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Artificial Intelligence in Neglected Tropical Diseases: Current Applications, Challenges, and Opportunities

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A Systematic Review of Artificial Intelligence in Neglected Tropical Diseases: Current Applications, Challenges, and Opportunities

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[***]This work is dedicated to the memory of our colleague and friend, Dr Arnaud Nguembang Fadja, whose essential contribution to this article and whose profound influence on our lives will always be remembered. Rest in peace, Arnaud
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ABSTRACT

Neglected tropical diseases (NTDs) *affect more than one billion people globally*, disproportionately burdening populations in low-resource tropical and subtropical regions worldwide. Recent advances in artificial intelligence (AI) offer considerable opportunities to strengthen NTD prevention and control, yet the scope and translational readiness of AI applications across this disease portfolio remain incompletely characterized. Thus, we conducted a systematic review of peer-reviewed studies applying AI methods to NTD-related problems, searching Scopus and Web of Science (WoS) databases, extracting data on disease focus, AI methodology, validation strategy, performance metrics, and implementation context. A thematic synthesis of predefined application categories was performed to characterize research trends, geographic distribution of NTD research capacity, and funding priorities, following PRISMA guidelines. We identified 289 studies, dominated by diagnosis (41.5%), surveillance (17%), prognosis (14.2%), outbreak prediction (10%), treatment monitoring (7.3%), drug discovery (6.2%), and policy planning (3.8%); over 70% employed supervised machine learning or deep learning on imaging, clinical, or epidemiological data, with discrimination metrics reported more often than calibration, external validation, or prospective evaluation. Research activity is concentrated in a small number of countries, notably Brazil and India, with limited representation from sub-Saharan Africa and South-East Asia, and few studies addressed deployment considerations such as data governance, health-system integration, explainability, and fairness. AI holds substantial promise for NTD control and elimination, but the evidence base reveals methodological, geographic, and translational gaps; future research should prioritize robust validation, transparent reporting, equity-aware design, and engagement with endemic-country stakeholders, supported by investment in data infrastructure, local capacity, and governance.

Keywords: Neglected Tropical Diseases, Artificial Intelligence, Deep Learning, Machine Learning, Digital Health, Diagnostics, Prognosis, Surveillance, Outbreak Prediction, Policy Planning, Global Health

1 Introduction

Neglected tropical diseases (NTDs) comprise a diverse group of parasitic, bacterial, and viral infections that disproportionately affect the world's populations experiencing extreme poverty and marginalization[1,2]. More than a billion people are estimated to require interventions against at least one NTD in their lifetime, with the highest burdens concentrated in sub-Saharan Africa, South Asia, and Latin America[3,4]. These diseases perpetuate cycles of poverty and stigma by causing chronic disability, reduced productivity, and impaired social participation[5–7]. Despite their immense collective burden, NTDs have historically received limited political attention, funding, and research investment compared with human immunodeficiency virus (HIV), tuberculosis, or malaria[8–10]. NTDs encompass 21 conditions according to the World Health Organization (WHO) grouping convention with markedly heterogeneous transmission dynamics, clinical manifestations, and programmatic control needs (see Supplementary Information Table S1).

Several conditions, including lymphatic filariasis, schistosomiasis, onchocerciasis, and soil-transmitted helminthiases, remain highly endemic, while others such as Guinea worm disease are approaching eradication, demonstrating both progress and fragility in global control efforts[11–13]. The persistence of many NTDs reflects entrenched inequities in health systems, water and sanitation infrastructure, and access to essential medicines[14–16], compounded by the biological and epidemiological diversity of NTD pathogens (see Supplementary Information B.1).

These complexities create significant analytical and operational challenges. Their diffuse burden, chronic course, and frequent underreporting limit the effectiveness of conventional diagnostic and surveillance approaches (see Supplementary Information A.3 for DALYs (Disability-Adjusted Life Years)). In this context, Artificial Intelligence (AI), the simulation of human intelligence in machines to perform tasks such as learning, reasoning, and decision-making[17,18], and its subset, Machine Learning (ML), which enables systems to learn from data without explicit programming[19,20], offer promising avenues to enhance NTD control and research.

AI applications are increasingly being investigated across infectious diseases, including diagnostics, outbreak prediction, treatment monitoring, etc. Within the NTD domain, a growing number of studies suggest the potential of approaches such as parasite detection using Computer Vision[21,22], forecasting of disease incidence and transmission dynamics[23–25], and supporting aspects of drug discovery through Deep Learning (DL) methods[26–28]. Despite these encouraging developments, the overall evidence base remains relatively limited and heterogeneous in scope. Many studies have tended to focus on individual diseases, specific methodological paradigms, or geographically bounded settings, and have only rarely been situated within a broader, integrative analytical framework.

Prior reviews have begun to address this need, though each from a specific viewpoint that this work builds upon. Ward et al.[29] examined AI-assisted microscopy for soil-transmitted helminths and schistosomiasis, demonstrating strong diagnostic feasibility and calling for alignment with WHO target product profiles, though their scope remained confined to two diseases and a single modality. Talimi et al.[30] conducted a systematic review of AI in cutaneous leishmaniasis diagnosis, identifying

seven research gaps from a body of literature comprising only seven eligible studies, underscoring how nascent the field remains even at the level of individual diseases. At a broader scale, Parija and Poddar[31] highlighted the transformative power of AI across parasitic disease control, spanning diagnostics, drug discovery, and predictive modelling, while Vaisman et al.[32] drew attention to the ethical and implementation challenges of deploying AI diagnostics in low-resource settings. Collectively, these efforts reveal a field that is growing but remains fragmented across diseases, modalities, and analytical dimensions.

