinguishes this work from existing literature. Section 3 details the methodological framework used in this study. Section 4 provides an overview of AI-based interventions in Lassa fever management, while Section 4.7 discusses applications in disease control and treatment optimization. Section 4.8 highlights practical AI use cases in broader pandemic management. Section 5 focuses on performance limitations and their potential resolutions, followed by Section 5.2, which explores ongoing and future research efforts. Finally, Section 6 concludes the paper.

2 Related review articles

Artificial intelligence (AI) has transformed epidemic preparedness and response by improving the speed, precision, and scope of data analysis. Its applications now span early outbreak detection, clinical diagnosis, drug discovery, and large-scale surveillance.

A growing body of literature demonstrates how machine learning (ML), deep learning (DL), and natural language processing (NLP) models have accelerated disease intelligence during crises such as COVID-19, Ebola, and influenza. Despite these advances, comprehensive reviews that systematically assess AI's role in the context of Lassa fever remain limited. The present section therefore positions this study within the broader landscape of AI-driven epidemic research, identifies existing knowledge gaps, and clarifies how this review extends prior work.

2.1 Review of existing literature

Table 1 summarises representative review papers addressing AI techniques in epidemic prediction, detection, and management. Earlier works, such as Ajagbe et al. [19] and Zeng et al. [20], examined AI frameworks for COVID-19 and other respiratory pandemics, emphasising computer-vision and time-series models but not haemorrhagic fevers. Reviews like Madueme et al. [21] and Samson et al. [22] introduced mathematical and ML models for Lassa fever, whereas Ibrahim et al. [23] explored algorithmic principles underlying Naive Bayes, logistic regression, support vector machine (SVM),

Table 1 Related review papers

Ref	Year	Main focus	Specific details
[19]	2024	Analysis of 45 papers on deep learning techniques for pandemic detection and prediction	● Convolutional Neural Networks (CNN) ● Deep Learning and Machine Learning ● Internet of Things (IoT)
[26]	2024	Overview of AI in combating healthcare challenges in Africa	● Impact of AI integration in Sub-Saharan Africa ● Challenges in AI health technology ● Emerging trends in AI-driven healthcare
[21]	2024	Mathematical models for Lassa fever	● Review of five categories of mathematical models ● Challenges identified: model heterogeneity, data quality, and gaps in understanding transmission and intervention dynamics
[22]	2023	Machine learning algorithms for Lassa fever	● Medium Gaussian SVM ● Ensemble Boosted and Bagged Trees ● Exponential Gaussian Process Regression (GPR)
[27]	2023	Detection and diagnosis of Lassa fever using Bayesian Belief Networks	● Focus on viral haemorrhagic fevers ● Prediction using supervised ML and Bayesian networks
[24]	2023	Advances in AI for infectious-disease surveillance	● Adoption of AI ● Data source, volume, and quality ● Limitations and challenges
[25]	2023	Computational approaches to prevention and surveillance of Lassa fever	● Use of bioinformatics and molecular pipelines ● Statistical models including Bayesian and forest methods
[16, 28]	2022	Pandemic prediction models	● Fuzzy logic ● SVM and neural networks
[23]	2021	Role of ML algorithms in disease diagnosis	● Pros and cons of Naive Bayes, logistic regression, SVM, and CNN
[20]	2021	Application of AI-enabled public-health surveillance	● Data sources for computational model development ● Use of ML in disease simulation and prediction
[29]	2020	COVID-19, AI, and big data	● Evaluation of CNN accuracy of 93.3% on 13,975 images
[30]	2020	Application of deep learning and ML in healthcare	● Benefits of DL and ML for large-scale health data analysis
[31]	2019	Societal issues of AI in medicine	● Legislation, interpretability, ethics, and fairness
[32, 33]	2019, 2023	AI for epidemic trend prediction	● Use of generative adversarial networks for epidemic-trend forecasting
[34]	2018	Review of Lassa-fever outbreaks in Nigeria	● Epidemiological profile, determinants, and public-health response

and convolutional neural networks (CNNs) for general disease detection. More recent surveys [24–26] reviewed computational or public-health approaches to epidemic surveillance in Africa but offered only passing references to Lassa fever. Collectively, these studies reveal a strong emphasis on respiratory or vector-borne diseases while highlighting a clear shortage of focused analyses on viral haemorrhagic fevers.

2.2 Focused examples of AI in epidemic management

To contextualise AI's evolving role, Table 2 presents a comparative feature analysis of prior reviews, highlighting their thematic coverage and methodological emphasis. Existing surveys have extensively examined machine-learning techniques for COVID-19, Ebola, and influenza but seldom for Lassa fever. Most emphasised algorithmic performance, architecture, or ethics without linking these to disease-specific data challenges such as scarcity, quality, and geographic bias. Only a few studies, particularly those by Madueme et al. [21], Samson et al. [22], and MacIntyre et al. [27], have explicitly explored AI in the context of viral haemorrhagic fevers, identifying major research gaps in feature selection, benchmarking, and multimodal fusion.

2.3 Summary of identified gaps

In summary, the literature on AI in epidemic control reveals extensive progress in model development but limited synthesis of how these advances translate to Lassa-fever research. Most prior reviews concentrate on algorithmic performance or general public-health surveillance without discussing contextual barriers such as scarce datasets, data heterogeneity, and ethical governance in endemic regions. By integrating lessons from broader epidemic AI research and explicitly addressing these neglected areas, the present review fills a unique gap and provides a unified framework for applying artificial-intelligence techniques to Lassa-fever monitoring, diagnosis, and intervention.

3 Review methodology

This section describes the methodological framework adopted for this review, based on the procedures outlined in [45–47]. A step-by-step illustration is presented in Fig. 1. The process began by acknowledging the expanding role of AI in tackling a broad range of global health challenges. Accordingly, we constructed guiding research questions, selecting specific terms associated with AI and health to support a focused literature search.

A structured strategy was then implemented to identify, screen, and select pertinent literature. This involved evaluating and synthesizing the extracted studies and reporting the synthesized outcomes accordingly. The review followed the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines, which promote consistency and transparency in reviewing and reporting scientific evidence. PRISMA provides a well-established structure for documenting systematic reviews and meta-analyses [48–50]. Additional methodological procedures are elaborated in the sections that follow.

3.1 Literature review questions

To effectively investigate the role of AI in addressing Lassa fever, it is crucial to first understand its key components. Accordingly, we carried out an initial review of scholarly literature aimed at identifying prior reviews focused on AI applications for pandemic

Table 2 Comparative feature coverage in related AI review literature

Ref	Year	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13
[35]	2024	Yes	No	No	No	Yes	Yes	No	Yes	No	No	No	No	Yes
[36]	2024	Yes	No	No	Yes	No	No	No	Yes	Yes	Yes	Yes	No	Yes
[37]	2023	Yes	No	Yes	Yes	No	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
[27]	2023	Yes	No	No	Yes	No	No	No	Yes	Yes	Yes	Yes	No	Yes
[38]	2023	Yes	No	No	Yes	No	No	No	Yes	Yes	Yes	Yes	No	Yes
[39]	2023	Yes	No	No	Yes	No	No	No	Yes	No	Yes	Yes	No	Yes
[19]	2023	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No	No	Yes
[40]	2023	Yes	No	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	No	Yes
[41]	2022	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	No	Yes
[20]	2021	Yes	No	Yes	Yes	No	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
[42]	2021	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	No	No
[43]	2021	Yes	No	Yes	Yes	No	No	Yes	Yes	Yes	Yes	No	No	Yes
[44]	2021	Yes	No	Yes	Yes	No	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Current	2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes

Legend: C1 = Machine learning techniques, C2 = Security considerations, C3 = Comparative frameworks, C4 = Review design explained, C5 = AI Architecture described, C6 = Models tailored to Lassa fever, C7 = Benchmarking of performance, C8 = Data quality and accessibility, C9 = Field implementation, C10 = Ethical and social aspects, C11 = Multimodal intelligence methods, C12 = Cross-disease comparisons, C13 = Early warning & predictive insights response. This section outlines the findings of that review. Although various related works exist, we observed limited comprehensive coverage on three major themes: AI system architectures suited for deployment, recent advances in AI technologies, and robust security frameworks for AI applications. These observed gaps shaped the development of the following core research questions:

1. Which AI algorithms have shown the most promise for predicting Lassa fever outbreaks using historical and real-time data?
2. How can AI-based models support the identification of high-risk zones for Lassa fever transmission?
3. What data types (e.g., clinical, environmental, socio-economic) are essential for building reliable AI-driven surveillance systems for Lassa fever?
4. What approaches can ensure the integrity and consistency of datasets used for training and validating AI models?
5. How can heterogeneous data sources (e.g., medical records, geospatial imagery) be integrated into a cohesive AI-powered surveillance framework?
6. What are the practical considerations for embedding AI-based surveillance solutions into existing public health infrastructures?
7. In what ways can AI models be optimized for use in resource-constrained environments with limited computing capacity and network access?
8. What ethical principles should be considered when deploying AI systems for public health surveillance of Lassa fever?
9. Which performance metrics are most appropriate for assessing the effectiveness of AI models in Lassa fever monitoring?
10. What unresolved challenges and emerging opportunities exist in enhancing AI-based solutions for pandemic preparedness and response?

Following the formulation of these questions, a second-stage literature review was conducted to assess whether these topics had been sufficiently explored and synthesized in existing review literature. Upon discovering that many of these questions had either been underexplored or not addressed, we proceeded to the article selection and screening phase.

3.2 Search and selection strategy

To ensure comprehensive coverage, the selection of articles was guided by well-defined criteria focusing on studies related to pandemics, epidemics, artificial intelligence (AI), and Lassa fever. Below is a summary of the process used to identify the final set of reviewed publications:

1. A comprehensive literature search was conducted across multiple databases to ensure broad coverage of both biomedical and computational research relevant to artificial intelligence applications for Lassa fever. Scopus was prioritized for its extensive interdisciplinary indexing and citation analytics, while IEEE Xplore and the ACM Digital Library provided focused access to studies in engineering, computing, and machine learning. PubMed and the NCBI databases (including GenBank and GEO) were consulted to identify biomedical, genomic, and transcriptomic studies related to Lassa virus biology and diagnostics. Web of Science was used to retrieve high-impact epidemiological and cross-disciplinary research, while MDPI and SpringerLink

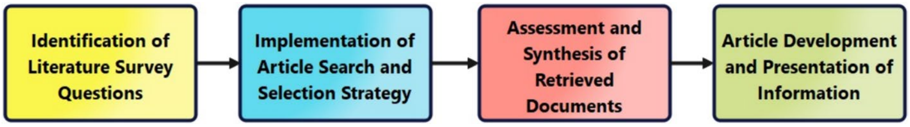

Fig. 1 Flow process of the review methodology [45]

offered access to open-access, peer-reviewed literature. Finally, Google Scholar served as a complementary source for cross-verification, capturing preprints, reports, and recently indexed materials not yet archived in traditional databases.

2. Based on an initial scoping review, key search phrases such as 'Artificial Intelligence,' 'Lassa fever,' 'Machine Learning,' 'Disease Detection,' 'Epidemic Forecasting,' 'Deep Learning,' and 'Security' were identified. Boolean logic operators ("AND", "OR") were applied to refine and optimize the search queries.
3. These keyword-based queries were executed across all selected repositories to gather a broad and relevant document base.
4. The search initially produced over 22,000 articles. We narrowed this pool using a 20-year publication window and keywords like but not limited to 'AI,' 'Pandemic,' and 'Lassa fever'. Manual screening was applied to shortlist candidate studies of potential relevance.
5. These shortlisted articles were further analyzed to determine their distinctiveness, as discussed in Section 2. Final selection was based on a quality assessment, followed by detailed reading and synthesis.

3.3 Evaluation and synthesis of information

To ensure the consistency and validity of the included literature, we applied specific inclusion and exclusion benchmarks as described below.

3.3.1 Inclusion criteria

1. The study must be peer-reviewed and published in a reputable academic journal or presented at a recognized scholarly conference.
2. The content must specifically address the use of AI in controlling or managing pandemics.
3. The study must provide substantial discussion on the selected keywords, not just brief mentions.

3.3.2 Exclusion criteria

1. Articles lacking full-text access were excluded from consideration.
2. Publications that merely listed keywords without substantive analysis were omitted.
3. Non-peer-reviewed sources such as preprints, reports, lecture slides, and proposals were excluded due to insufficient scholarly rigor.

After initial filtering, we conducted a further quality assessment:

1. Relevance was scored using a structured evaluation checklist.
2. Each article was cross-referenced with the research questions presented in Section 3.1.
3. A unified assessment protocol was applied to maintain consistency across all included studies.

From the initial 250 documents, 171 met the criteria for final inclusion and were used to support this review.

3.4 Article structuring and information presentation

Following the synthesis of topic-specific insights for each keyword and research objective, the structure of this article was organized as follows:

1. Using the PRISMA framework as a guide, the manuscript was organized into seven major sections aligned with the research themes. Due to the lack of standalone results or discussion sections in most studies, synthesized findings were integrated into each section, with a final conclusion summarizing open challenges and future research pathways.
2. The synthesized literature was grouped according to the research questions, with each section evaluating strengths, limitations, and trends in the application of AI techniques.
3. A final review of the manuscript was performed to ensure logical coherence and alignment with the article's goal of offering a structured overview of AI-driven strategies in epidemic response, particularly Lassa fever.

This structured approach ensured clarity, relevance, and logical flow throughout the paper, thus enabling a more effective presentation of AI's contributions to Lassa fever management.

4 AI in Lassa fever management: Techniques, applications, case studies, and databases

The emergence and spread of infectious diseases such as COVID-19, Ebola, Lassa fever, and influenza pose substantial challenges that necessitate swift, coordinated, and scalable public health responses. These outbreaks often overwhelm health systems and highlight the urgent need for technologies capable of real-time data analysis, forecasting, and efficient resource planning. AI has become an essential enabler in this context, offering advanced capabilities to detect, manage, and control infectious disease outbreaks effectively [26]. Applications of AI in pandemic settings, including Lassa fever, extend across fields such as epidemiology, clinical decision support, and public health administration, contributing significantly to improved outbreak preparedness and response [20].

In the midst of an outbreak, rapid access to relevant data can determine whether containment is successful or if widespread transmission ensues. The authors in [29] noted that AI systems are capable of processing large datasets with greater speed and accuracy than traditional analytical methods, enabling earlier detection of emerging patterns. During the COVID-19 crisis, AI tools were widely employed to track virus dissemination by aggregating and analyzing information from heterogeneous sources, including online media, news platforms, and official public health updates [51–53]. These real-time analytical tools supported the identification of infection hotspots, monitored containment efficacy, and offered predictive insights to guide timely interventions. As such, AI's capacity for rapid pattern recognition, forecasting, and data-driven decision support has made it indispensable in pandemic response strategies [52].

In the case of Lassa fever, researchers are applying AI-driven methods to develop advanced diagnostic systems, early-warning tools, and data-informed treatment planning models. These systems incorporate techniques such as machine learning, deep learning, and natural language processing to interpret diverse datasets, including electronic health records, genomic sequences, and diagnostic images [54–56]. Such capabilities allow for timely disease detection, better surveillance accuracy, and optimized clinical decision-making, ultimately strengthening overall public health resilience.

Fig. 2 provides a structured overview of various branches under AI, highlighting five major domains: Machine Learning, Deep Learning, Natural Language Processing, Bayesian Network and Probabilistic Models, and Expert Systems and Rule-Based Approaches. Each domain is further categorized into specific techniques or models. Machine Learning encompasses Supervised, Unsupervised, and Reinforcement Learning; Deep Learning includes networks such as CNNs, RNNs, Transformer Models, and Hybrid Models; Natural Language Processing deals with tasks like Text Classification and Machine Translation; Bayesian Networks and Probabilistic Models cover probabilistic reasoning; while Expert Systems focus on rule-based decision-making. Notably, each of these domains will be discussed in subsequent sections with focus on their role and application in Lassa fever management.

4.1 Machine learning in Lassa fever management

Machine learning (ML), which is recognized as a subset of AI, has been regarded as a transformative approach in epidemic management, including for diseases such as Lassa fever. Through the use of large datasets and sophisticated algorithms, patterns and insights that typically remain undetected by traditional analytical methods have been identified [57, 58]. In the study by [59], both ML and Deep Learning techniques were employed to control COVID-19, with AI being applied in areas such as case prediction, diagnostic analysis, and treatment planning.