The objective of this review is to systematically characterize the scope, methodological maturity, and translational readiness of artificial intelligence (AI) applications across the full portfolio of WHO-listed NTDs. Specifically, we established a conceptual taxonomy of AI applications spanning individual-level and population-level domains. We further seek to determine: (i) which NTDs and AI application domains have received the greatest research investment and which remain comparatively neglected; (ii) how research outputs, dataset provenance, funding priorities, and collaborative networks are geographically distributed relative to disease burden and global health needs; and (iii) the extent to which existing AI research adheres to methodological standards required for translation, including robust validation, calibration, uncertainty quantification, and transparent reporting. By identifying key methodological, geographic, and socio-technical gaps, this review aims to establish an evidence-based foundation for prioritizing future AI research, investment, and capacity-building efforts that advance equitable AI innovation and align with the WHO 2030 NTD roadmap.

To address these gaps, we present a systematic and integrative review of AI applications across all WHO-listed NTDs. We combine a structured taxonomy of use cases with a thematic synthesis of predefined application categories, publication trends, geographic concentration, funding patterns, and collaboration dynamics. Rather than cataloging technical performance alone, we situate these findings within the broader context of global NTD mitigation efforts, explicitly linking methodological advances to questions of implementation, equity, and alignment with the WHO 2030 roadmap[33]. In doing so, we aim to provide a foundation for more deliberate, inclusive, and impact-oriented AI research across the NTD landscape.

This paper is organized as follows: Section 2 presents the results; Section 3 synthesizes the evidence, discusses its implications for research and practice, and concludes with recommendations for future work; and Section 4 describes the systematic review methods.

2 Results

We present the findings of this systematic review organized around a conceptual taxonomy developed to situate AI research within the broader NTD landscape. This structure is complemented by analyses of research activity trends, application domains, geographic focus, funding patterns, collaboration dynamics, and alignment with global NTD priorities.

2.1 Conceptual Taxonomy of AI Applications

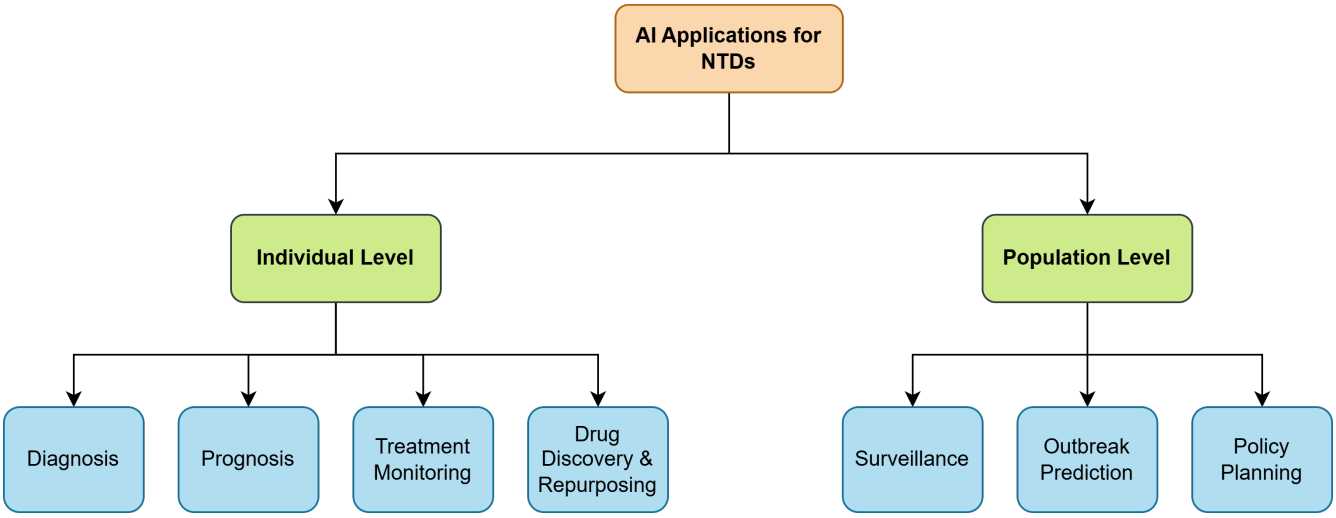
One of the primary focus of this work is a conceptual organization that taxonomizes AI applications in NTDs according to analytical scope and data granularity (Figure 1). Rather than organizing studies by disease or algorithm type alone, the taxonomy distinguishes two overarching domains that reflect fundamentally different units of analysis and intervention targets. Individual-level applications operate on patient-specific data, supporting clinical decision-making along the patient care pathway. Population-level applications, by contrast, draw on aggregated epidemiological, environmental, or spatiotemporal data to inform public health action at the scale of communities and health systems[34,35]. This distinction captures not only differences in data modality and model architecture, but also in the intended end-users, deployment contexts, and policy implications of AI tools.

The taxonomy provides the conceptual structure used to organize the evidence identified in this review and serves as the framework for the sections that follow. Building on this structure, the next we first examine AI/ML methods across the major NTD use cases and then broaden the analysis to the wider research landscape, including publication trends, geographic distribution, data sources, and patterns of collaboration. This progression from conceptual categorization to landscape-level analysis helps contextualize both current applications of AI in NTDs and the broader structural factors shaping the field[34,35].

2.2 Individual-Level Applications

Individual-level AI systems assist clinicians and laboratory personnel by analyzing patient-centric data, including microscopy images, radiological scans, molecular profiles, and clinical records. Spanning diagnostic decision-making, prognostic modelling, treatment monitoring, and drug discovery, these tools are designed to augment clinical workflows and improve patient outcomes[22,36–38]. Next we elaborate on the major themes and innovations within each of these patient-centred application areas.

Diagnostics represents the most extensively studied application of AI in NTDs, and the literature reflects both the breadth of approaches that have been explored and the unevenness of progress across diseases. We organized the evidence into



four broad methodological domains. The first two cover clinical and serological ML models for early screening, alongside microscopy-based DL for parasite detection. The remaining domains focus on radiomics and multimodal biomarker discovery, as well as ecological or surveillance-linked diagnostic support. These are further grouped into eight clusters by shared modality, model family, and data source (see Supplementary Information Table S2).