These technological capabilities have been harnessed to support enhanced surveillance systems, improve forecasting models, accelerate drug discovery processes, and facilitate effective contact tracing and epidemiological analysis. Furthermore, remote monitoring

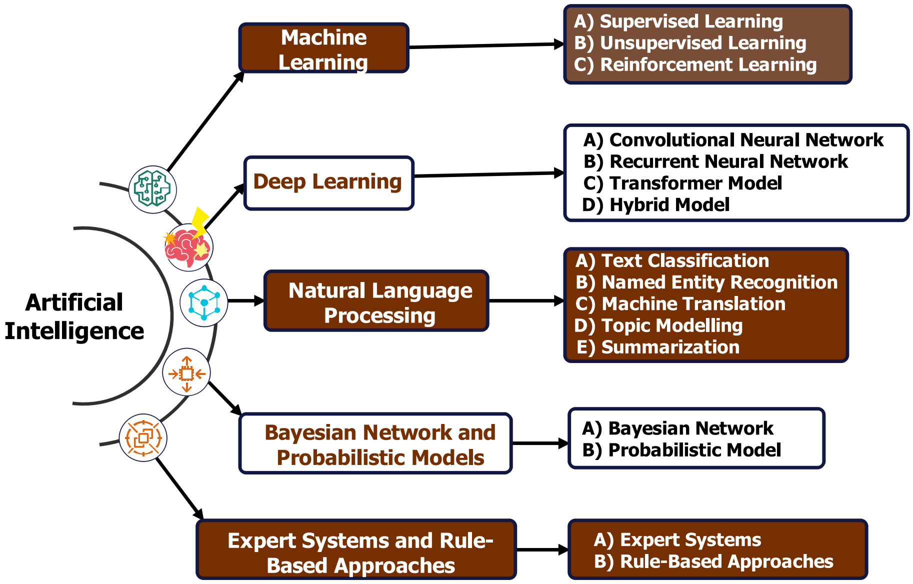

Fig. 2 Different AI techniques

and telemedicine solutions have been enabled by ML, allowing advanced healthcare interventions to be extended even to resource-constrained settings [44, 60].

Through ML algorithms, systems have been enabled to learn from data, recognize complex patterns, and make data-driven predictions without the need for explicit programming [61]. The literature has documented extensive applications of ML techniques in pandemic and disaster response efforts [41, 62–64]. In the case of Lassa fever, ML has been considered pivotal for early diagnosis, outbreak forecasting [65–67], patient monitoring, and the optimization of resource distribution [68–71]. ML algorithms are typically categorized into supervised learning, unsupervised learning, and reinforcement learning. In the following sections, the focus will be directed toward the application of ML in the management of Lassa fever.

4.1.1 Supervised learning algorithms

Supervised learning is an approach in AI, commonly applied in the healthcare domain for tasks such as disease classification, prognosis evaluation, and risk prediction. This methodology is based on the use of labeled datasets, where both input variables and their corresponding outcomes are predefined [72, 73]. Once trained, these models can infer outcomes for previously unseen inputs, making them particularly valuable in decision-support tools for clinical environments.

These learning algorithms are suited for many predictive tasks, such as both classification (e.g., identifying infection status) and regression (e.g., estimating recovery duration). Common supervised learning models include logistic regression, decision trees, support vector machines (SVM), random forests, and deep neural networks. Additional algorithms such as Naive Bayes, linear regression, K-Nearest Neighbors (KNN), and Gradient Boosting Machines are also widely used, with each method offering unique advantages depending on the data structure and clinical context [74, 75]. Table 3 outlines various supervised learning models and their specific roles in managing Lassa fever.

In Lassa fever management, supervised learning algorithms are particularly useful in:

1. Diagnosis prediction: ML models can be trained using comprehensive patient data, including symptoms, medical history, and biomarkers, to estimate the likelihood of Lassa fever infection. This helps healthcare providers make quick and informed decisions, especially in regions with limited laboratory resources [82].
2. Prognosis monitoring: Post-diagnosis, machine learning models assist in tracking disease progression and forecasting potential complications by analyzing patient vitals and treatment responses. This predictive insight can guide clinicians in adjusting treatment plans [83].

Table 3 Supervised ML algorithms in Lassa fever management

Supervised learning algorithms	Description	Use case for Lassa fever
Logistic regression	A basic classification algorithm used for binary outcomes (e.g., infected or not infected) [76–78]	Early diagnosis based on symptoms
Support vector machines (SVM)	Classifies data points by finding the best boundary between classes [79]	Classifying severity of infection
Random forests	Uses multiple decision trees to improve predictive performance	Diagnosis and risk prediction [80, 81]
Neural networks	Learns complex patterns in data through layers of neurons [74]	Predicting long-term prognosis based on vitals

A typical workflow for applying a supervised learning algorithm to Lassa fever management includes the following steps:

1. Input: Collect relevant patient data such as fever, bleeding, fatigue, and other clinical indicators.
2. Feature extraction: Identify and select key features that are most indicative of Lassa fever, which could include specific biomarkers, environmental factors, and symptom patterns.
3. Model training: Train a machine learning model using a dataset comprising historical patient records with known Lassa fever diagnoses [84].
4. Prediction: Apply the trained model to a new patient's data to predict whether they have Lassa fever and assess the likely severity of their condition.
5. Model improvement: Incorporate feedback from clinical use to continuously refine and improve the model's performance for greater accuracy and reliability.

Supervised learning's ability to process large volumes of data and uncover patterns makes it a powerful tool in advancing diagnostic and management strategies for Lassa fever, contributing to faster response times and improved patient outcomes.

4.1.2 Unsupervised learning algorithms

Unsupervised learning refers to a category of machine learning that processes data without predefined labels, aiming to identify hidden structures, patterns, or relationships in the dataset. Unlike supervised methods, which depend on known input–output pairs, unsupervised techniques work directly with unlabeled data to extract meaningful insights. These approaches are particularly useful in tasks such as clustering, anomaly detection, and exploring latent data structures that are not easily discernible through manual analysis [57].

Some widely used algorithms in this category include K-Means, Hierarchical Clustering, Principal Component Analysis (PCA), and t-Distributed Stochastic Neighbor Embedding (t-SNE). Additional models such as Autoencoders, Association Rule Learning (e.g., Apriori), DBSCAN (Density-Based Spatial Clustering of Applications with Noise), Gaussian Mixture Models (GMM), Self-Organizing Maps (SOM), and Latent Dirichlet Allocation (LDA) are also prominent. These algorithms enable the discovery of natural groupings and underlying relationships within complex datasets, often revealing insights that do not depend on prior categorization. Table 4 presents a selection of key unsupervised learning techniques and their roles in managing Lassa fever-related data.

In Lassa fever management, unsupervised learning has proven to be instrumental in:

1. Outbreak pattern discovery: Leveraging environmental and epidemiological data such as temperature, rodent population metrics, and humidity levels, unsupervised learning can identify geographical regions at an elevated risk for Lassa fever outbreaks. This

Table 4 Unsupervised ML algorithms in Lassa fever management

Unsupervised learning algorithms	Description	Use case for Lassa fever
K-Means clustering	Groups data into clusters based on similarity [72, 85]	Identifying outbreak clusters based on environmental data
Hierarchical clustering	Builds a tree-like structure of nested clusters [73, 86]	Grouping patients by symptom severity
Principal component analysis (PCA)	Reduces the dimensionality of data for easier visualization [87]	Identifying key environmental factors contributing to outbreaks

information is critical for preemptive public health measures and resource allocation [58].

2. Symptom grouping: By analyzing patient data, unsupervised learning models can identify clusters of symptoms that might represent distinct disease presentations or levels of severity, helping refine diagnostic criteria and treatment plans [60].

A typical workflow for applying an unsupervised learning algorithm to Lassa fever management includes the following steps:

1. Input: Collect environmental data such as humidity, rodent population density, and vegetation coverage.
2. Clustering: Group data points into clusters based on shared characteristics, revealing underlying structures in the data.
3. Pattern discovery: Use the model to detect hidden patterns that indicate potential high-risk areas for Lassa fever outbreaks.
4. Output: Generate a visual representation, such as a risk map, highlighting regions with a higher probability of outbreaks.

Unsupervised learning's capacity to analyze data without the need for labeled outputs makes it a powerful approach for discovering patterns that support proactive healthcare strategies, enhancing the monitoring and management of Lassa fever outbreaks.

4.2 Reinforcement learning algorithms

Reinforcement Learning (RL) is a specialized machine learning paradigm where an agent learns to make optimal decisions by interacting with its environment. Unlike supervised and unsupervised approaches, RL is driven by feedback mechanisms, rewards for correct actions and penalties for suboptimal ones, that guide the learning process over time. Through continuous interaction and adaptation, the agent improves its strategy to maximize cumulative rewards in varied and often unpredictable scenarios [88, 89].

Several prominent RL algorithms include Q-Learning, Deep Q-Networks (DQN), Policy Gradient techniques, Actor-Critic frameworks, Proximal Policy Optimization (PPO), and the REINFORCE algorithm [90, 91]. Each of these methods offers unique mechanisms for modeling the relationship between agent actions and environmental feedback. They also differ in how they manage the balance between exploration (trying unfamiliar strategies) and exploitation (relying on previously successful actions). Table 5 provides an overview of these reinforcement learning approaches and their relevance to Lassa fever intervention and management.

In Lassa fever management, reinforcement learning has shown significant potential in the following areas:

Table 5 Reinforcement learning algorithms in Lassa fever management

Reinforcement learning algorithms	Description	Use case for Lassa fever
Q-learning	A model-free algorithm that learns the value of actions for a given state [92]	Optimizing vaccination distribution during outbreaks
Deep Q-networks (DQN)	Combines Q-Learning with deep learning to handle large state spaces [92]	Resource allocation in regions with varying outbreak severity
Proximal policy optimization (PPO)	A policy optimization method that ensures stable and efficient training	Dynamic quarantine strategies balancing health and economic impacts

1. Resource allocation: RL can dynamically allocate resources such as healthcare workers, vaccines, and hospital beds during an outbreak. By analyzing real-time data on infection rates, population density, and hospital capacity, RL algorithms learn to prioritize areas or patients that require urgent attention, thus optimizing outcomes [81, 83].
2. Dynamic containment strategies: RL can be used to simulate and develop effective containment strategies, such as quarantines and travel restrictions. By iterating on these simulations, the algorithm identifies strategies that minimize infection spread while considering socio-economic factors [91].

A typical workflow for applying a reinforcement learning algorithm to Lassa fever management includes:

1. Environment: Create a simulation representing a region affected by a Lassa fever outbreak. The simulation includes variables such as population density, infection rates, healthcare resources, and socio-economic factors.
2. Actions: Define possible actions the agent can take, such as allocating medical supplies, imposing quarantines, deploying healthcare workers, or initiating public health campaigns.
3. Reward: Establish a reward mechanism, where positive feedback is given for reduced infection rates, lower mortality, or efficient resource usage, and penalties are applied for adverse outcomes such as overburdened hospitals or uncontrolled spread.
4. Learning loop: The agent iteratively interacts with the environment, evaluating the outcomes of its actions, and updates its policy to improve future decisions. Over time, the agent learns to optimize its strategy for effective Lassa fever management.

Reinforcement learning's ability to model and adapt to dynamic systems makes it a powerful tool for addressing complex challenges in Lassa fever management, such as outbreak response, resource prioritization, and containment planning. By integrating RL into healthcare systems, decision-making can become more data-driven, efficient, and adaptive.

4.3 Deep learning algorithms

Deep learning (DL), a subfield of AI, uses deep neural networks composed of multiple layers to automatically extract patterns and features from raw data. In contrast to traditional machine learning approaches that often depend on manual feature engineering, DL is particularly adept at modeling complex, nonlinear relationships in high-dimensional datasets. This strength makes DL highly applicable in areas such as medical diagnostics, image recognition, time-series forecasting, and decision support-critical components in both healthcare and epidemic control [82, 83, 93–95].

In the context of epidemic management, DL contributes to more efficient feature extraction, reducing the need for manual data preprocessing and accelerating analytical workflows. It is also highly scalable, capable of processing extensive datasets, including real-time health monitoring data. Furthermore, its adaptability allows models to be fine-tuned for emerging diseases and evolving outbreak scenarios.

Despite these advantages, several limitations affect the application of DL in managing Lassa fever. One major constraint is the requirement for large volumes of labeled training data, which may be difficult to obtain in low-resource settings. Additionally, DL models are computationally intensive, often requiring significant processing power and access to high-performance hardware such as GPUs. Another challenge is interpretability-DL models are frequently criticized as "black boxes," making it difficult to explain or justify their decisions during clinical assessments.

Nonetheless, DL offers considerable promise in supporting epidemic preparedness and response. Its use in diagnosing, monitoring, and predicting Lassa fever outbreaks may lead to earlier interventions and improved public health outcomes.

4.3.1 Convolutional neural networks (CNNs)

Convolutional Neural Networks (CNNs) are a class of deep learning models that excel in processing grid-like data, particularly images and spatially-organized datasets. By leveraging convolutional layers, CNNs automatically detect hierarchical patterns in data, such as edges, textures, and shapes. This capability makes CNNs highly effective for medical image analysis, where subtle patterns may reveal critical diagnostic information [35, 82, 83]. Pooling layers, combined with fully connected layers, ensure that the extracted features are refined and interpreted for accurate predictions or classifications. CNNs are widely used in healthcare due to their ability to process complex visual data with minimal human intervention, enabling more accurate, consistent, and scalable diagnostic processes.

Table 6 highlights specific use cases of CNNs in Lassa fever management.

In Lassa fever management, CNNs have shown promise in the following applications:

1. Medical image diagnosis: CNNs can analyze radiological images, such as X-rays, CT scans, or MRI scans, to detect abnormalities associated with Lassa fever complications. For example, they can identify internal bleeding, organ swelling, or tissue damage indicative of severe infection [35, 83].
2. Outbreak detection: By analyzing satellite or aerial imagery, CNNs can detect environmental factors such as rodent population density or changes in vegetation, which may signal regions at heightened risk of outbreaks. These insights support preemptive public health interventions [82].
3. Histopathological analysis: CNNs can assist in analyzing biopsy or tissue samples under a microscope, identifying specific cellular damage patterns linked to Lassa fever.

A typical workflow for applying CNNs to Lassa fever management includes the following steps:

1. Input: Obtain relevant medical images (e.g., X-rays, MRI scans) or environmental data (e.g., satellite imagery).
2. Convolutional layers: Use these layers to detect intricate patterns such as organ lesions, swelling, or environmental features like rodent habitats.

Table 6 Applications of CNNs in Lassa fever management

Application area	Description	Use case for Lassa fever
Medical image analysis	Analyzing radiological images to detect anomalies [96]	Identifying organ damage, such as internal bleeding or swelling, from X-rays or CT scans
Outbreak prediction	Processing satellite or aerial imagery to monitor environmental factors	Detecting rodent population density or habitat changes linked to outbreak risk
Histopathological studies	Analyzing tissue samples for microscopic patterns	Identifying cellular-level damage caused by Lassa fever

3. Pooling layers: Apply pooling operations (e.g., max pooling) to reduce the spatial dimensions of feature maps, focusing on the most critical patterns and reducing computational complexity.
4. Fully connected layers: Translate the refined features into actionable insights, such as classifying an image as indicative of healthy tissue or infected tissue.
5. Output: Generate predictions, such as disease severity, infection status, or outbreak probability in a given region.

CNNs' ability to process complex visual data autonomously has revolutionized healthcare diagnostics [97–99]. For Lassa fever, the integration of CNNs into diagnostic and outbreak monitoring systems can enhance precision and speed, ultimately supporting timely and effective public health interventions.

4.3.2 Recurrent neural networks (RNNs)

RNNs are regarded as a class of deep learning models that have been specifically designed for the processing of sequential data, where the order of inputs is known to significantly influence the output. In contrast to feedforward neural networks, RNNs are structured with feedback connections within their hidden layers, allowing information from prior inputs to be retained. Through this architecture, temporal dependencies across input sequences can be effectively captured, a feature that is critical for tasks involving time-series analysis or data characterized by inherent chronological structure. Advanced variants of RNNs, such as Long Short-Term Memory (LSTM) networks and Gated Recurrent Units (GRUs), have been introduced to enhance the model's capacity to manage long-range dependencies while addressing limitations such as the vanishing gradient problem [100–102].

In healthcare, RNNs have become increasingly useful for applications like patient monitoring, epidemic trend forecasting, and analyzing chronological patterns in clinical datasets. Table 7 provides examples of how RNNs are being leveraged for Lassa fever analysis and prediction.

A typical workflow for applying RNNs to Lassa fever management includes the following steps:

1. Input: Collect time-series data, such as patient vitals (e.g., fever, blood pressure, heart rate) or environmental metrics (e.g., rodent activity, temperature fluctuations).
2. Hidden layers: The RNN processes the sequential data, retaining information about previous inputs to identify trends and patterns.
3. Output: Generate predictions, such as the likelihood of disease progression (e.g., from mild to severe symptoms) or forecasts of future outbreak locations.

Table 7 Applications of RNNs in Lassa fever management

Application area	Description	Use case for Lassa fever
Patient symptom tracking	Analyzing temporal data of symptoms to predict disease progression	Predicting worsening symptoms (e.g., mild fever escalating to severe hemorrhagic conditions)
Outbreak monitoring	Processing real-time environmental and patient data to identify trends	Predicting future outbreak hotspots using IoT sensor data
Treatment response analysis	Tracking patient responses to interventions over time	Adjusting treatment plans dynamically based on response trends

4. Feedback loop: Refine the model using updated data from real-world monitoring and patient records to improve accuracy and adapt to evolving conditions.

The ability of RNNs to analyze and interpret sequential data makes them an invaluable tool in the fight against Lassa fever. By enabling more precise tracking of patient symptoms and outbreak dynamics, RNNs contribute to faster, more effective responses in disease management and control.

4.3.3 Transformer models

Transformer models represent a significant advancement in deep learning architectures, originally introduced for natural language processing (NLP) tasks. Unlike traditional sequential models such as RNNs, transformers utilize a self-attention mechanism that enables them to process entire sequences of data in parallel, capturing both local and global dependencies without the need for sequential processing. This capability makes transformers highly effective for analyzing sequential and multivariate data, particularly in complex scenarios where relationships across long distances in the data are critical.

Transformers have become invaluable tools in various domains, including healthcare, where their versatility and efficiency enable them to process and integrate diverse data types for actionable insights. Table 8 highlights the key applications of transformer models in the management of Lassa fever [103].

A typical workflow for applying transformer models in Lassa fever management includes the following steps:

1. Input: Collect diverse data sources, such as patient vitals, symptom profiles, environmental metrics (e.g., temperature, humidity), and genomic data of the virus.
2. Attention mechanism: The transformer applies its self-attention mechanism to assign weights to different inputs, focusing on the most relevant features for the prediction task.
3. Output: Generate predictions, such as outbreak risk maps, patient outcome probabilities, or likelihood of virus mutations.
4. Model refinement: Use feedback from real-world applications and updated datasets to improve the model's accuracy and adaptability.

4.3.4 Hybrid models

In many scenarios, combining different deep learning architectures leads to superior performance by leveraging the strengths of each model [104–106]. Hybrid architectures are especially beneficial in complex applications where diverse types of data and tasks are involved. Table 9 outlines examples of hybrid models and their applications in the management of Lassa fever.

Table 8 Applications of transformer models in Lassa fever management

Application area	Description	Use case for Lassa fever
Genomic data analysis	Analyzing viral genomic sequences to track mutations and predict variants	Assisting in vaccine development and understanding virus evolution
Multivariate data integration	Processing multiple data sources simultaneously to identify complex patterns	Predicting outbreak risks by combining patient symptoms, environmental factors, and healthcare data
Symptom-outcome correlation	Mapping patient symptoms to possible disease outcomes with high accuracy	Anticipating complications based on initial clinical presentations

Deep learning models, whether standalone or in hybrid configurations, provide robust tools for combating Lassa fever. Their ability to integrate diverse data types and perform complex analyses enhances early diagnosis, outbreak monitoring, and disease management, ultimately improving patient outcomes and public health responses.

4.4 Natural language processing (NLP) algorithms

NLP is recognized as a branch of artificial intelligence that enables the interpretation, analysis, and generation of human language by computational systems. Within the context of public health emergencies such as pandemics, NLP has been employed to extract meaningful insights from large volumes of unstructured textual data, including clinical documentation, scientific literature, news articles, and content derived from social media platforms [111–113].

The utility of NLP methodologies becomes particularly pronounced during disease outbreaks, such as Lassa fever, where unstructured text sources are frequently encountered. Through the application of these techniques, automated extraction of relevant information from heterogeneous textual inputs is facilitated, thereby enabling real-time tracking of disease progression and analysis of public discourse. Typical NLP applications include text classification, sentiment analysis, named entity recognition (NER), machine translation, topic modeling, and text summarization [114].

4.4.1 Text classification and sentiment analysis

Text classification is defined as the process by which predefined categories are assigned to textual data, whereas sentiment analysis is concerned with the identification of emotional polarity conveyed within the content-typically categorized as positive, negative, or neutral. These methods are regarded as particularly valuable for deriving actionable insights from unstructured information sources, including media reports, social media platforms, and electronic health records [111, 115, 116].

In relation to Lassa fever management, both text classification and sentiment analysis offer promising applications, as outlined in the following areas:

1. Public sentiment monitoring: During Lassa fever outbreaks, analyzing social media posts and news reports can help gauge public fear, misinformation, or panic, allowing healthcare organizations to take timely actions.
2. Patient records analysis: Text classification models can be trained to automatically analyze patient records and classify them based on severity, risk factors, or treatment outcomes.

A typical workflow for applying text classification and sentiment analysis in Lassa fever management includes the following steps:

Table 9 Applications of hybrid models in Lassa fever management

Hybrid model type	Description	Use case for Lassa fever
CNN-RNN hybrid [107, 108]	Combines spatial feature extraction from images with sequential data analysis	Predicting disease progression from organ damage images and patient vitals
Transformer-CNN hybrid [109, 110]	Integrates transformers for multivariate analysis with CNNs for image processing	Comprehensive outbreak modeling using patient data and environmental images
Transformer-RNN hybrid	Uses transformers for attention-based feature selection and RNNs for sequential predictions	Advanced forecasting of disease spread and patient recovery timelines

1. Input: Text from social media, news articles, or patient records.
2. Preprocessing: Text is cleaned, tokenized, and vectorized (converted to numerical format).
3. Classification model: The text is classified based on the task (e.g., outbreak severity, patient condition, or public sentiment).
4. Output: Category (e.g., high-risk patient, public concern level) or sentiment (positive, negative, neutral).

4.4.2 Named entity recognition (NER)

NER is a technique that identifies and classifies named entities within a text (e.g., person names, dates, medical conditions, locations). It is particularly useful for information extraction, especially from medical literature and clinical data [95, 117–119].

Applications in Lassa Fever:

1. Medical data extraction: NER models can automatically identify key details from clinical reports, such as symptoms, treatments, and disease progression in Lassa fever patients.
2. Outbreak reporting: NER can extract important entities like disease names, affected regions, and case numbers from news articles or government reports, helping track and monitor outbreaks [120].

A typical workflow for applying NER analysis in Lassa fever management includes the following steps:

1. Input: A text document (e.g., clinical report, research paper).
2. Entity recognition: The NER model identifies important entities such as patient names, symptoms, and treatments.
3. Entity classification: These entities are classified into categories (e.g., person, disease, location).
4. Output: Structured information (e.g., patient symptoms, disease progression).

4.4.3 Machine translation

Machine translation enables the automatic translation of text from one language to another [121–123]. This can be extremely useful in global pandemics like Lassa fever, where data and reports are often available in multiple languages. Applications in Lassa Fever:

1. Cross-language medical collaboration: During an outbreak, data on Lassa fever might be available in multiple languages. Machine translation can help researchers and medical professionals collaborate across regions and linguistic barriers.
2. Patient communication: In multilingual regions, machine translation is employed to facilitate communication between healthcare providers and patients who speak different languages.

A typical workflow for applying Machine Translation in Lassa fever management includes the following steps:

1. Input: A document in one language (e.g., a research paper in French).

2. Translation model: The NLP model translates the text into another language (e.g., English).
3. Output: The translated document.

4.4.4 Topic modeling

Topic modeling is an unsupervised NLP technique that automatically detects abstract topics in a collection of documents. It helps in organizing and summarizing large volumes of text by identifying recurring themes [124–127]. Applications in Lassa Fever:

1. Research paper analysis: Topic modeling can analyze thousands of research papers on Lassa fever to identify emerging trends, common themes, or areas of consensus.
2. Public discussion monitoring: Topic modeling can be applied to social media posts and news articles to understand public discussions around Lassa fever.

A typical workflow for applying Topic Modeling in Lassa fever management includes the following steps:

1. Input: A large corpus of text (e.g., scientific papers or social media posts).
2. Modeling: The model identifies key topics and groups related documents together.
3. Output: A list of topics (e.g., vaccine research, public health measures) with associated documents.

4.4.5 Summarization

Summarization techniques in NLP allow for extracting the most important information from large texts. Summarization can be extractive (selecting key sentences) or abstractive (generating a condensed version of the text) [128–133]. Applications in Lassa Fever:

1. Research paper summarization: Automated summarization can help researchers quickly get the gist of new studies on Lassa fever without having to read through entire papers.
2. News and policy updates: Summarization can condense long government reports or news updates, helping the public or healthcare officials stay informed with minimal reading time.

A typical workflow for applying Summarization in Lassa fever management includes the following steps:

1. Input: A long text document (e.g., a research paper or news report).
2. Modeling: The NLP model condenses the text, keeping the key information.
3. Output: A shorter version of the text that captures the main points.

4.5 Bayesian networks and probabilistic models

Bayesian networks and probabilistic models provide powerful frameworks for modeling uncertainty and causal relationships in complex systems [134–136]. These approaches are particularly valuable for understanding and managing pandemics, such as Lassa fever, where various environmental, biological, and social factors interact dynamically to influence disease transmission [21, 25, 137]. By quantifying uncertainties and representing causal dependencies, these models offer insight into the mechanisms underlying disease spread and support evidence-based decision-making. Bayesian networks and probabilistic models' key concepts include:

1. Bayesian networks (BN): A Bayesian network is a probabilistic graphical model that depicts a set of variables and their interdependencies through a directed acyclic graph (DAG). In this structure, nodes represent random variables, while edges illustrate the conditional relationships among them. In the case of Lassa fever modeling, such variables might include environmental factors, rodent population density, and frequency of human interaction.
2. Probabilistic models: These models provide a mathematical framework to quantify uncertainty, enabling predictions of outcomes based on observed data. By calculating probabilities of various scenarios, probabilistic models facilitate reasoning about potential future events.

Bayesian networks and probabilistic models have diverse applications in addressing Lassa fever outbreaks, including:

1. Epidemiological risk assessment: These models estimate the likelihood of outbreaks by analyzing factors such as population density, climatic conditions, and rodent behavior.
2. Transmission dynamics: By modeling interactions between variables, these frameworks elucidate how factors like environmental changes and human behavior contribute to virus spread.
3. Public health decision-making: Bayesian networks and probabilistic models support resource allocation and response planning, optimizing strategies for outbreak containment and prevention.

A structured workflow guides the development and application of probabilistic models for Lassa fever management:

1. Define variables: Identify key variables influencing disease dynamics, such as rodent populations, human activities, and environmental conditions.
2. Determine probability distributions: Assign probability distributions to each variable, representing uncertainties and variabilities in the data.
3. Construct model: Develop a probabilistic model by defining relationships between variables, simulating possible outbreak scenarios.
4. Inference and updating: Incorporate observed data to refine probability estimates, improving model accuracy in predicting outbreaks.
5. Decision support: Use the model to inform public health strategies, guiding resource deployment and preventive measures.

Similarly, the workflow for constructing and applying Bayesian networks in Lassa fever management involves:

1. Define nodes: Clearly define the variables (nodes) and their dependencies, such as environmental conditions, rodent populations, human contact with rodents, and outbreak occurrences.
2. Data collection and preprocessing: Gather reliable data from experiments, surveys, or databases. Preprocess the data to handle missing values and remove noise.

3. Construct model: Establish the network structure, specifying causal relationships between nodes. For instance, environmental conditions influence rodent populations, which in turn affect human contact and outbreak risks.
4. Parameter learning and validation: Use Bayes' theorem to update prior distributions with observed data. Validate the network with domain experts to ensure accuracy.
5. Decision support: Perform probabilistic inference to predict outcomes, query conditional probabilities, and inform public health interventions.

By leveraging these tools, public health officials can enhance their understanding of disease dynamics, optimize resource allocation, and implement timely interventions. These models contribute significantly to outbreak preparedness, fostering resilience and effective response strategies in the face of Lassa fever epidemics.

4.6 Comparison of the different approaches

The consolidated comparison presented in Table 10 highlights how diverse artificial-intelligence paradigms collectively advance the control and management of Lassa fever across diagnostic, predictive, and surveillance domains. Classical machine-learning models, particularly supervised approaches such as logistic regression, support-vector machines, and random forests-remain strong for structured clinical data analysis, delivering accuracies above 75–95 % when adequate labeled datasets exist. Unsupervised and reinforcement-learning techniques complement these by uncovering latent outbreak clusters and enabling adaptive resource allocation in dynamic epidemic environments. Deep-learning frameworks, especially convolutional and recurrent architectures, demonstrate high precision (AUC   0.85−0.98) for image-based diagnosis and temporal forecasting, while transformer models extend these capabilities to multimodal and genomic data integration. Probabilistic and expert-system paradigms contribute interpretability and causal reasoning for decision support in low-data settings, and natural-language-processing methods expand situational awareness through automated information extraction, multilingual communication, and knowledge summarization. Overall, Table 10 illustrates that each AI category offers complementary strengths, ranging from accuracy and scalability to transparency and linguistic adaptability, hence emphaszing the importance of hybrid and context-sensitive frameworks that integrate these techniques for a more robust, ethical, and data-driven Lassa-fever response.