Dengue diagnostics have attracted the largest volume of work. Clinical, genomic, and haematology-based models spanning Support Vector Machines (SVMs), random forests, gradient boosting, Artificial Neural Networks (ANNs), and online learning paradigms report accuracies of 72–100% for early case detection and severity stratification[39–44]. A parallel cluster focuses on microscopy-based blood-smear analysis, where Convolutional Neural Networks (CNNs), U-Net, Faster R-CNN, RetinaNet, and YOLO-based pipelines routinely achieve accuracies above 95%[45–49]. Both lines of work are constrained by small cohorts, limited external validation, and geographic concentration in South Asia and Brazil, and the microscopy systems face additional challenges from variability in staining quality and device-specific imaging conditions.

Chagas disease diagnostics are similarly driven by microscopy-based DL. ResNet variants, U-Net derivatives, and residual segmentation models detect and localize trypomastigotes with reported accuracies of 98–100% and Dice coefficients above 0.8[49–52], while YOLOv8-based pipelines achieve mAP_{50} values above 0.95[48]. Complementary work on cellphone-captured triatomine images has extended these capabilities to vector identification, supporting entomological surveillance[53]. Leishmaniasis diagnostics draw on a similar technical repertoire: YOLO detectors, CNN classifiers, AdaBoost learners, and biosensor pipelines trained on Giemsa slides or SPR sensorgrams reporting variable sensitivity (52–100%) and specificity up to 98% across studies in Ethiopia, Iran, and Brazil[21,54–57]. Dataset size and geographic isolation remain the primary limiting factors in both diseases.

Schistosomiasis presents one of the most methodologically diverse diagnostic landscapes. Digital microscopy platforms, including the Schistoscope with Faster R-CNN and CNN-based egg detection, achieve sensitivities of 80–96%[22,58]. Structured clinical ML frameworks using CatBoost, LightGBM, and XGBoost enable early risk prediction with accuracies near 87%[59], while radiomics and spectral learning approaches applied to ultrasound or X-ray absorption data predict hepatic fibrosis with Area Under the Curve (AUC) values approaching 0.97–0.99[38,60]. CNN-based environmental classification has further enabled identification of intermediate snail hosts and cercariae with up to 99% accuracy[61], extending diagnostic utility to transmission monitoring.

Among other NTDs, CNN-based egg detection for soil-transmitted helminths achieves around 97% accuracy on microscopy images[62]. Trachoma detection and grading using mobile and texture-enhanced CNNs with Gabor features and AutoML pipelines reports accuracies of 88–98% across African datasets[63–65]. Leprosy diagnostic tools combining explainable CNN architectures with Grad-CAM visualization have reached accuracies up to 98%[66–68].

Across these clusters, AI consistently demonstrates diagnostic promise, but the evidence base shares a common profile of limitations: small and geographically narrow datasets, inconsistent metric reporting, and rare external or prospective validation. Progress toward deployable tools will require standardized benchmarks, potentially multi-country data sharing, and validation studies conducted in the community and primary-care settings using prospective data where NTD burden is highest.

Prognostic AI for NTDs on the other hand has developed primarily through individual-level applications targeting early risk stratification, clinical triage, and prediction of disease progression (see Supplementary Information Table S3). The evidence is most mature for dengue, where clinical and laboratory features including dyspnoea, plasma leakage, thrombocytopenia, platelet dynamics, and early haematological indices, retain consistent prognostic value when combined with supervised learning methods such as logistic regression, tree-based ensembles, SVMs, Bayesian networks, and multilayer perceptrons. These approaches support earlier identification of high-risk patients, prediction of transfusion requirements, and risk-stratified care in resource-constrained settings[45,69–73].

Interpretable and hybrid ML approaches are increasingly used to improve clinical actionability alongside predictive accuracy. Explainable gradient boosting models with SHapley Additive exPlanations (SHAP) analysis have been applied to anticipate blood component transfusion needs in hospitalized dengue patients, achieving AUC values near 0.8 while surfacing clinically intuitive drivers including platelet count, haematocrit, and bleeding risk[73]. Metabolomics-integrated pipelines combining random forests, logistic regression, and dimensionality reduction have further uncovered host-derived metabolic signatures linked to severe dengue progression, implicating lipid metabolism, oxidative stress, and inflammatory pathways[74]. Bayesian belief networks and explainable DL have similarly been used to identify mechanistic correlates of poor outcomes, including cytokine modules and humoral endotypes associated with severe or chronic disease manifestations such as schistosomiasis-related morbidity[75–77].

Prognostic inference has also been extended beyond the individual patient through quantitative imaging, radiomics, and spatial modelling. Ultrasound-derived radiomic pipelines predict progression of schistosomal liver fibrosis with AUC values approaching 0.97[38], and while complementary epidemiological ultrasound studies are not AI-driven, they provide critical prognostic ground truth by linking structural pathology and lesion burden to long-term morbidity in urogenital schistosomiasis[78]. Hybrid ML geostatistical models integrating Kriging with tree-based learners predict spatial distributions of schistosomiasis seropositivity with R^2 values up to 0.87, identifying high-risk transmission zones associated with environmental and socioeconomic drivers[79]. Environmental and meteorological forecasting frameworks using XGBoost, random forests, and ensemble classifiers have been applied similarly to dengue, capturing seasonal severity dynamics across Asia and South America[80,81].

Despite these advances, clinical translation remains limited by narrow training populations, sparse longitudinal data, and insufficient attention to calibration, interpretability, and prospective validation. Many prognostic models draw on retrospective single-country cohorts, omit serotype-specific effects, or conflate individual-level prognosis with population-level forecasting. Progress will require multi-site longitudinal cohorts, harmonized outcome definitions, routine external validation, and wider adoption of interpretable and causally-informed architectures. These limitations also highlight the need for approaches that extend beyond static risk prediction toward continuous monitoring of patients over the course of care.