Furthermore, the performance evaluation of these models for infectious-disease applications must be standardised to ensure comparability and reproducibility. In prior Lassa-fever studies, indicators such as accuracy, sensitivity, specificity, F1-score, and area under the receiver operating characteristic curve (AUC) were reported inconsistently. Table 10 summarises typical accuracy ranges, yet contextual interpretation is critical for drawing meaningful conclusions in health-related decision-making. A brief explanation of these metrics are as follows:

1. Accuracy quantifies the proportion of correctly classified instances among all samples and is suitable when class distributions are balanced. However, in Lassa-fever datasets where confirmed positive cases are often scarce relative to negatives, accuracy alone can be misleading.
2. Sensitivity (Recall) measures the proportion of true positives correctly identified and is particularly crucial for early outbreak detection, screening, and triage systems,

Table 10 AI Technique Matrix for Lassa-fever management: use-cases, data needs, reported performance, and principal limitations

AI method (Representative models)	Primary Lassa-fever use-case(s)	Typical data requirements	Reported accuracy range	Principal limitation(s)
Supervised ML (Logistic Regression, SVM, Random Forest, MLP/NN)	Early diagnosis; prognosis stratification; outbreak risk prediction; triage support	Labeled tabular records: demographics, symptoms, vitals, labs; spatiotemporal covariates (weather, rodent proxies); curated feature sets	Accuracy: 75–95% (task/dataset dependent); F1/AUC: 0.78—0.96	Needs labeled data; performance sensitive to class imbalance and data quality; potential dataset shift across regions; explainability varies by model
Unsupervised ML (K-Means/HC, PCA, GMM)	Cluster high-risk areas; patient phenotype discovery; anomaly detection in streams	Unlabeled tabular + environmental layers; geospatial rasters; EHR text embeddings	Clustering quality via silhouette, Davies-Bouldin	Interpretability of clusters; choice of *k* and distance metrics; results sensitive to scaling and noise; no direct "accuracy" notion
Reinforcement learning (Q-Learning, DQN, PPO)	Dynamic resource allocation (beds, kits, workforce); adaptive containment policies	Simulated/real-time state signals: case counts, capacity, mobility; reward design	N/A (policy learning); report reward gains or regret reduction	Reward shaping and realism of simulators; data sparsity for on-policy learning; computational cost; transfer to real settings
CNNs	Medical image support (e.g., signs of complications); satellite/aerial imagery for environmental risk proxies (habitats, land-use)	Labeled image sets (radiology, microscopy) or geospatial imagery with outbreak labels/proxies; preprocessing pipelines	Accuracy: 85–98%; AUC: 0.85—0.98	Requires sizable labeled image corpora; domain shift across devices/sites; limited temporal reasoning; compute-intensive training
RNNs/LSTM/GRU	Time-series forecasting of cases; symptom trajectory modeling; streaming sensor fusion (IoT)	Sequential tabular/time-series: daily/weekly cases, vitals, mobility, climate; careful handling of missingness and lags	Accuracy/F1 for sequence classification: 70–95%	Vanishing/exploding gradients for long horizons; data scarcity; sensitivity to non-stationarity; needs careful validation to avoid leakage
Transformers	Genomic sequence analysis (mutation patterns); multimodal fusion (clinical + environmental + text); outbreak risk scoring	Tokenized sequences (genomes, text), multivariate time-series; larger data budgets; alignment across modalities	Accuracy/AUC: 80–97%; F1: 0.80—0.95 (task dependent)	High compute/memory needs; potential overfitting on small LF datasets; model opacity; complex data integration
Bayesian networks Probabilistic models	Causal risk assessment; scenario analysis; transparent outbreak reasoning	Structured variables (environmental, host, rodent, contact); expert priors; conditional tables	Accuracy/AUC: 80–100% reported in select studies; calibration and posterior diagnostics emphasized	Eliciting reliable priors/structure; sensitivity to missing/biased inputs; scalability for high-dimensional CPTs

Table 10 (continued)

AI method (Representative models)	Primary Lassa-fever use-case(s)	Typical data requirements	Reported accuracy range	Principal limitation(s)
Expert systems/rule-based	Triage, preliminary diagnosis support; protocol guidance; checklists	Curated rules/knowledge base derived from guidelines and expert input; codified symptom/lab thresholds	Reported agreement with experts or decision accuracy on cases	Rule brittleness; maintenance burden; limited adaptability to new evidence; no learning from data by default
Text classification (NLP)	Syndromic surveillance from media/EHR text; case triage notes; misinformation flagging	Labeled text (notes, reports, posts); tokenization and embeddings; balanced classes	Accuracy/F1: 75–95%	Labeling costs; domain shift across sources; handling negation and abbreviations; bias in text corpora
Named entity recognition (NLP)	Extract entities (symptoms, drugs, locations, dates) from reports for structured dashboards	Annotated corpora with biomedical entities; domain-specific tag sets; de-identification pipeline	F1: 0.70—0.92	Performance drops out-of-domain; ambiguity and overlapping entities; requires domain annotation effort
Machine translation (NLP)	Cross-language alerts, guidance, records; multilingual coordination across West Africa	Parallel or comparable corpora; domain adaptation for medical terminology	BLEU: 20–35 (low-resource); human adequacy/fluency preferred	Terminology fidelity; low-resource languages; hallucinations; privacy of clinical text
Topic modeling (NLP)	Trend mining from literature/news; thematic monitoring of public discourse	Large unlabeled text corpora; preprocessing; model selection (LDA/CTM)	Typically reported in terms of coherence (C_v) and stability	Topic interpretability; sensitivity to preprocessing; temporal drift
Summarization (NLP)	Condense situation reports, policy briefs, clinical updates	Domain text for extractive/abstractive models; evaluation references if available	ROUGE-1: 35–50; human judgment recommended	Factuality risks (abstractive); omission of caveats; domain adaptation needed

where failing to detect an actual case has serious consequences for containment and treatment.

3. Specificity measures the proportion of true negatives correctly identified and is vital for avoiding false alarms in low-prevalence settings, ensuring that limited laboratory or field resources are not misallocated.
4. Precision represents the proportion of correctly predicted positive cases among all predicted positives. In predictive surveillance, precision helps quantify the reliability of an alert signal or case forecast.
5. F1-Score is the harmonic mean of precision and sensitivity, balancing both false positives and false negatives. It is preferred when positive and negative classes are imbalanced, as is common in Lassa-fever case reporting.
6. Area Under the Curve (AUC) summarises model discrimination ability across all decision thresholds, describing how effectively the model separates infected from non-infected or high-risk from low-risk samples. AUC is particularly useful for

models producing probabilistic outputs, such as logistic regression, neural networks, or ensemble classifiers.

In the Lassa-fever context, *sensitivity* is the most critical metric for early case detection and outbreak prediction, whereas *specificity* is more relevant for confirmatory diagnostics and screening programs. For continuous-risk or probabilistic forecasting tasks, *AUC* provides a comprehensive measure of discriminative performance. For imbalanced surveillance data, the *F1-score* offers the most stable indicator of overall predictive quality. To promote consistency, subsequent studies should explicitly report these metrics using stratified cross-validation and, when feasible, include confidence intervals to quantify uncertainty in performance estimates.

4.7 AI in treatment, control, and prevention optimization

AI is transforming healthcare by optimizing treatment, control, and prevention strategies, through personalized, data-driven approaches that enhance patient outcomes. This section explores AI's diverse applications in medical interventions, from tailoring treatment plans to accelerating vaccine discovery, all powered by advanced computational methods and patient-specific data. Typical AI flow in Lassa fever management is shown in Fig. 3

1. Personalizing treatment plans using patient-specific data AI enables precision medicine by tailoring treatment plans to individual patient's based on their genetic, clinical, and lifestyle data. By analysing vast datasets including genomic profiles, medical history, and real-time physiological metrics-AI can predict the most effective treatments optimize drug dosages and minimize adverse effects. Additionally, AI driven systems allow for continuous monitoring, and dynamic treatment adjustments, ensuring responsive patient centred care [139].
2. Drug discovery and re-purposing through AI algorithms. AI has revolutionalize drug discovery by rapidly identifying potential compounds and predicting molecular interactions more efficiently than traditional methods. Machine learning models analyze extensive chemical databases to uncover novel drug candidates while also facilitating drug reporposing to identifying existing medications for new therapeutic uses. By integrating clinical and preclinical data, AI streamlines treatment development, reducing cost and time to market [140, 141].
3. Monitoring and predicting treatment outcomes. AI-powered models enhance the monitoring and prediction of treatment by integrating data from wearable devices, electronic health records, and laboratory test. Deep learning algorithms analyze these data streams to forecast treatment success or detect early signs of adverse reactions, enabling proactive clinical adjustment. This predictive capability ensures timely interventions and improve patient outcomes [142].
4. Predictive analytics for resource allocation in high-risk areas. AI-powered predictive analytics optimize resource distribution, particularly in regions with limited healthcare infrastructure or during public health crisis. By analyzing historical trends and real-time data, AI predicted the demand for critical resources, such as ventilators, ICU beds, and medical supplies, ensuring efficient allocation and preventing shortages. This capability is vital for emergency preparedness and response [143].

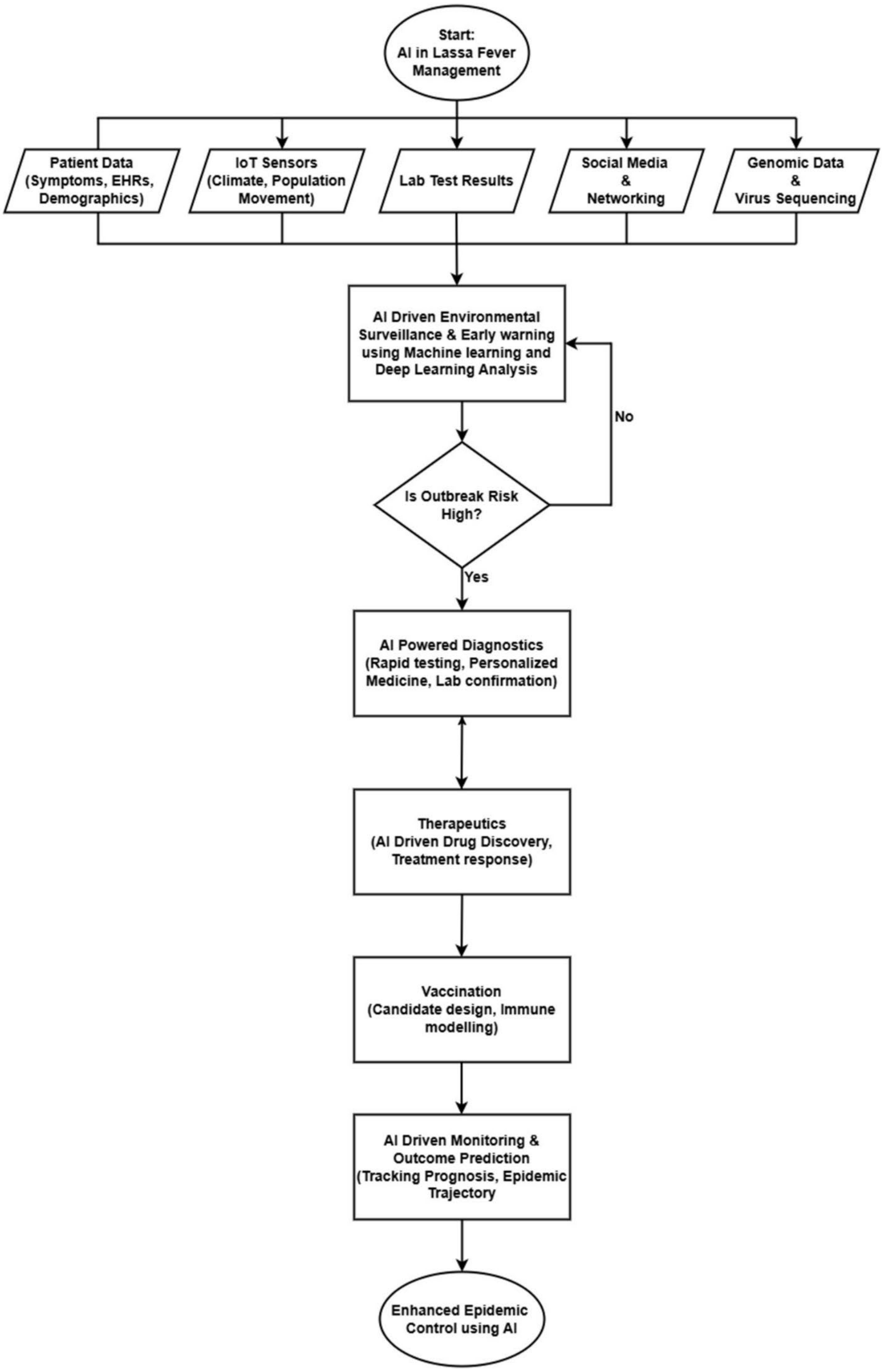

Fig. 3 AI flow in LASSA fever management

5. Using AI to accelerate vaccine candidate discovery. AI accelerates vaccine development by analyzing genetic data, pathogen structures, and immunological responses. By rapidly identifying promising vaccine candidates, AI reduces research time and cost while optimizing formulations for safety and efficacy. AI also facilitates vaccine trial designs and post- market surveillance ensuring broader protection against emerging infectious threats [144].

6. Analyzing genetic variations of the Lassa virus for targeted vaccine design. AI is playing a crucial role in developing vaccines for rapidly mutating viruses, such as the Lassa virus. By sequencing viral genomes and identifying key genetic markers, AI models can simulate how different genetic variations affect vaccine efficiency, enabling the development of more robust vaccines effective across various strains. This approach is essential for diseases like Lassa fever, where viral evolution poses significant challenges to vaccine development [143].

4.8 Case studies of AI in addressing pandemics

AI is transforming the landscape of disease prevention, diagnosis, and treatment by introducing cutting-edge solutions to persistent healthcare challenges. Through tools like predictive analytics, vaccine development models, and precision medicine applications, AI-based systems contribute to improved efficiency, effectiveness, and equity in delivering healthcare services. As AI technologies advance, their integration into clinical and public health infrastructures is paving the way for a more responsive and data-informed approach to healthcare delivery.

This section reviews documented use cases of AI in pandemic response as discussed in the literature.

4.8.1 Successful AI deployments in epidemic management

Artificial Intelligence (AI) has shown significant promise in enhancing epidemic response through improved disease surveillance, outbreak prediction, diagnostics, and intervention strategies. During the COVID-19 pandemic, for example, the company BlueDot leveraged machine learning and natural language processing (NLP) to examine large-scale data from news outlets, airline travel records, and official health bulletins, allowing for early detection of disease spread [20]. Similarly, platforms like HealthMap provided near real-time monitoring of disease outbreaks and contributed to more timely public health responses [145].

In the case of Ebola, AI systems were employed for predictive modeling to detect potential outbreak zones and optimize resource distribution-reducing delays and improving outcomes [81]. For influenza, AI-driven models, particularly those built using recurrent neural networks (RNNs), improved forecasting accuracy by incorporating information from clinical data, environmental factors, and online media platforms [146]. These examples demonstrate AI's versatility in processing complex, multi-source data to support dynamic and adaptive epidemic management efforts.

4.8.2 Lessons learned from previous outbreaks

From past outbreaks, several critical lessons have emerged regarding AI's role in epidemic control, which are listed as follows:

1. Data integration and quality: The effectiveness of AI hinges on the availability of high-quality, diverse datasets [147]. For example, integrating environmental, clinical, and socio-economic data was critical in predicting and managing Zika virus outbreaks [148].
2. Real-time analysis: During the H1N1 pandemic, AI systems that provided real-time analysis and actionable insights were more effective in guiding public health interventions [145].

3. Interdisciplinary collaboration: Collaborations between data scientists, epidemiologists, and healthcare professionals significantly improved AI models' accuracy and usability, as seen in SARS and MERS outbreaks [20].
4. Ethical and privacy considerations: Maintaining data privacy and addressing ethical concerns were paramount in ensuring public trust and adoption of AI tools during outbreaks like COVID-19 [81].
5. Scalability and adaptability: Flexible AI systems capable of adapting to different diseases and regions proved essential for sustained impact [146].

These lessons emphasize the need for robust data infrastructure, ethical frameworks, and cross-sectoral collaboration to maximize AI's potential in epidemic management.

4.8.3 Real-world examples of AI impact in Lassa fever control

We provide a number of examples where AI has been used for Lassa fever control as follows:

1. Predictive analytics: The authors in [149] developed an ensemble deep learning model combining RNN, LSTM, and GRU to predict Lassa fever outbreaks. By integrating weather data (e.g., temperature, humidity) with historical outbreak data, the model achieved improved prediction accuracy, enabling proactive public health responses. Similarly in [150], a Bayesian Belief Network was used, achieving 100 % accuracy in outbreak predictions, showcasing the reliability of probabilistic models in disease forecasting .
2. Real-time surveillance: In [148], the authors implemented a real-time surveillance system using machine learning algorithms for early warning and monitoring. This system improved the timeliness of reporting and tracking cases, enabling faster containment measures .
3. Diagnostic innovations: The approach in [151] involved the deployment of supervised machine learning techniques to diagnose Lassa fever based on clinical signs, significantly enhancing diagnostic accuracy. In a different study, the authors in [35] developed a CNN-based model that analyzed blood smear images for Lassa fever detection, achieving high diagnostic precision and expediting laboratory workflows .
4. Geospatial analysis: Regression analysis and spatial modeling was used in [87] to identify geographic clustering and urban-rural dynamics of Lassa fever outbreaks. These insights facilitated targeted public health interventions in hotspots. While these AI deployments have demonstrated notable successes, challenges such as data scarcity, model biases, and integration with existing healthcare systems remain areas for improvement.

While these AI deployments have demonstrated notable successes, challenges such as data scarcity, model biases, and integration with existing healthcare systems remain areas for improvement. Table 11 presents a summary of selected real-world examples of AI techniques used in the management of Lassa fever.

4.8.4 Publicly available Lassa-fever datasets

To promote transparency, reproducibility, and cross-validation of artificial-intelligence models, this section consolidates publicly available datasets that underpin Lassa-fever research across genomic, transcriptomic, and epidemiological domains. Open data

Table 11 Real-world examples of AI techniques used in the management of Lassa fever

Ref.	County	Key features	AI technique(s)	Context	Focus	Success	Challenges and future improvements
[81]	Nigeria	Predictive analytics for outbreak forecasting	XGBoost, Random Forest	Outbreak Prediction	Lassa Fever	Increased predictive accuracy for epidemic trends	Data scarcity and the need for computational resources
[146]	Nigeria, UK	Forecasting outbreak progression	Decision Tree, k-NN	Resource Allocation and Detection	Lassa Fever	Reduced response times for outbreak management	Model biases and limitations in real-time deployment
[148]	West Africa	Real-time surveillance system for outbreak tracking	Machine Learning, Statistical ML	Early Warning and Monitoring	Lassa Fever	Improved timeliness in reporting and tracking cases	Data integration and privacy concerns
[87]	Ondo State, Nigeria	Analyzed urban versus rural dynamics, linking ecological variables (e.g., population, nighttime light intensity) to outbreaks	Regression Analysis, Spatial Modeling	Geographic clustering and urban trend identification	Lassa Fever	Highlighted urban hotspots for Lassa fever, influencing targeted public health strategies	Data accuracy challenges from secondary sources; need for proactive urban rodent control strategies
[149]	Nigeria	Developed an ensemble deep learning model combining RNN, LSTM, and GRU to predict Lassa fever outbreaks. Integrated Lassa fever data with weather data (temperature, humidity, precipitation)	Recurrent Neural Networks (RNN), Long Short-Term Memory (LSTM), Gated Recurrent Unit (GRU)	Outbreak Prediction	Lassa Fever	Improved prediction accuracy by integrating diverse data sources (weather and disease cases)	Data preprocessing challenges (missing values); ensuring model scalability and real-time applicability
[74]	West Africa	Used machine learning algorithms (Naive Bayes, Decision Trees, Random Forest) to predict Lassa fever outbreaks based on patient data	Naive Bayes, Decision Trees, Random Forest	Outbreak prediction	Lassa Fever	High accuracy in predicting outbreaks based on patient symptoms and demographic data	Dataset limitations, need for more data integration
[150]	Nigeria	Used a Bayesian Belief Network to predict Lassa fever outbreaks, achieving 100% accuracy	Bayesian Belief Network	Outbreak prediction	Lassa Fever	Achieved 100% accuracy in predictions, demonstrating potential for high reliability	Data quality concerns; dataset curation needed

Table 11 (continued)

Ref.	County	Key features	AI technique(s)	Context	Focus	Success	Challenges and future improvements
[151]	West Africa	Machine learning techniques were employed to diagnose Lassa fever and viral hemorrhagic fevers based on clinical signs	Supervised Machine Learning	Disease Diagnosis	Lassa Fever and Viral Hemorrhagic Fevers	Improved diagnostic accuracy, facilitating faster interventions	Lack of standardized clinical data across different regions
[161]	Global	Designed an AI-based diagnostic system for Lassa fever, integrating rule-based approaches for infection prediction	Rule-Based AI Systems	Disease Diagnosis	Lassa Fever	Improved decision-making in healthcare settings	Complexity in implementing real-time systems in low-resource areas
[35]	Nigeria	Developed a CNN-based model utilizing blood smear images to predict Lassa fever	Convolutional Neural Networks (CNN)	Disease Diagnosis	Lassa Fever	Achieved high accuracy in detecting Lassa fever using microscopic images	Limited access to high-quality image datasets for model training
[162]	Nigeria	Designed a hybridized intelligent framework driven by the integration of NN, Fuzzy logic (FL) and Case Based Reasoning (CBR)	fuzzy logic, NN and rule based technique	Disease Diagnosis	Lassa Fever	Quick and reliable diagnosis for Lassa fever	Opaque relations between rules

repositories are essential for training, validating, and benchmarking predictive algorithms used in early warning, diagnosis, and outbreak forecasting. Table 12 provides a summary of key datasets, their provenance, scope, and access details and these are discussed as follows:

1. Genomic repositories: The National Center for Biotechnology Information (NCBI) Virus and GenBank databases host hundreds of complete and partial Lassa virus (LASV) genome sequences from both human and rodent hosts, representing multiple viral lineages circulating across West Africa [152, 153]. These records support phylogenetic and molecular epidemiology studies that trace viral evolution, lineage diversity, and inter-regional transmission. Similarly, the Pathosystems Resource Integration Center (PATRIC)-now integrated into the BV-BRC Bioinformatics Resource Center-provides curated LASV genomic assemblies and functional annotations, facilitating machine-learning applications in viral classification, feature selection, and epitope prediction [154]. Together, these repositories provide a foundation for applying deep-learning and probabilistic models to study genome variability and mutation dynamics in Lassa virus.

Table 12 Publicly available Lassa-fever datasets supporting reproducibility. Sizes reflect values reported by each source or are dynamically updated

Dataset / Resource	Size / Scope	Key attributes (Examples)	Provenance	Access URL
NCBI Virus / GenBank (LASV)	Dynamic (> hundreds of LASV segments)	Complete or partial Lassa virus S and L segments; strain, host (human / rodent), country, year; FASTA files with metadata	NCBI Virus / GenBank (public submissions)	https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/
BV-BRC (LASV genomes collection)	Dynamic curated set	Annotated LASV genomes with proteins, epitopes, and metadata; bulk download via FTP	NIAID Bacterial and Viral Bioinformatics Resource Center (BV-BRC)	https://bv-brc.org/
GEO GSE225258 (LASV vaccine RNA-seq)	RNA-seq experiment (2023)	Expression profiling of LASV vaccine response in non-human primates; FASTQ and processed counts with sample annotations	NCBI Gene Expression Omnibus (GEO)	https://www.ncbi.nlm.nih.gov/gds
BMC genomics	∼65 human samples (RNA-seq + microarray)	Transcriptomic data for LASV and Marburg infection; infected vs. uninfected samples; processed expression matrices	BMC Genomics (open repository)	https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-15-960
Kenema government hospital (Sierra Leone)	Multi-year clinical and laboratory records	Patient demographics, Ag/IgM/IgG status, outcome, and ribavirin treatment history	Kenema Government Hospital / PLOS Data in Brief	https://figshare.com/articles/dataset/7911068
Zenodo Nigeria Lassa Epidemiology (2018-2021)	SPSS dataset (∼ 4.5 MB)	De-identified records with case counts by state and demographic variables	Zenodo (open repository)	https://zenodo.org/records/7309567
Nextstrain Lassa fever builds	Dynamic phylogenetic collection	Curated and time-resolved LASV phylogenies built from GenBank submissions; includes metadata harmonization	Nextstrain project (open access)	https://nextstrain.org/blog/2025-02-21-rabies-lassa-yellow-fever-resources
Representative GenBank accessions (Togo Lineage)	4 complete LASV segments	Example isolates (MF990886-MF990889) with metadata for strain and collection year	CDC / GenBank submission archive	https://wwwnc.cdc.gov/eid/article/24/3/pdfs/17-1905-combined.pdf
NCDC Nigeria data portal / situation Reports	Weekly national reports + CSV datasets (when available)	Case counts by state/LGA, fatality rates, trends, and geo-coded registries via API or CSV	Nigeria Centre for Disease Control (NCDC)	https://dataportal.ncdc.gov.ng/dataset https://ncdc.gov.ng/

2. Transcriptomic and immunological datasets: Host-response and vaccine-related transcriptomic data are increasingly available through repositories such as the Gene Expression Omnibus (GEO). Studies profiling immune responses to hemorrhagic fever viruses have revealed key transcriptional signatures that inform vaccine design and immunomodulation strategies. For example, Wang et al. [155] profiled vaccine-induced immune responses in humans and non-human primates, providing analytical templates for LASV vaccine research. Likewise, Caballero et al. [156] generated transcriptome profiles of cells infected with Lassa and Marburg viruses, offering critical insights into early host-pathogen interactions and differential gene regulation. Such datasets underpin supervised and unsupervised learning approaches used to

classify disease severity, identify prognostic biomarkers, and integrate multi-omic data for improved diagnostic models.

3. Clinical and epidemiological data: Clinical and population-level datasets provide essential ground truth for validating predictive models. The Kenema Government Hospital (KGH) dataset in Sierra Leone contains long-term serological and clinical records of confirmed LASV infections, supporting studies on viral load, immune status, and mortality predictors [157]. Complementing this, recent epidemiological data from Nigeria, such as those described by Dambazau [158], document spatiotemporal trends in confirmed Lassa-fever cases during the 2024 outbreak in Kaduna State. Aggregated national reports from the Nigeria Centre for Disease Control (NCDC) further include weekly case counts, fatality rates, and geographic distribution patterns useful for spatiotemporal modeling and reinforcement-learning simulations. Collectively, these datasets enable modelers to evaluate detection accuracy and sensitivity across varied epidemiological settings.
4. Integrated and visualization platforms: Integrated bioinformatics resources such as Nextstrain combine publicly deposited genomic sequences with curated metadata to produce real-time phylogenetic visualizations of LASV evolution [159]. These open frameworks enhance reproducibility by allowing AI models to ingest harmonized sequence data and temporal annotations for training dynamic phylogeographic networks. Additionally, research into intracellular receptor pathways provides molecular context for AI-assisted feature engineering; for instance, Jae and Brummelkamp [160] identified host factors involved in hemorrhagic fever virus entry, contributing to the annotation of genomic and proteomic datasets accessible through NCBI and BV-BRC.

Overall, the datasets outlined in Table 12 collectively provide genomic, transcriptomic, and epidemiological foundations for data-driven modeling of Lassa fever. While their availability represents major progress in open science, persistent gaps remain in data completeness, geographic representation, and standardized metadata annotation. Expanding cross-border data sharing-while observing ethical, privacy, and consent frameworks-will be key to improving the robustness and generalizability of future AI-driven Lassa-fever studies.

5 Performance constraints, future directions, and emerging trends

Ongoing advancement and refinement of AI methods are essential for promoting more effective, ethical, and responsible applications in public health. Nevertheless, several obstacles, such as concerns over data privacy, bias, and whether diverse, high-quality datasets are available, which must be addressed to fully realize the benefits of AI while upholding ethical principles. Progress in this domain will depend on coordinated efforts among policymakers, healthcare practitioners, and technology developers, who will address these barriers and expand AI's impact in healthcare.

Through thoughtful implementation and international cooperation, AI is poised to play a key role in enhancing preparedness and improving equity in responses to future public health emergencies. This section introduces the core challenges and emerging developments that are shaping AI performance and adoption in this evolving field.

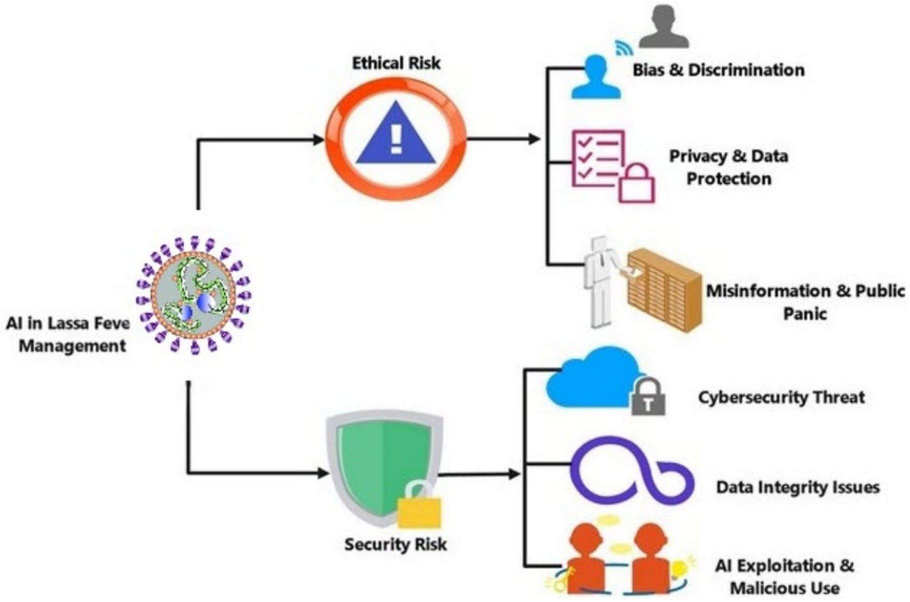

Fig. 4 Constraints in AI adoption for Lassa fever management

5.1 Performance constraints

Fig. 4 depicts key challenges impacting how AI systems perform in the context of Lassa fever management.

1. Data quality and availability: AI outcome reliability is largely determined by the quality and completeness of the data used during training and validation. When data are inconsistent, insufficient, or biased, model performance is often degraded, resulting in unreliable predictions. To enhance the reliability of AI systems, the establishment of unified and standardized data collection practices is considered essential [161]. In outbreak-prone and resource-limited settings-such as those observed during the Ebola epidemic-data collection has frequently been conducted in a fragmented or incomplete manner [163, 164], thereby undermining model accuracy [165].
2. Scalability and computational requirements: Implementing AI models typically demands high computational power and robust infrastructure-resources that are scarce in many low-income or remote settings [81, 165]. Without reliable internet, sufficient processing capacity, or adequately trained personnel, deploying AI solutions becomes impractical. Additionally, biased training data can perpetuate inequities, especially in areas like treatment discovery where model outputs may not generalize across diverse populations [166].
3. Interpretability and explainability: Many advanced AI systems function as "black boxes," providing limited insight into their internal reasoning processes. This lack of transparency can hinder trust among clinicians and stakeholders. Implementing explainable AI frameworks can improve user confidence and facilitate accountability in decision-making [20].
4. Ethical and privacy considerations: The use of sensitive health data introduces significant ethical and legal risks. Issues such as privacy breaches, unauthorized data usage, or unintended consequences from model outputs necessitate strict adherence to privacy-preserving protocols and ethical AI standards [148]. Recent advances in privacy-preserving and ethical-AI methods provide actionable strategies to

mitigate bias, protect patient data, and strengthen community trust in Lassa-fever research. Differential privacy (DP) mechanisms, which introduce statistical noise to model outputs or gradients, have been successfully piloted in African health data-sharing initiatives to ensure compliance with local and international data-protection laws while maintaining analytical validity [167]. In parallel, federated-learning (FL) frameworks have been evaluated across multiple healthcare institutions in Africa to train AI models collaboratively without exchanging raw data [168, 169]. These deployments showed that FL can harmonise heterogeneous electronic-health-record (EHR) sources for disease surveillance while satisfying cross-border ethical-review requirements. Moreover, federated learning (FL) enables multi-institutional model training without exchanging raw records. Large, real-world healthcare deployments during COVID-19 demonstrated that FL improves generalizability across hospitals while keeping data local, and recent African pilots (e.g., chest-imaging networks across several countries) show feasibility in low-resource settings relevant to West Africa [170]. These patterns suggest FL is a viable option where raw EHRs cannot leave facilities such as Kenema Government Hospital or Nigerian referral centers [170]. Furthermore, community-engagement and consent frameworks developed during Ebola responses in Sierra Leone offer grounded governance mechanisms (e.g., community liaison teams, consent dialogues, feedback loops) that increase trust and clarify data-use boundaries for surveillance and research and these align with WHO outbreak-ethics guidance and can be adapted to Lassa fever [171].

5. Integration with existing health eystems: Effective implementation of AI tools requires seamless integration into current healthcare infrastructure. This can be hindered by lack of interoperability standards, resistance to new technologies, and the need for specialized training among healthcare professionals [146, 172]. Ensuring coordinated interaction between AI and conventional medical workflows is essential for maximizing benefit.
6. Misinformation and disinformation: During pandemics, the spread of false information can significantly undermine public health efforts. AI-based tools can support early detection of misinformation and assist in managing targeted public education campaigns to mitigate its effects [145].
7. Cybersecurity threats: AI systems used in healthcare are increasingly vulnerable to cyberattacks, including data breaches and adversarial inputs. Robust cybersecurity frameworks are needed to protect patient data and maintain system trustworthiness [161].
8. Bias and discriminatory outcomes: If not properly monitored, AI models may replicate or even amplify existing societal biases, disproportionately impacting vulnerable or marginalized groups. Regular audits and bias mitigation techniques are essential to promote fairness [150].
9. Job displacement and overdependence on technology: The expansion of AI in healthcare raises concerns about automation replacing human roles and excessive reliance on technology. Workforce reskilling and balanced integration strategies are needed to ensure sustainable and ethical deployment [35].