Thus, treatment monitoring encompasses the longitudinal assessment of therapeutic adherence, treatment response, and disease progression across the course of care (see Supplementary Information Table S4). Compared with diagnostics and surveillance, this remains one of the least developed application domains in AI for NTDs, reflecting the scarcity of longitudinal follow-up datasets and the operational difficulty of collecting repeated measurements in endemic low-resource settings. Existing studies primarily rely on imaging, clinical, and serological data to support objective evaluation of treatment outcomes and patient follow-up[82].

Evidence is available across several diseases, though studies remain sparse and heterogeneous. In leprosy, CNN-based analysis of skin lesion images achieved 91.6% accuracy in evaluating treatment progression, providing a rapid and objective complement to clinical assessment[83]. For cutaneous leishmaniasis, SVM-based models have been used to identify predictors of treatment non-adherence and therapeutic unresponsiveness, achieving 86.3% accuracy while highlighting the role of adverse effects and regimen complexity[35]. In rabies control programmes, Bayesian modelling of longitudinal serological data from vaccinated dog populations in Cambodia has supported optimization of vaccination schedules required to maintain protective immunity over time[84].

Across these applications, AI demonstrates meaningful potential to support longitudinal care and therapeutic evaluation in NTDs. However, a consistent profile of limitations emerges: small and geographically narrow datasets, regional heterogeneity in health infrastructure, and a near absence of prospective validation. The prioritization of robust longitudinal datasets, standardized outcome definitions, accessible multi-source AI tools tailored to endemic low-resource contexts, and integration with routine care pathways to enable scalable and equitable AI-assisted treatment monitoring in support of global NTD elimination goals is be vital. Beyond clinical monitoring and patient-level decision support, AI is also increasingly being applied earlier in the translational pipeline to accelerate therapeutic development.

Drug discovery for NTDs faces structural constraints including limited commercial incentives, sparse bioactivity data, and fragmented research infrastructure. AI and computational modelling are increasingly used to address these barriers by

accelerating *in silico* screening, enabling systematic repurposing, and improving candidate prioritization across the discovery pipeline (see Supplementary Information Table S5).

In silico screening now underpins much of NTD drug discovery, combining structure and ligand-based virtual screening with ML models that capture non-linear relationships between chemical structure and biological activity[85–87]. Graph neural networks (GNNs) have shown particular promise for antiprotozoal discovery by improving hit enrichment and scaffold diversity[26], while DL-based image analysis enables automated phenotypic screening in leishmaniasis and schistosomiasis assays[28,54]. Advances in protein structure prediction, notably AlphaFold, have expanded the tractable target space by enabling high-throughput docking against previously unresolved NTD proteins[88]. In parallel, drug repurposing leverages existing safety profiles and open compound libraries such as the malaria and Pathogen Boxes, with fexinidazole for human African trypanosomiasis offering a well-documented example of successful computational-to-clinical translation[89–91].

Downstream of screening, computational prioritization focuses on selecting candidates with favorable trade-offs among potency, selectivity, drug-likeness, and safety. Multi-parameter optimization frameworks combine physicochemical rules, drug-likeness metrics, and AI-based Absorption, Distribution, Metabolism, Excretion, and Toxicity (ADMET) predictions to triage compounds early and reduce downstream attrition[92–94]. For parasitic diseases, integrating high-content phenotypic data with multitask and uncertainty-aware learning improves data efficiency and supports mechanism-of-action inference across parasite life stages[26,54]. Collectively, these approaches are shifting NTD drug discovery from fragmented, target-specific efforts toward more integrated, data-driven pipelines that balance biological novelty with translational feasibility.

2.3 Population-Level Applications

Population-level applications complement patient-centred tools by operating at the scale of communities and health systems. Integrating spatiotemporal, environmental, and vector-related data streams, these approaches support disease surveillance, outbreak prediction, and strategic resource allocation[34,53,95]. Next we expound on how such tools contribute to programmatic decision-making and the strengthening of NTD control efforts.

Amongst these application domains, population-level surveillance is central to NTD control and elimination, guiding hotspot detection and the allocation of scarce public-health resources (see Supplementary Information Table S6). AI and ML have strengthened these capabilities by integrating heterogeneous data streams, including epidemiological reports, environmental and climatic predictors, vector ecology, remote sensing, genomic variation, and digital trace data, into models that capture complex spatiotemporal dynamics[96–99].

Spatial risk mapping illustrates operational utility across a range of settings. In Costa Rica, combining generalized additive models for location, scale and shape with random forest improved dengue risk estimation across 32 cantons[100], while Radial Basis Function Network with Darts Game Optimizer models applied in India, Peru, and the United States achieved high accuracy but limited geographic transferability[101]. For schistosomiasis, models integrating remote sensing imagery with field survey data demonstrated strong predictive performance, though uneven geographic coverage constrained scalability[102]. Environmental and vector ecology predictors further refine surveillance models: Imbalanced-XGBoost has been applied to rabies risk mapping in Morocco[103], a CNN with integrated differential equations to schistosomiasis trends in China[104], and SVM and random forest models to the distribution of the sand fly *Phlebotomus papatasi* in Iran[97]. Genomic-informed ML approaches have also been used to predict virulence-related genes in *Leishmania* strains, illustrating the integration of pathogen genomics into population-level risk assessment[96].

Integrated decision-support systems extend these capabilities by combining diverse data modalities. Ensemble classifiers such as the dengue disease prediction model synthesize epidemiological and digital trace information[105], while hybrid genetic algorithm[106] and Bayesian particle swarm optimization approaches[107] improve predictive accuracy but remain geographically constrained. In Brazil, Bayesian network models applied to clinical and demographic data have demonstrated potential for targeted leprosy reaction surveillance, though reliance on genetic features limits broader deployment[108]. Remote sensing-informed hotspot prediction using deep transfer learning with AlexNet CNN has shown high accuracy for dengue early warning in Taiwan[99], and ML-driven environmental models using the Normalized Difference Vegetation Index, Normalized Difference Water Index, Land Surface Temperature, and Tropical Rainfall Measuring Mission rainfall data have successfully predicted oviposition activity of *Aedes aegypti* in Argentina, outperforming conventional linear approaches[98].

Across these applications, AI-enabled surveillance shows meaningful potential, but persistent structural challenges, including data gaps, inconsistent reporting standards, and limited interoperability between health information systems, must be addressed before these tools can support reliable, routine public-health decision-making. Building on these foundations, a closely related body of work focuses on anticipating future transmission dynamics rather than describing current or historical patterns.

Outbreak prediction combines AI tools with mechanistic models to forecast the location, timing, and magnitude of NTD cases.

This integration enables cost-effective interventions before outbreaks fully manifest (see Supplementary Information Table S7)[24,109,110]. Its primary aim is to generate actionable early warnings that support preemptive public health responses in resource-limited settings, thereby reducing the health and economic burden of outbreaks.

The evidence base is dominated by dengue forecasting, where the value of integrating demographic and meteorological data with case reports is well established. Specifically, ML models including SVMs and Bayesian formulations perform reliably in data-scarce contexts.[111–113], whereas ensemble tree methods such as random forest, gradient boosting, and logitboost excel at handling heterogeneous features and supporting variable importance ranking.[114–116]. DL architectures, including recurrent neural networks with long short-term memory and gated recurrent unit variants for multivariate time series have demonstrated meaningful gains in predictive accuracy. Similarly, CNNs utilizing aerial or satellite imagery have shown success across dengue-endemic regions, including Malaysia, Bangladesh, India, Indonesia, Mexico, and the United States.[24,110,114,117–119]. Hybrid architectures that couple mechanistic epidemiological models with ML surrogates have been used to blend interpretability with predictive power, supporting early warning system development in Mexico, the United States, and Bangladesh[109,120].

In practice, model selection depends on data richness and operational context. Tree ensembles remain robust under data sparsity, while DL models are more demanding of data volume and sensitive to reporting lags. Hybrid strategies that augment routine surveillance with low-cost local digital signals, combined with transparent external validation, are most likely to produce deployable early warning systems[115,121].

Lastly, policy planning represents the least studied application domain in this review, yet the available evidence points to meaningful opportunities for AI to support data-driven resource allocation, intervention optimization, and guideline development (see Supplementary Information Table S8).

Several illustrative applications span different diseases and contexts. In China, AI-driven risk surveillance models for schistosomiasis have demonstrated the ability to adapt to varying geographical and socio-cultural contexts, supporting more targeted mass drug administration strategies[122]. Spatial modelling of baseline endemicity for lymphatic filariasis in Nigeria has informed control program planning, advocacy, and resource prioritization[123]. The SisLeish information system applies standardized data collection and AI-assisted analysis to facilitate real-time leishmaniasis monitoring and guide regional collaboration across 16 countries in the Americas[124]. Deep neural networks applied to unstructured outbreak reports from sources such as ProMED-mail have shown how natural language processing can extract policy-relevant signals for emerging infectious diseases[125].

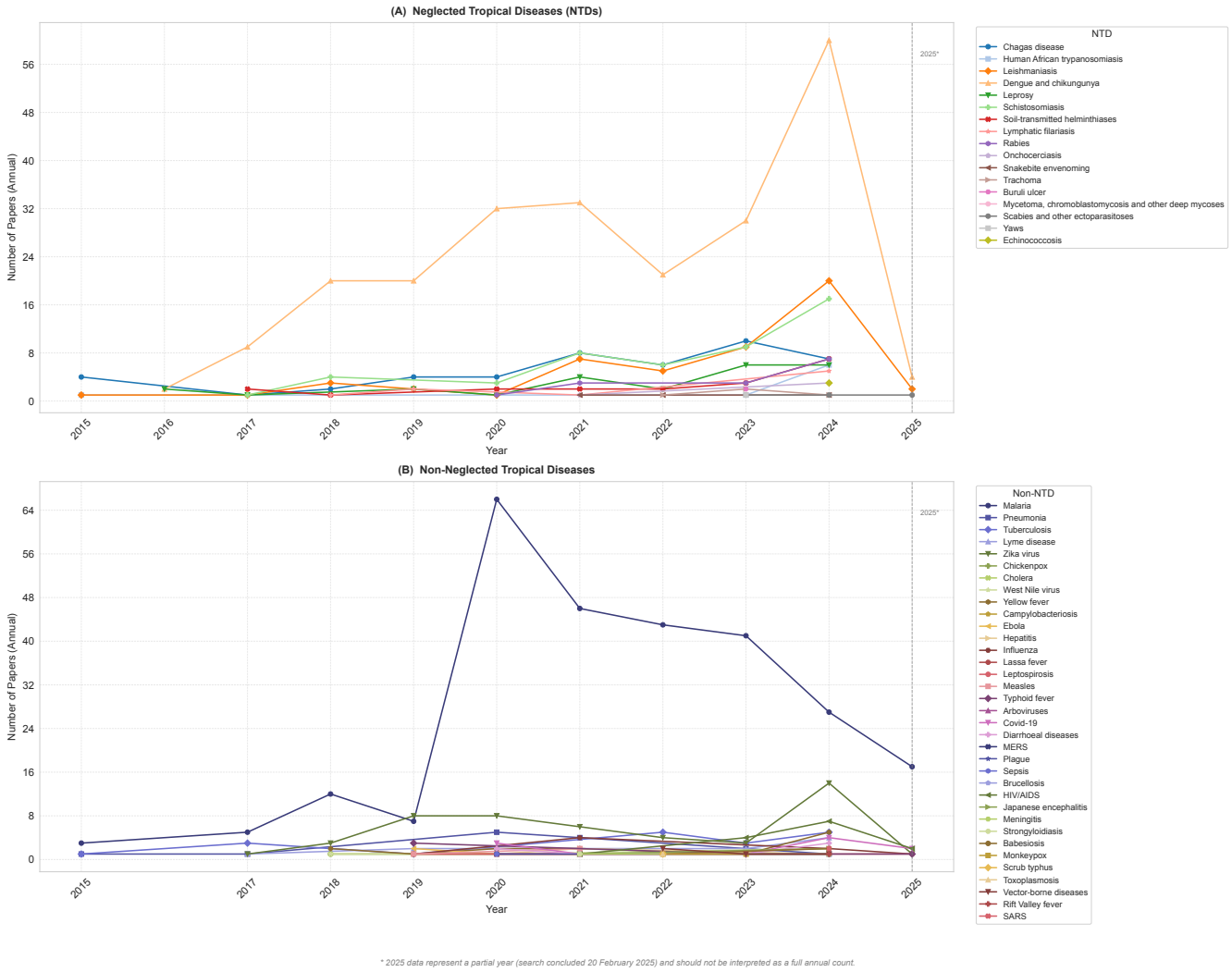
Beyond surveillance and risk mapping, AI has been explored as a tool for strengthening healthcare workforce capacity. In Nigeria, AI-assisted training frameworks for female genital schistosomiasis have been used to improve diagnostic accuracy and competency among health workers through on-site support tools[126].