5.2 Future directions and emerging trends

AI is increasingly recognized as a transformative tool in the fight against Lassa fever, offering innovative approaches for early detection, prevention, and disease control. As AI technologies continue to evolve, various forward-looking strategies and trends are emerging, with significant potential for improving Lassa fever response and management [35, 161, 173–176]. This section explores future research directions and promising developments identified in current literature, and these are identified as follows:

1. Advances in disease surveillance and predictive Modeling Machine learning-powered predictive systems are expected to improve disease monitoring by enabling earlier identification of outbreak signals [173, 174]. These systems can synthesize data from diverse sources, such as weather patterns, demographics, and historical case reports, to estimate outbreak risk and guide public health interventions. The integration of Internet of Things (IoT) sensors will further strengthen real-time data acquisition, boosting prediction accuracy [35].
2. Next-generation diagnostic tools AI-based diagnostic platforms are being developed to support rapid Lassa fever detection, even in settings with limited infrastructure. Innovations such as portable biosensors, automated laboratory devices, and AI-enhanced test kits are expected to enable quicker, point-of-care diagnostics. Additionally, AI can assist in analyzing genomic data to detect viral mutations, supporting the design of more accurate diagnostic solutions [176].
3. Tailored treatments and vaccine innovation Personalized healthcare, supported by AI, has the potential to optimize Lassa fever treatment by leveraging individualized clinical and genetic data [175]. AI-driven platforms can also expedite vaccine research through candidate identification and simulation-based optimization, which can reduce both development costs and timeframes [174].
4. Community education and outreach via AI tools AI-enabled technologies such as mobile apps, intelligent chatbots, and social media analytics are playing an increasing role in educating communities. These tools can disseminate timely and localized information about symptoms, prevention, and treatment, while combating misinformation. NLP technologies enhance accessibility by supporting multiple languages and culturally relevant communication [35].
5. AI and remote healthcare integration Combining AI with telehealth services offers a pathway to extend medical support to remote and underserved populations affected by Lassa fever [173]. AI applications can assist in clinical decision-making, remote diagnostics, and patient monitoring, enhancing access to timely and appropriate care [175].
6. Ethical, regulatory, and trust considerations As AI is adopted more widely, it is critical to address challenges related to data protection, algorithmic fairness, and user trust. Developing clear ethical frameworks and privacy-preserving mechanisms, along with stakeholder engagement, will be key to responsible implementation [176].
7. Strengthening research and local capacity Building interdisciplinary partnerships across fields such as AI, epidemiology, virology, and public health will be essential to tackle the complexity of Lassa fever [174]. Investment in local infrastructure, skill development, and training will empower healthcare systems and communities to harness AI technologies more effectively [35].

8. Emerging techniques in AI research Recent innovations such as federated learning, explainable AI, and reinforcement learning offer new opportunities for managing Lassa fever [173]. Federated learning supports collaborative model development without compromising privacy. Explainable AI fosters model transparency and trust, while reinforcement learning offers dynamic strategies for managing resources and interventions during outbreaks [175].

The future of AI in combating Lassa fever is poised for significant progress, driven by technological innovation, ethical alignment, and interdisciplinary collaboration. By addressing current limitations and embracing cutting-edge approaches, AI can play a transformative role in reducing the disease burden in affected regions.

6 Conclusion

This review has presented an exploration of how artificial intelligence (AI) contributes to epidemic management, with a particular emphasis on its application to Lassa fever, a persistent and endemic health concern in West Africa. Through the lens of various AI methodologies, we have explored their roles in enhancing surveillance, diagnostics, and treatment strategies. Key successes include predictive analytics for outbreak detection and AI-driven innovations in vaccine development, showcasing the transformative role AI can play in epidemic response. Despite these advancements, there remain considerable challenges to the effective integration of AI into epidemic control efforts. These include data limitations, inconsistencies in data quality, significant computational demands, scalability issues, and risks related to cybersecurity. In the context of Lassa fever, these challenges are further exacerbated by limited epidemiological data and variability in disease presentation, which complicate the development and deployment of AI-based tools. Overcoming these barriers requires coordinated engagement among researchers, public health professionals, technology developers, and policy stakeholders to ensure that AI solutions are ethically sound, trustworthy, and context-appropriate. Future research should prioritize the creation of robust AI architectures that can manage data constraints, provide greater interpretability, and support scalable deployment. Cross-disciplinary partnerships will be essential in tailoring AI innovations to local healthcare needs and epidemiological realities. By promoting responsible implementation and fostering collaborative global efforts, AI can become an indispensable resource in improving epidemic preparedness and health system resilience. In conclusion, this review highlights the importance of sustained innovation and investment in AI-centered approaches for epidemic control. When implemented strategically and ethically, AI holds great promise for advancing global health security and enabling timely, equitable, and proactive responses to future public health emergencies.

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References

1. Simon van Teutem: Our World in Data. Online. Accessed: 10 March 2025 (2025). https://ourworldindata.org/data-insights/the-un-projects-that-africas-population-will-double-by-2070
2. World Health Organization: Lassa fever. Online. Accessed: 10 March 2025 (2025). https://www.who.int/news-room/fact-sheets/detail/lassa-fever
3. Centers for Disease Control and Prevention: Lassa Fever. Online. Accessed: 10 March 2025 (2025). https://www.cdc.gov/vhf/lassa/index.html
4. Richmond JK, Baglole DJ. Lassa fever: epidemiology, clinical features, and social consequences. BMJ. 2003;327(7426):1271–5. https://doi.org/10.1136/bmj.327.7426.1271.
5. Kamara AS, Fatoma P, Moseray A. The perspectives of healthcare professionals on the strategies, challenges, and community responses to health system response and interventions towards lassa fever infections and mortality in sierra leone. Risk Manage Healthc Policy. 2024;17:1127–49. https://doi.org/10.2147/rmhp.s455254.
6. World Health Organization Regional Office for Africa: Lassa fever. Online. Accessed: 10 March 2025 (2025). https://www.afro.who.int/health-topics/lassa-fever
7. NCDC: NCDC confirms 54 Lassa fever cases, 10 deaths. Online. Accessed: 10 March 2025 (2025). https://punchng.com/ncdc-confirms-54-lassa-fever-cases-10-deaths/
8. Aloke C, Obasi NA, Aja PM, Emelike CU, Egwu CO, Jeje O, et al. Combating lassa fever in west african sub-region: progress, challenges, and future perspectives. Viruses. 2023;15(1):146. https://doi.org/10.3390/v15010146.
9. Ferreira C, Doursout M-FJ, Balingit JS. Hemorrhagic fevers: candidates for pandemics,295–327. Springer, Switzerland 2023. https://doi.org/10.1007/978-3-031-10035-2_11
10. Yun NE, Walker DH. Pathogenesis of lassa fever. Viruses. 2012;4(10):2031–48. https://doi.org/10.3390/v4102031.
11. Garry RF. Lassa fever—the road ahead. Nat Rev Microbiol. 2022;21(2):87–96. https://doi.org/10.1038/s41579-022-00789-8.
12. Asogun DA, Günther S, Akpede GO, Ihekweazu C, Zumla A. Lassa fever. Infect Dis Clin North Am. 2019;33(4):933–51. https://doi.org/10.1016/j.idc.2019.08.002.
13. Peter OJ, Abioye AI, Oguntolu FA, Owolabi TA, Ajisope MO, Zakari AG, et al. Modelling and optimal control analysis of lassa fever disease. Inf Med Unlocked. 2020;20:100419. https://doi.org/10.1016/j.imu.2020.100419.
14. Kalra N, Verma P, Verma S. Advancements in ai based healthcare techniques with focus on diagnostic techniques. Comput Biol Med. 2024;179:108917. https://doi.org/10.1016/j.compbiomed.2024.108917.
15. Isiaka RM, Babatunde RS, Ajao JF, Yusuff SR, Popoola DD, Arowolo MO, et al. A study of impacts of artificial intelligence on covid-19 prediction, diagnosis, treatment, and prognosis. Adv Multidiscip sci Res J Publ. 2022;10(4):11–62. https://doi.org/10.22624/aims/maths/v10n4p2.

16. Attai K, Amannejad Y, Vahdat Pour M, Obot O, Uzoka F-M. A systematic review of applications of machine learning and other soft computing techniques for the diagnosis of tropical diseases. Trop Med Infect Dis. 2022;7(12):398. https://doi.org/10.3390/tropicalmed7120398.
17. Rasool S, Husnain A, Saeed A, Gill AY, Hussain HK. Harnessing predictive power: exploring the crucial role of machine learning in early disease detection. JURIHUM: J Inovasi dan Humaniora. 2023;1(2):302–15.
18. Celik B, Vanschoren J. Adaptation strategies for automated machine learning on evolving data. IEEE Trans Pattern Anal Mach Intell. 2021;43(9):3067–78. https://doi.org/10.1109/tpami.2021.3062900.
19. Ajagbe SA, Adigun MO. Deep learning techniques for detection and prediction of pandemic diseases: a systematic literature review. Multimed Tools Appl. 2023;83(2):5893–927. https://doi.org/10.1007/s11042-023-15805-z.
20. Zeng D, Cao Z, Neill DB. Artificial intelligence-enabled public health surveillance-from local detection to global epidemic monitoring and control, 437–453. Elsevier, San Diego, California 2021. https://doi.org/10.1016/b978-0-12-821259-2.00022-3
21. Madueme P-GU, Chirove F. A systematic review of mathematical models of lassa fever. Math Biosci. 2024;374:109227. https://doi.org/10.1016/j.mbs.2024.109227.
22. Samson T, Akingbade T, Orija J. Comparative analysis of mortality predictions from lassa fever in nigeria: a study using count regression and machine learning methods. Acadlore Transact AI and Mach Learn. 2023;2(4):204–11. https://doi.org/10.56578/ataiml020403.
23. Ibrahim I, Abdulazeez A. The role of machine learning algorithms for diagnosing diseases. J Appl Sci Technol Trends. 2021;2(01):10–9. https://doi.org/10.38094/jastt20179.
24. Brownstein JS, Rader B, Astley CM, Tian H. Advances in artificial intelligence for infectious-disease surveillance. N Engl J Med. 2023;388(17):1597–607. https://doi.org/10.1056/nejmra2119215.
25. Elughi GN, Oniha MI, Abimbola BS, Orukotan KE, Ahuekwe EF, Akinduti P. Computational approaches toward prevention and surveillance of Lassa fever in developing countries, 145–157. Springer, Switzerland 2023. https://doi.org/10.1007/978-3-031-33370-5_10
26. Oladipo EK, Adeyemo SF, Oluwasanya GJ, Oyinloye OR, Oyeyiola OH, Akinrinmade ID, et al. Impact and challenges of artificial intelligence integration in the african health sector: a review. Trends in Med Res. 2024;19(1):220–35. https://doi.org/10.3923/tmr.2024.220.235.
27. MacIntyre CR, Chen X, Kunasekaran M, Quigley A, Lim S, Stone H, et al. Artificial intelligence in public health: the potential of epidemic early warning systems. J Int Med Res. 2023;51(3):03000605231159335. https://doi.org/10.1177/03000605231159335.
28. Mbunge E, Batani J. Application of deep learning and machine learning models to improve healthcare in sub-saharan africa: emerging opportunities, trends and implications. Telemat Inf Reports. 2023;100097. https://doi.org/10.1016/j.teler.2023.100097.
29. Pham Q-V, Nguyen DC, Huynh-The T, Hwang W-J, Pathirana PN. Artificial intelligence (ai) and big data for coronavirus (covid-19) pandemic: a survey on the state-of-the-arts. IEEE access. 2020;8:130820–39. https://doi.org/10.1109/access.2020.3009328.
30. Battineni G, Sagaro GG, Chinatalapudi N, Amenta F. Applications of machine learning predictive models in the chronic disease diagnosis. J personal med. 2020;10(2):21. https://doi.org/10.3390/jpm10020021.
31. Vellido A. Societal issues concerning the application of artificial intelligence in medicine. Kidney Diseases. 2019;5(1):11–7.
32. Holzinger A, Langs G, Denk H, Zatloukal K, Müller H. Causability and explainability of artificial intelligence in medicine. Wiley Interdiscip Rev Data Mining Knowl Discov. 2019;9(4):1312. https://doi.org/10.1002/widm.1312.
33. Wong F, Fuente-Nunez C, Collins JJ. Leveraging artificial intelligence in the fight against infectious diseases. Science. 2023;381(6654):164–70. https://doi.org/10.1126/science.adh1114.
34. Okwor T, Ndu A, Okeke T, Aguwa E, Arinze-Onyia S, Chinawa A, et al. A review of lassa fever outbreaks in nigeria from 1969 to 2017: epidemiologic profile, determinants and public health response. Niger J Med. 2018;27(3):219–33. https://doi.org/10.4103/1115-2613.278784.
35. John-Otumu AM, Aliga AP, Etus C, Nwokonkwo OC, Oshoiribhor EO, Aniugo VO. An intelligent model for effective lassa fever prediction based on convolutional neural network. In: 2024 International Conference on Science, Engineering and Business for Driving Sustainable Development Goals (SEB4SDG), 2024:1–5. https://doi.org/10.1109/seb4sdg60871.2024.10629833 . IEEE
36. El Morr C, Ozdemir D, Asdaah Y, Saab A, El-Lahib Y, Sokhn ES. Ai-based epidemic and pandemic early warning systems: a systematic scoping review. Health Inf J. 2024;30(3):14604582241275844. https://doi.org/10.1177/14604582241275844.
37. Okpala I, Halse S, Kropczynski J. Machine learning methods for evaluating public crisis: Meta-analysis. In: 2022 International Conference on Computational Science and Computational Intelligence (CSCI), 2022:78–84. https://doi.org/10.1109/csci58124.2022.00019 . IEEE
38. Olawade DB, Wada OJ, David-Olawade AC, Kunonga E, Abaire O, Ling J. Using artificial intelligence to improve public health: a narrative review. Front Public Health. 2023;11:1196397. https://doi.org/10.3389/fpubh.2023.1196397.
39. Butt MJ, Malik AK, Qamar N, Yar S, Malik AJ, Rauf U. A survey on covid-19 data analysis using ai, iot, and social media. Sensors. 2023;23(12):5543. https://doi.org/10.3390/s23125543.
40. Jiao Z, Ji H, Yan J, Qi X. Application of big data and artificial intelligence in epidemic surveillance and containment. Intel med. 2023;3(1):36–43. https://doi.org/10.1016/j.imed.2022.10.003.
41. Heidari A, Jafari Navimipour N, Unal M, Toumaj S. Machine learning applications for covid-19 outbreak management. Neural Comput Appl. 2022;34(18):15313–48. https://doi.org/10.1007/s00521-022-07424-w.
42. Li W, Chai Y, Khan F, Jan SRU, Verma S, Menon VG, et al. A comprehensive survey on machine learning-based big data analytics for iot-enabled smart healthcare system. Mobile netw appl. 2021;26:234–52. https://doi.org/10.1007/s11036-020-01700-6.
43. Wang L, Zhang Y, Wang D, Tong X, Liu T, Zhang S, et al. Artificial intelligence for covid-19: a systematic review. Front Med. 2021;8:704256. https://doi.org/10.3389/fmed.2021.704256.
44. Hamilton AJ, Strauss AT, Martinez DA, Hinson JS, Levin S, Lin G, et al. Machine learning and artificial intelligence: applications in healthcare epidemiology. Antimicrob Stewardship & Healthc Epidemiol. 2021;1(1):28. https://doi.org/10.1017/ash.2021.192.