Taken together, these applications remain largely proof-of-concept, and the policy planning literature is notably thinner and less methodologically rigorous than other application domains. Translating these tools into routine policy use will require stronger integration with health information systems, engagement with policymakers in endemic countries, and evaluation frameworks that move beyond technical performance to assess real-world decision impact[122–126].

2.4 Landscape Analyses of AI in NTDs

Figure 2 is presented primarily to compare publication trends for common non-NTD infectious diseases with those of NTDs. As shown in the figure, we observed a consistent upward trajectory. In the early years (2015–2018), only a handful of papers appeared, reflecting proof-of-concept work and limited data availability[127–131]. This highlights how AI was initially tested on small datasets before being applied more broadly.

From 2018 onward, annual publication counts increased steadily across both panels, where each data point reflects the number of unique papers addressing a given disease in that year, with papers covering multiple diseases contributing once to each relevant disease category. In the non-NTD panel, malaria dominated throughout the study period, peaking at approximately 64 annual publications around 2020 before gradually declining to 16 by early 2025. It should be noted that malaria was explicitly included in the search strings as a high-burden comparator disease, and its prominence therefore reflects this methodological decision relative to other non-NTDs. Within the NTD panel, dengue and chikungunya showed the most pronounced annual growth, peaking at 58 publications in 2024, while leishmaniasis exhibited the next highest trajectory, reaching 18 papers in 2024. By contrast, the majority of NTDs, including trachoma, yaws, Buruli ulcer, and snakebite envenomation, remained at or near zero annual publications throughout the study period. This disparity demonstrates that AI research has been disproportionately concentrated in a small number of diseases, leaving many NTDs relatively underexplored despite their substantial disease burden.

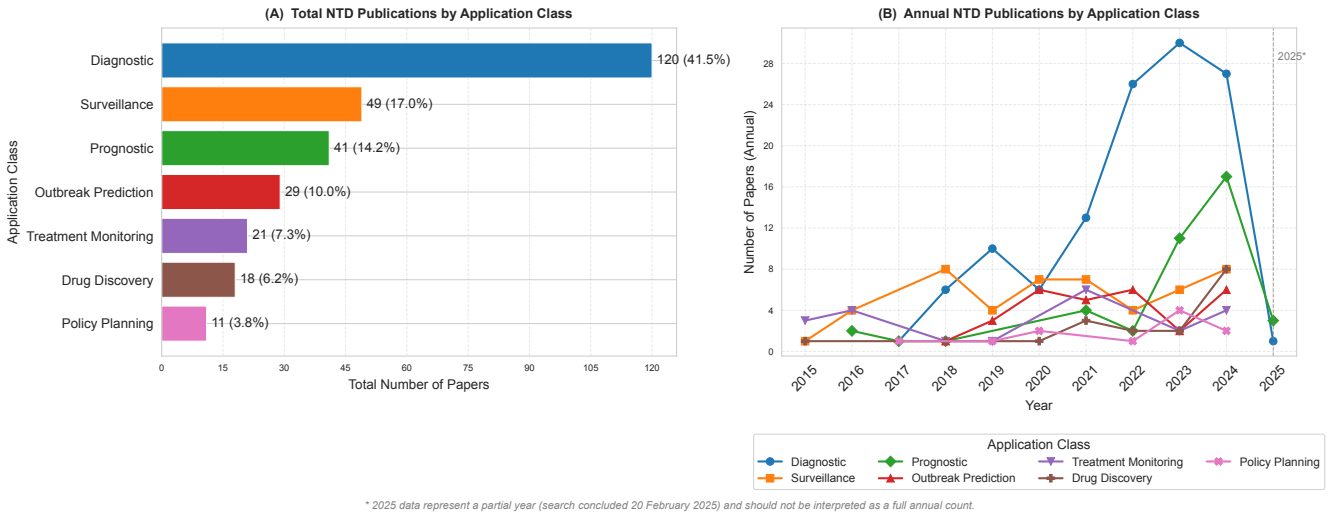


Furthermore, leishmaniasis, schistosomiasis, and leprosy show modest but visible growth compared with other conditions such as trachoma, yaws, or Buruli ulcer, which remain minimally represented[21,25,27,62,132–134]. Taken together, these temporal patterns show that AI for NTD research is growing but in an uneven manner. The field is expanding as digital health becomes more mainstream, yet most progress remains concentrated in a few diseases, leaving many high-burden NTDs with little AI research attention. This gap underscores the need for more targeted investments in underrepresented diseases if AI is to have equitable global health impact.