45. Alenoghena CO, Onumanyi AJ, Ohize HO, Adejo AO, Oligbi M, Ali SI, et al. ehealth: A survey of architectures, developments in mhealth, security concerns and solutions. Int J Environ Res Public Health. 2022;19(20):13071. https://doi.org/10.3390/ijerph192013071.
46. Alenoghena CO, Ohize HO, Adejo AO, Onumanyi AJ, Ohihoin EE, Balarabe AI, et al. Telemedicine: a survey of telecommunication technologies, developments, and challenges. J Sens Actuator Netw. 2023;12(2). https://doi.org/10.3390/jsan12020020.
47. Ohize HO, Onumanyi AJ, Umar BU, Ajao LA, Isah RO, Dogo EM, et al. Blockchain for securing electronic voting systems: a survey of architectures, trends, solutions, and challenges. Clust Comput. 2024;28(2):132. https://doi.org/10.1007/s10586-024-04709-8.
48. Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, Shamseer L, Tetzlaff JM, Akl EA, Brennan SE, et al. The prisma 2020 statement: an updated guideline for reporting systematic reviews. Bmj 2021;372 https://doi.org/10.1186/s13643-021-01626-4
49. Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. Updating guidance for reporting systematic reviews: development of the prisma 2020 statement. J Clin Epidemiol. 2021;134:103–12. https://doi.org/10.1016/j.jclinepi.2021.02.003.
50. Sarkis-Onofre R, Catalá-López F, Aromataris E, Lockwood C. How to properly use the prisma statement. Syst Rev. 2021;10:1–3. https://doi.org/10.1186/s13643-021-01671-z.
51. Agbehadji IE, Awuzie BO, Ngowi AB, Millham RC. Review of big data analytics, artificial intelligence and nature-inspired computing models towards accurate detection of covid-19 pandemic cases and contact tracing. Int J Environ Res Public Health. 2020;17(15):5330. https://doi.org/10.3390/ijerph17155330.
52. Achieng MS, Ogundaini OO. Big data analytics for integrated infectious disease surveillance in sub-saharan africa. South African J Inf Manage. 2024;26(1):1668. https://doi.org/10.4102/sajim.v26i1.1668.
53. Najjar R. Digital frontiers in healthcare: Integrating mhealth, ai, and radiology for future medical diagnostics 2024 https://doi.org/10.5772/intechopen.114142
54. Alrashdi I, Alqazzaz A. Synergizing ai, iot, and blockchain for diagnosing pandemic diseases in smart cities: challenges and opportunities. Sustain Machine Intell J. 2024;7:6–1. https://doi.org/10.61356/smij.2024.77106.
55. Zhao AP, Li S, Cao Z, Hu PJ-H, Wang J, Xiang Y, et al. Ai for science: predicting infectious diseases. J Safe Sci Resil. 2024. https://doi.org/10.1016/j.jnlssr.2024.02.002.
56. Ucar A, Karakose M, Kırımça N. Artificial intelligence for predictive maintenance applications: key components, trustworthiness, and future trends. Appl Sci. 2024;14(2):898. https://doi.org/10.3390/app14020898.
57. Shinde PP, Shah S. A review of machine learning and deep learning applications. In: 2018 Fourth International Conference on Computing Communication Control and Automation (ICCUBEA), 2018:1–6. https://doi.org/10.1109/iccubea.2018.8697857 . IEEE
58. Shailaja K, Seetharamulu B, Jabbar M. Machine learning in healthcare: a review. In: 2018 Second International Conference on Electronics, Communication and Aerospace Technology (ICECA), 2018:910–914. https://doi.org/10.1109/iceca.2018.8474918 . IEEE
59. Folorunso SO, Ogbuju E, Oladipo F. Artificial Intelligence and the control of COVID-19: a review of machine and deep learning approaches, 167–185. Springer, Switzerland 2021. https://doi.org/10.1007/978-3-030-69744-0_10
60. Nguyen NH, Picetti D, Dulai PS, Jairath V, Sandborn WJ, Ohno-Machado L, et al. Machine learning-based prediction models for diagnosis and prognosis in inflammatory bowel diseases: a systematic review. J Crohns Colitis. 2021;16(3):398–413. https://doi.org/10.1093/ecco-jcc/jjab155.
61. Syeda HB, Syed M, Sexton KW, Syed S, Begum S, Syed F, et al. Role of machine learning techniques to tackle the covid-19 crisis: systematic review. JMIR Med Inform. 2021;9(1):23811. https://doi.org/10.2196/23811.
62. Chamola V, Hassija V, Gupta S, Goyal A, Guizani M, Sikdar B. Disaster and pandemic management using machine learning: a survey. IEEE Internet Things J. 2021;8(21):16047–71. https://doi.org/10.1109/JIOT.2020.3044966.
63. Demertzis K, Taketzis D, Tsiotas D, Magafas L, Iliadis L, Kikiras P. Pandemic analytics by advanced machine learning for improved decision making of covid-19 crisis. Processes. 2021;9(8):1267. https://doi.org/10.3390/pr9081267.
64. Lalmuanawma S, Hussain J, Chhakchhuak L. Applications of machine learning and artificial intelligence for covid-19 (sars-cov-2) pandemic: a review. Chaos Solitons & Fractals. 2020;139:110059. https://doi.org/10.1016/j.chaos.2020.110059.
65. Williamson B. Digital education governance: data visualization, predictive analytics, and 'real-time' policy instruments. J Educ Policy. 2015;31(2):123–41. https://doi.org/10.1080/02680939.2015.1035758.
66. Mishra N, Silakari S. Predictive analytics: A survey, trends, applications, oppurtunities & challenges. Int J Comput Sci Inf Technol. 2012;3(3):4434–8.
67. Selvan C, Balasundaram S. Data analysis in context-based statistical modeling in predictive analytics. In: Handbook of research on engineering, business, and healthcare applications of data science and analytics, 96–114. IGI Global Scientific Publishing, 2021. https://doi.org/10.4018/978-1-7998-3053-5.ch006
68. Johnson MR, Naik H, Chan WS, Greiner J, Michaleski M, Liu D, et al. Forecasting ward-level bed requirements to aid pandemic resource planning: lessons learned and future directions. Health Care Manag Sci. 2023;26(3):477–500. https://doi.org/10.1007/s10729-023-09639-2.
69. Shi P, Helm JE, Chen C, Lim J, Parker RP, Tinsley T, et al. Operations (management) warp speed: rapid deployment of hospital-focused predictive/prescriptive analytics for the covid-19 pandemic. Prod Oper Manag. 2023;32(5):1433–52. https://doi.org/10.1111/poms.13648.
70. Al-Turjman F. AI-powered cloud for COVID-19 and other infectious disease diagnosis. Pers Ubiquit Comput. 2021;27(3):661–4. https://doi.org/10.1007/s00779-021-01625-1.
71. Kaur A, Gupta S, Kumar D. Ai-powered predictive modelling for disease diagnostics. In: Genomic Intelligence, pp. 154–170. CRC Press
72. Mooney SJ, Pejaver V. Big data in public health: terminology, machine learning, and privacy. Annu Rev Public Health. 2018;39(1):95–112. https://doi.org/10.1146/annurev-publhealth-040617-014208.
73. Bansal S, Chowell G, Simonsen L, Vespignani A, Viboud C. Big data for infectious disease surveillance and modeling. J Infect Dis. 2016;214(suppl-4):375–9. https://doi.org/10.1093/infdis/jiw400.
74. Bakari S, Malgwi YM, Abu KP, Mohammed U. Lassa fever predictive model using machine learning techniques. Int J Comput Sci Mathemat Theory (IJCSMT). 2024;10(4):365–71.

75. Nwankwo W, Adigwe W, Umezuruike C, Acheme ID, Nwankwo CP, Ojei E, Oghorodi D. Application of support vector machine to lassa fever diagnosis. In: Hu, Z., Zhang, Q., He, M. (eds.) Advances in Artificial Systems for Logistics Engineering III, pp. 165–177. Springer, Cham 2023. https://doi.org/10.1007/978-3-031-36115-9_16
76. Long J, Shelhamer E, Darrell T. Fully convolutional networks for semantic segmentation. In: Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition, 2015:3431–3440.https://doi.org/10.1109/cvpr.2015.7298965
77. Chen JH, Asch SM. Machine learning and prediction in medicine—beyond the peak of inflated expectations. N Engl J Med. 2017;376(26):2507–9. https://doi.org/10.1056/NEJMp1702071.
78. Al-Mustapha AI, Adesiyan IM, Orum TG, Ogundijo OA, Lawal AN, Nzedibe OE, et al. Lassa fever in nigeria: epidemiology and risk perception. Sci Rep. 2024;14(1):27669. https://doi.org/10.1038/s41598-024-78726-3.
79. Amer M, Goldstein M, Abdennadher S. Enhancing one-class support vector machines for unsupervised anomaly detection. In: Proceedings of the ACM SIGKDD Workshop on Outlier Detection and Description, 2013:8–15. https://doi.org/10.1145/2500853.2500857
80. Alsentzer E, Murphy JR, Boag W, Weng W-H, Jin D, Naumann T, McDermott M. Publicly available clinical bert embeddings. arXiv preprint arXiv:1904.03323 2019
81. Quezada DA, Akwafuo S, Halyal S. Harnessing machine learning for predictive analytics: a case study of lassa fever outbreaks in nigeria. In: 2024 10th International Conference on Control, Decision and Information Technologies (CoDIT), 2024:377–382. https://doi.org/10.1109/codit62066.2024.10708095 . IEEE
82. LeCun Y, Bengio Y, Hinton G. Deep learning nature. 2015;521(7553):436–44. https://doi.org/10.1038/nature14539.
83. Litjens G, Kooi T, Bejnordi BE, Setio AAA, Ciompi F, Ghafoorian M, et al. A survey on deep learning in medical image analysis. Med Image Anal. 2017;42:60–88. https://doi.org/10.1016/j.media.2017.07.005.
84. Esteva A, Kuprel B, Novoa RA, Ko J, Swetter SM, Blau HM, et al. Dermatologist-level classification of skin cancer with deep neural networks. Nature. 2017;542(7639):115–8. https://doi.org/10.1038/nature21056.
85. Lopes AM, Andrade JP, Machado JT. Multidimensional scaling analysis of virus diseases. Comput Methods Programs Biomed. 2016;131:97–110. https://doi.org/10.1016/j.cmpb.2016.03.029.
86. Redding DW, Gibb R, Dan-Nwafor CC, Ilori EA, Yashe RU, Oladele SH, et al. Geographical drivers and climate-linked dynamics of lassa fever in Nigeria. Nat Commun. 2021;12(1):5759. https://doi.org/10.1038/s41467-021-25910-y.
87. Cadmus S, Taiwo OJ, Akinseye V, Cadmus E, Famokun G, Fagbemi S, et al. Ecological correlates and predictors of lassa fever incidence in ondo state, nigeria 2017–2021: an emerging urban trend. Scientific Reports. 2023;13(1):20855. https://doi.org/10.21203/rs.3.rs-3363536/v1.
88. AlMahamid F, Grolinger K. Reinforcement learning algorithms: an overview and classification. In: 2021 IEEE Canadian Conference on Electrical and Computer Engineering (CCECE), 2021:1–7 https://doi.org/10.1109/ccece53047.2021.9569056 . IEEE
89. Vlachogiannis JG, Hatziargyriou ND. Reinforcement learning for reactive power control. IEEE Trans Power Syst. 2004;19(3):1317–25. https://doi.org/10.1109/tpwrs.2004.831259.
90. Shuvo SS, Symum H, Ahmed MR, Yilmaz Y, Zayas-Castro JL. Multi-objective reinforcement learning based healthcare expansion planning considering pandemic events. IEEE J Biomed Health Inform. 2023;27(6):2760–70. https://doi.org/10.1109/JBHI.2022.3187950.
91. AM AR, R S A deep learning-based preventive measures of covid-19 in a crowd using reinforcement model over gan for enhanced efficiency. In: 2023 Third International Conference on Advances in Electrical, Computing, Communication and Sustainable Technologies (ICAECT), 2023:1–8. https://doi.org/10.1109/ICAECT57570.2023.10118327
92. Bhattacharya A, Mitra A. Development and repurposing of drugs against covid-19 using artificial intelligence. Comput Intell Pandemics:Tools Methods Face New Strains of COVID-19. 2023;9:139. https://doi.org/10.1515/9783110767681-007.
93. Reza SM, Bradley D, Aiosa N, Castro M, Lee JH, Lee B-Y, et al. Deep learning for automated liver segmentation to aid in the study of infectious diseases in nonhuman primates. Acad Radiol. 2021;28:37–44. https://doi.org/10.1016/j.acra.2020.08.023 .
94. Arulkumaran K, Deisenroth MP, Brundage M, Bharath AA. Deep reinforcement learning: a brief survey. IEEE Signal Process Mag. 2017;34(6):26–38. https://doi.org/10.1109/msp.2017.2743240.
95. Li J, Sun A, Han J, Li C. A survey on deep learning for named entity recognition. IEEE Trans Knowl Data Eng. 2020;34(1):50–70. https://doi.org/10.1109/tkde.2020.2981314.
96. Chu WT, Reza SM, Anibal JT, Landa A, Crozier I, Bağci U, et al. Artificial intelligence and infectious disease imaging. J Infect Dis. 2023;228(Supplement-4):322–36. https://doi.org/10.1093/infdis/jiad158.
97. Varshni D, Thakral K, Agarwal L, Nijhawan R, Mittal A. Pneumonia detection using cnn based feature extraction. In: 2019 IEEE International Conference on Electrical, Computer and Communication Technologies (ICECCT), 2019:1–7. https://doi.org/10.1109/icecct.2019.8869364 . IEEE
98. Wu Y-H, Gao S-H, Mei J, Xu J, Fan D-P, Zhang R-G, et al. Jcs: An explainable covid-19 diagnosis system by joint classification and segmentation. IEEE Trans Image Process. 2021;30:3113–26. https://doi.org/10.1109/tip.2021.3058783.
99. Ouyang X, Huo J, Xia L, Shan F, Liu J, Mo Z, et al. Dual-sampling attention network for diagnosis of covid-19 from community acquired pneumonia. IEEE Trans Med Imaging. 2020;39(8):2595–605. https://doi.org/10.1109/tmi.2020.2995508.
100. Lipton ZC, Berkowitz J, Elkan C A critical review of recurrent neural networks for sequence learning. arXiv preprint arXiv:1506.00019 2015
101. Yu Y, Si X, Hu C, Zhang J. A review of recurrent neural networks: Lstm cells and network architectures. Neural Comput. 2019;31(7):1235–70. https://doi.org/10.1162/neco_a_01199.
102. Zhang H, Wang Z, Liu D. A comprehensive review of stability analysis of continuous-time recurrent neural networks. IEEE Transact Neural Netw Learn Syst. 2014;25(7):1229–62. https://doi.org/10.1109/tnnls.2014.2317880.
103. Attai K, Ekpenyong M, Amannah C, Asuquo D, Ajuga P, Obot O, et al. Enhancing the interpretability of malaria and typhoid diagnosis with explainable ai and large language models. Tropical Medicine and Infectious Disease. 2024;9(9):216. https://doi.org/10.20944/preprints202408.0966.v1.
104. Osia SA, Shamsabadi AS, Sajadmanesh S, Taheri A, Katevas K, Rabiee HR, et al. A hybrid deep learning architecture for privacy-preserving mobile analytics. IEEE Internet Things J. 2020;7(5):4505–18. https://doi.org/10.1109/jiot.2020.2967734.
105. Salur MU, Aydin I. A novel hybrid deep learning model for sentiment classification. IEEE Access. 2020;8:58080–93. https://doi.org/10.1109/access.2020.2982538.