Building on the temporal analysis, we next examined how studies are distributed across application categories (Figure 3). Panel A shows the total publication counts across all years, while Panel B shows the corresponding annual trends. Diagnostics dominate the literature, accounting for 120 publications in total (41.5%), and Panel B shows that this category drove most of the growth observed after 2020, peaking at 30 annual publications in 2023 before declining. This shows that AI research in NTDs has primarily focused on patient-level diagnosis, reflecting both the availability of imaging data and the feasibility of applying computer vision methods such as CNNs[22,39,51,135–137].

Surveillance is the second most represented category, with 49 total publications (17.0%), though Panel B shows that annual counts remained relatively flat throughout the study period, fluctuating between 4 and 8 papers per year. This is worth noting because it indicates a steady but modest recognition of AI's role in monitoring transmission and supporting public health decision-making[138–140].

Prognostic applications account for 41 publications in total (14.2%) and Panel B reveals a late but notable increase, with annual counts rising to 17 papers in 2024. This suggests that researchers are beginning to shift attention toward predicting disease



** 2025 data represent a partial year (search concluded 20 February 2025) and should not be interpreted as a full annual count.*

progression and treatment outcomes, an area that directly supports patient management[23,25,141].

Other categories, including outbreak prediction (29, 10.0%), treatment monitoring (21, 7.3%), drug discovery (18, 6.2%), and policy planning (11, 3.8%), each remain considerably smaller in total volume and show no sustained upward trajectory in Panel B. These low numbers are important because they reveal untapped opportunities: AI has clear potential in drug repurposing, adherence monitoring, and resource allocation, but these areas are still nascent[24,26,28,34,35,114,115,142–145].

Overall, these trends indicate that the evolution of AI for NTDs has been guided more by technical feasibility and data availability than by comprehensive public health priorities. Bridging this gap requires expanding investment beyond diagnostics to areas where system-level impact could be greatest.

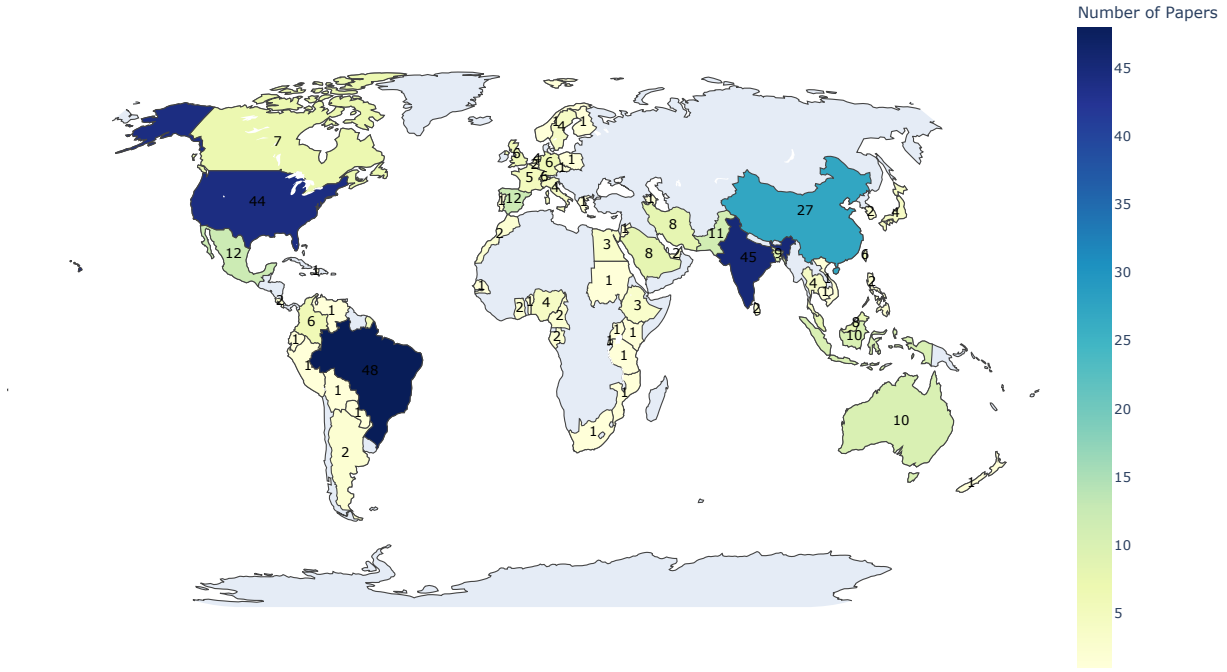
To understand where this research is being led, we analyzed author affiliations by country (Figure 4). A small set of countries contributes the majority of publications: Brazil, India, and the United States together account for over two-thirds of research output on AI in NTDs, with China also contributing substantially. For instance, Brazil has developed AI tools for schistosomiasis and dengue[22,37]; India has produced forecasting and modeling work on dengue[23,140]; China has advanced radiomics-based diagnostics for schistosomiasis[38]; and in the United States, cross-continental collaborations have yielded insights into dengue immune profiling[138] and automated vector identification for Chagas disease[53].

Several European countries and Australia produced mid-range outputs, typically between 5 and 12 papers each. In Africa, we observed contributions from Nigeria, Egypt, Cameroon, Ethiopia, South Africa, and several other countries with smaller counts. For example, Nigerian and European researchers co-developed automated frameworks for urogenital schistosomiasis microscopy[36,95], while Egypt has contributed classification pipelines for hepatic schistosomiasis fibrosis[146,147]. South African teams have investigated genetic variants in schistosomiasis[148].

The publication distribution (Figure 4) suggests that research activity is influenced more by technical feasibility and data availability than by disease burden or mortality risk. Conditions with accessible and well-curated datasets, such as dengue, are more frequently represented in the AI literature, whereas high-burden but data-limited diseases such as rabies and visceral leishmaniasis remain comparatively underrepresented.

Taken together, these results show that leadership is not limited to high-income countries. Middle-income countries with high NTD burdens, particularly Brazil and India, have become major hubs of AI research. This is encouraging because it aligns research activity with disease need. At the same time, participation remains uneven across many other endemic countries, underscoring the need to broaden geographic representation and strengthen research capacity in underrepresented regions.