106. Hassan MM, Gumaei A, Alsanad A, Alrubaian M, Fortino G. A hybrid deep learning model for efficient intrusion detection in big data environment. Inf Sci. 2020;513:386–96. https://doi.org/10.1016/j.ins.2019.10.069.
107. Khadhim BJ, Kadhim QK, Shams WK, Ahmed ST, Alsiadi WW. Diagnose covid-19 by using hybrid cnn-rnn for chest x-ray. Indonesian J Elect Eng Comp Sci. 2023;29(2):852–60. https://doi.org/10.11591/ijeecs.v29.i2.pp852-860.
108. Islam MM, Islam MZ, Asraf A, Al-Rakhami MS, Ding W, Sodhro AH. Diagnosis of covid-19 from x-rays using combined cnn-rnn architecture with transfer learning. BenchCouncil Transact Benchmarks Stand Eval. 2022;2(4):100088. https://doi.org/10.1016/j.tbench.2023.100088.
109. Naidji MR, Elberrichi Z. A novel hybrid vision transformer cnn for covid-19 detection from ecg images. Computers. 2024;13(5):109. https://doi.org/10.3390/computers13050109.
110. Yang Y, Zhang L, Ren L, Wang X. Mmvit-seg: a lightweight transformer and cnn fusion network for covid-19 segmentation. Comput Methods Programs Biomed. 2023;230:107348. https://doi.org/10.1016/j.cmpb.2023.107348.
111. Feldman J, Thomas-Bachli A, Forsyth J, Patel ZH, Khan K. Development of a global infectious disease activity database using natural language processing, machine learning, and human expertise. J Am Med Inform Assoc. 2019;26(11):1355–9. https://doi.org/10.1093/jamia/ocz112.
112. Sun S, Luo C, Chen J. A review of natural language processing techniques for opinion mining systems. Information fusion. 2017;36:10–25. https://doi.org/10.1016/j.inffus.2016.10.004.
113. Zeng Z, Shi H, Wu Y, Hong Z. Survey of natural language processing techniques in bioinformatics. Comput Math Methods Med. 2015;2015(1):674296. https://doi.org/10.1155/2015/674296.
114. Li J, Sun A, Han J, Li C. A survey on deep learning for named entity recognition. IEEE Trans Knowl Data Eng. 2022;34(1):50–70. https://doi.org/10.1109/TKDE.2020.2981314.
115. Yi J, Nasukawa T, Bunescu R, Niblack W Sentiment analyzer: extracting sentiments about a given topic using natural language processing techniques. In: Third IEEE International Conference on Data Mining. ICDM-03, pp. 427–434. IEEE Comput. Soc, 2003. https://doi.org/10.1109/icdm.2003.1250949 . IEEE
116. Lauriola I, Lavelli A, Aiolli F. An introduction to deep learning in natural language processing: models, techniques, and tools. Neurocomputing. 2022;470:443–56. https://doi.org/10.1016/j.neucom.2021.05.103.
117. Baigang M, Yi F. A review: development of named entity recognition (ner) technology for aeronautical information intelligence. Artif Intell Rev. 2022;56(2):1515–42. https://doi.org/10.1007/s10462-022-10197-2.
118. Sun P, Yang X, Zhao X, Wang Z. An overview of named entity recognition. In: 2018 International Conference on Asian Language Processing (IALP), 2018:273–278. https://doi.org/10.1109/ialp.2018.8629225 . IEEE
119. Mohit B. Named entity recognition. In: natural language processing of semitic languages, pp. 221–245. Springer, ??? 2014. https://doi.org/10.1007/978-3-642-45358-8_7
120. Barros JM, Duggan J, Rebholz-Schuhmann D. Disease mentions in airport and hospital geolocations expose dominance of news events for disease concerns. Journal of biomedical semantics. 2018;9:1–11. https://doi.org/10.1186/s13326-018-0186-9.
121. Singh SP, Kumar A, Darbari H, Singh L, Rastogi A, Jain S. Machine translation using deep learning: an overview. In: 2017 International Conference on Computer, Communications and Electronics (comptelix), 2017:162–167 https://doi.org/10.1109/comptelix.2017.8003957 . IEEE
122. Liu Y, Zhang J. Deep learning in machine translation. Deep Learn Nat Lang Process, 2018:147–183 https://doi.org/10.1007/978-981-10-5209-5_6
123. Popel M, Tomkova M, Tomek J, Kaiser Ł, Uszkoreit J, Bojar O, et al. Transforming machine translation: a deep learning system reaches news translation quality comparable to human professionals. Nat Commun. 2020;11(1):4381. https://doi.org/10.1038/s41467-020-18073-9.
124. Abdelrazek A, Eid Y, Gawish E, Medhat W, Hassan A. Topic modeling algorithms and applications: a survey. Inf Syst. 2023;112:102131. https://doi.org/10.1016/j.is.2022.102131.
125. Vayansky I, Kumar SA. A review of topic modeling methods. Inf Syst. 2020;94:101582. https://doi.org/10.1016/j.is.2020.101582.
126. Barde BV, Bainwad AM. An overview of topic modeling methods and tools. In: 2017 International Conference on Intelligent Computing and Control Systems (ICICCS), 2017:745–750. https://doi.org/10.1109/iccons.2017.8250563 . IEEE
127. Churchill R, Singh L. The evolution of topic modeling. ACM Comput Surv. 2022;54(10s):1–35. https://doi.org/10.1145/3507900.
128. Widyassari AP, Rustad S, Shidik GF, Noersasongko E, Syukur A, Affandy A. Review of automatic text summarization techniques & methods. J King Saud Univ-Comput Inf Sci. 2022;34(4):1029–46. https://doi.org/10.1016/j.jksuci.2020.05.006.
129. Nenkova A, McKeown K. A survey of text summarization techniques. Mining text data, 2012:43–76 https://doi.org/10.1007/978-1-4614-3223-4_3
130. Gambhir M, Gupta V. Recent automatic text summarization techniques: a survey. Artif Intell Rev. 2017;47(1):1–66. https://doi.org/10.1007/s10462-016-9475-9.
131. Watanangura P, Vanichrudee S, Minteer O, Sringamdee T, Thanngam N, Siriborvornratanakul T. A comparative survey of text summarization techniques. SN Comput Sci. 2023;5(1):47. https://doi.org/10.1007/s42979-023-02343-6.
132. Andhale N, Bewoor LA. An overview of text summarization techniques. In: 2016 International Conference on Computing Communication Control and Automation (ICCUBEA), 2016:1–7. https://doi.org/10.1109/iccubea.2016.7860024 . IEEE
133. Wibawa AP, Kurniawan F. A survey of text summarization: techniques, evaluation and challenges. Nat Lang Process J. 2024;7:100070. https://doi.org/10.1016/j.nlp.2024.100070.
134. Cai B, Kong X, Liu Y, Lin J, Yuan X, Xu H, et al. Application of bayesian networks in reliability evaluation. IEEE Trans Industr Inf. 2018;15(4):2146–57. https://doi.org/10.1109/tii.2018.2858281.
135. Boudali H, Dugan JB. A continuous-time bayesian network reliability modeling, and analysis framework. IEEE Trans Reliab. 2006;55(1):86–97. https://doi.org/10.1109/tr.2005.859228.
136. Kwag S, Gupta A, Dinh N. Probabilistic risk assessment based model validation method using bayesian network. Reliab Eng Sys Safe. 2018;169:380–93. https://doi.org/10.1016/j.ress.2017.09.013.
137. Klitting R, Kafetzopoulou LE, Thiery W, Dudas G, Gryseels S, Kotamarthi A, et al. Predicting the evolution of the lassa virus endemic area and population at risk over the next decades. Nat Commun. 2022;13(1):5596. https://doi.org/10.1038/s41467-022-33112-3.

139. Schork NJ. Artificial intelligence and personalized medicine. Precis Med Cancer Ther. 2019:265–283 https://doi.org/10.1007/978-3-030-16391-4_11
140. Tanoli Z, Vähä-Koskela M, Aittokallio T. Artificial intelligence, machine learning, and drug repurposing in cancer. Expert Opin Drug Discov. 2021;16(9):977–89. https://doi.org/10.1080/17460441.2021.1883585.
141. Darabseh E, Tarhan İE. Cloud-based ai role in intelligent pharmaceutical manufacturing facilities. In: The International Symposium for Production Research, 2023;116–128. https://doi.org/10.1007/978-3-031-53991-6_9 . Springer
142. Krittanawong C, Johnson KW, Rosenson RS, Wang Z, Aydar M, Baber U, et al. Deep learning for cardiovascular medicine: a practical primer. Eur Heart J. 2019;40(25):2058–73. https://doi.org/10.1093/eurheartj/ehz056.
143. Obermeyer Z, Powers B, Vogeli C, Mullainathan S. Dissecting racial bias in an algorithm used to manage the health of populations. Science. 2019;366(6464):447–53. https://doi.org/10.1126/science.aax2342.
144. Srivastava R. Applications of artificial intelligence in medicine. Explor Res Hypothesis Med. 2024;9(2):138–46.
145. Chen H, Zeng D, Buckeridge DL, Izadi MI, Verma A, Okhmatovskaia A, et al. Ai for global disease surveillance. IEEE Intell Syst. 2009;24(6):66–82. https://doi.org/10.1109/mis.2009.126.
146. Oluwole AS, Nkonyana T. Forecasting lassa fever outbreak progression with machine learning. In: 2022 International Conference on Electrical, Computer, Communications and Mechatronics Engineering (ICECCME), 2022;1–5. https://doi.org/10.1109/iceccme55909.2022.9987787 . IEEE
147. Folorunso S, Ogundepo E, Basajja M, Awotunde J, Kawu A, Oladipo F, et al. Fair machine learning model pipeline implementation of covid-19 data. Data Intelligence. 2022;4(4):971–90. https://doi.org/10.1162/dint_a_00182.
148. Wattamwar A, Akwafuo S, Mistry V. Data-driven real-time surveillance system for tracking disease outbreaks: a case study of lassa fever outbreak. In: 2024 IEEE 12th International Conference on Healthcare Informatics (ICHI), 2024;344–349 https://doi.org/10.1109/ichi61247.2024.00051 . IEEE
149. Oluwadare SA, Adegun IP, Orogun OA, Boyinbode OK, Oyekanmi EO. The design of ensemble deep learning model for the prediction of lassa fever outbreak using multiple data sources. Int J Res Eng Sci (IJRES). 2024;12(3):365–71.
150. Aina E, Olutayo B, Oladunni D, Bamidele K. A bayesian linear regression model for predicting lassa fever in nigeria: a case study of ondo state. Int J Novel Res Dev (IJNRD). 2024;9(4):289–98.
151. Alile SO. A supervised machine learning approach for diagnosing lassa fever and viral hemorrhagic fever types reliant on observed signs. Life. 2022;3:4.
152. Andersen KG, Shapiro B, Matranga CB, Sealfon R, Lin AE, Moses LM, et al. Clinical sequencing uncovers origins and evolution of lassa virus. Cell. 2015;162(4):738–50. https://doi.org/10.1016/j.cell.2015.07.020.
153. Sogoba N, Feldmann H, Safronetz D. Lassa fever in west africa: evidence for an expanded region of endemicity. PLoS Negl Trop Dis. 2012;6(3):1476. https://doi.org/10.1371/journal.pntd.0001476.
154. Davis JJ, Wattam AR, Aziz RK, Brettin T, Butler R, Butler RM, et al. The patric bioinformatics resource center: expanding data and analysis capabilities. Nucleic Acids Res. 2020;48(D1):606–12.
155. Wang I-M, Bett AJ, Cristescu R, Loboda A, Meulen J. Transcriptional profiling of vaccine-induced immune responses in humans and non-human primates. Microb Biotechnol. 2012;5(2):177–87.
156. Caballero IS, Yen JY, Hensley LE, Honko AN, Goff AJ, Connor JH. Lassa and marburg viruses elicit distinct host transcriptional responses early after infection. BMC Genomics. 2014;15(1):960. https://doi.org/10.1186/1471-2164-15-960.
157. Shaffer JG, Grant DS, Schieffelin JS, Boisen ML, Goba A, Hartnett JN, et al. Lassa fever in post-conflict sierra leone. PLoS Negl Trop Dis. 2014;8(3):2748. https://doi.org/10.1371/journal.pntd.0002748.
158. Dambazau Z. Epidemiology of lassa fever in kaduna state, nigeria: Insights from the 2024 outbreak. Int J Infect Dis. 2025;152:107578. https://doi.org/10.1016/j.ijid.2024.107578.
159. Hadfield J, Megill C, Bell SM, Huddleston J, Potter B, Callender C, et al. Nextstrain: real-time tracking of pathogen evolution. Bioinformatics. 2018;34(23):4121–3. https://doi.org/10.1093/bioinformatics/bty407.
160. Jae LT, Brummelkamp TR. Emerging intracellular receptors for hemorrhagic fever viruses. Trends Microbiol. 2015;23(7):392–400. https://doi.org/10.1016/j.tim.2015.04.006.
161. Imanov E, Asengi FJ. Artificial intelligence for lassa fever diagnosis system. In: International Conference on Theory and Applications of Fuzzy Systems and Soft Computing, 2020;540–547. https://doi.org/10.1007/978-3-030-64058-3_67 . Springer
162. Nnebe SE, Okoh NAO, John-Otumu AMG, Oshoiribhor EO. A neuro-fuzzy case based reasoning framework for detecting lassa fever based on observed symptoms. American J Artificial Intell. 2019;3(1):9–16. https://doi.org/10.11648/j.ajai.20190301.12.
163. Liang W, Tadesse GA, Ho D, Fei-Fei L, Zaharia M, Zhang C, et al. Advances, challenges and opportunities in creating data for trustworthy ai. Nat Mach Intell. 2022;4(8):669–77. https://doi.org/10.1038/s42256-022-00516-1.
164. Roshania R, Mallow M, Dunbar N, Mansary D, Shetty P, Lyon T, et al. Successful implementation of a multicountry clinical surveillance and data collection system for ebola virus disease in west africa: findings and lessons learned. Global Health Sc Practice. 2016;4(3):394–409. https://doi.org/10.9745/ghsp-d-16-00186.
165. Kwofie SK, Adams J, Broni E, Enninful KS, Agoni C, Soliman ME, et al. Artificial intelligence, machine learning, and big data for ebola virus drug discovery. Pharmaceuticals. 2023;16(3):332. https://doi.org/10.3390/ph16030332.
166. Forna A, Dorigatti I, Nouvellet P, Donnelly CA. Comparison of machine learning methods for estimating case fatality ratios: an ebola outbreak simulation study. PLoS ONE. 2021;16(9):0257005. https://doi.org/10.1371/journal.pone.0257005.
167. Dyda A, Purcell M, Curtis S, Field E, Pillai P, Ricardo K, Weng H, Moore JC, Hewett M, Williams G, et al. Differential privacy for public health data: an innovative tool to optimize information sharing while protecting data confidentiality. Patterns 2021;2(12) https://doi.org/10.1016/j.patter.2021.100366
168. Gupta[1] S, Nadakuditi S. Healthvigil: harnessing federated ai for cross-border pandemic intelligence & preemptive intervention. In: ICT for Global Innovations and Solutions: International Conference, ICGIS 2025, Virtual Event, April 26-27, 2025, Proceedings, p. 435. Springer, ??? (2025). https://doi.org/10.1007/978-3-032-02853-2_32 . Springer Nature
169. Saad NA, Hassan MI, Doutoum MAI, Saad AA. Federated adaptive epidemiological learning (fael): a novel ai framework for covid-19 pandemic preparedness in africa 2025 https://doi.org/10.21203/rs.3.rs-7308097/v1
170. Dayan I, Roth HR, Zhong A, Harouni A, Gentili A, Abidin AZ, et al. Federated learning for predicting clinical outcomes in patients with covid-19. Nat Med. 2021;27(10):1735–43. https://doi.org/10.1038/s41591-021-01506-3.

171. Dada S, McKay G, Mateus A, Lees S. Lessons learned from engaging communities for ebola vaccine trials in sierra leone: reciprocity, relatability, relationships and respect (the four r's). BMC Public Health 2019:19(1) https://doi.org/10.1186/s12889-019-7978-4
172. Aung YY, Wong DC, Ting DS. The promise of artificial intelligence: a review of the opportunities and challenges of artificial intelligence in healthcare. Br Med Bull. 2021;139(1):4–15. https://doi.org/10.1093/bmb/ldab016.
173. Sarkar D, Majumdar R, Le D. The state of CDNs today and what AI-assisted CDN means for the future, 2023;97–110. https://doi.org/10.1002/9781119836667.ch6
174. Olan F, Arakpogun EO, Jayawickrama U, Suklan J, Liu S. Sustainable supply chain finance and supply networks: the role of artificial intelligence. IEEE Trans Eng Manage. 2024;71:13296–311. https://doi.org/10.1109/TEM.2021.3133104.
175. Olan F, Suklan J, Arakpogun EO, Robson A. Advancing consumer behavior: the role of artificial intelligence technologies and knowledge sharing. IEEE Trans Eng Manage. 2024;71:13227–39. https://doi.org/10.1109/TEM.2021.3083536.
176. Adelakun, AJ, Alese BK, Thompson AF-B, Alowolodu OD case studies in AIoMT applications: a secure medical cyber-physical system for the monitoring and diagnosis of lassa fever. In: Handbook of Security and Privacy of AI-Enabled Healthcare Systems and Internet of Medical Things, pp. 429–444. CRC Press. Florida.

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