Building on the patterns observed in author affiliations, we next examined where the underlying datasets utilized in the surveyed paper were sourced from (Figure 5). While the authorship distribution section showed that scientific leadership extends beyond high-income settings with Brazil, India, and other middle-income countries emerging as key contributors, the distribution of datasets reveals a more uneven landscape. Most datasets, unsurprisingly, originate from a limited high disease-burdened regions, particularly Brazil, India, China, and select sites in North America, where digital infrastructure, funding readiness, and research capacity are more established. In contrast, many high-burden areas in sub-Saharan Africa, Southeast Asia, and parts of Latin



America remain sparsely represented in the available data.

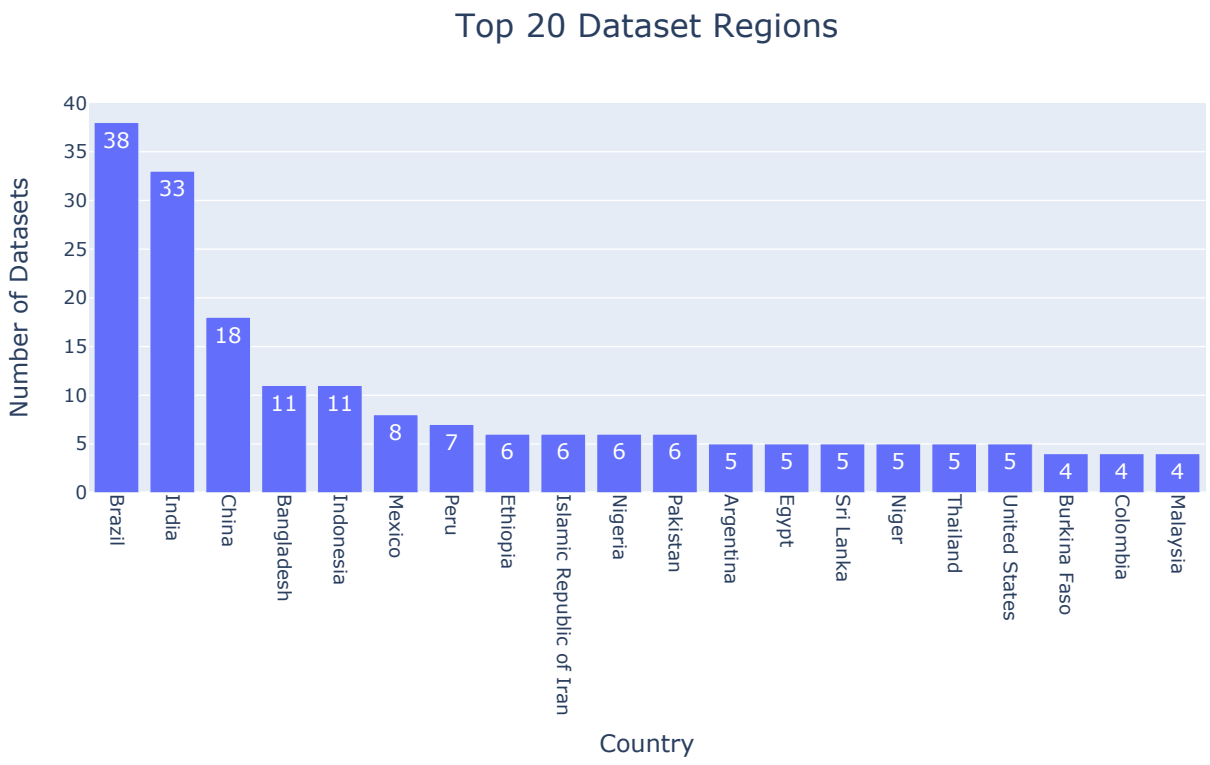
This geographic skew has important ramifications for model validity and healthcare access equity. Because AI systems trained on geographically narrow datasets often struggle to generalize to new epidemiological and ecological contexts, tools developed in well-resourced settings may underperform when deployed in underrepresented endemic regions due to *data distribution shifts*. The patterns in (Figure 5) therefore highlight a critical gap: the need for more inclusive, locally generated datasets and for investment in infrastructure that enables data production and management within endemic communities. Strengthening regional data ecosystems, expanding field-based data collection, and adopting collaborative approaches such as federated learning will be essential for ensuring that AI tools are robust, context-appropriate, and aligned with the global distribution of NTD burden.

Furthermore, we investigated how funding flows intersect with disease areas and institutional affiliations (Figure 6). We found that a small set of organizations dominates the landscape. National agencies in Brazil, such as Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), provide the bulk of funding for Chagas disease research, which primarily flows to Brazilian universities and institutes[22,37]. This shows how strong national investment has enabled Brazil to take a leadership role in AI for NTD research, particularly for diseases of regional importance.

We also observed substantial contributions from the US National Institutes of Health (NIH), the National Science Foundation (NSF), and the Bill and Melinda Gates Foundation. Their funding is distributed across multiple diseases, including schistosomiasis and soil-transmitted helminthiases, and connects to leading universities in North America and Europe[138,148]. This demonstrates how large, well-resourced funders shape global research priorities and sustain high-profile collaborations.

Philanthropic and multinational actors, such as the Gates Foundation, the European Union, and Johnson & Johnson, appear as cross-cutting supporters. These connections highlight the role of non-state actors in diversifying funding streams and linking research across regions.

At the institutional level, Brazilian universities and research institutes (e.g., Universidade de São Paulo, Universidade Federal,



Fundação Oswaldo Cruz) account for a large share of visible affiliations[53,140]. This indicates that endemic-country institutions are not only participants but also primary recipients of national research support. In contrast, *institutions in Africa and South East Asia are less visible in this network*, underscoring the need to expand direct investment in these regions for AI research for NTDs[36,95].

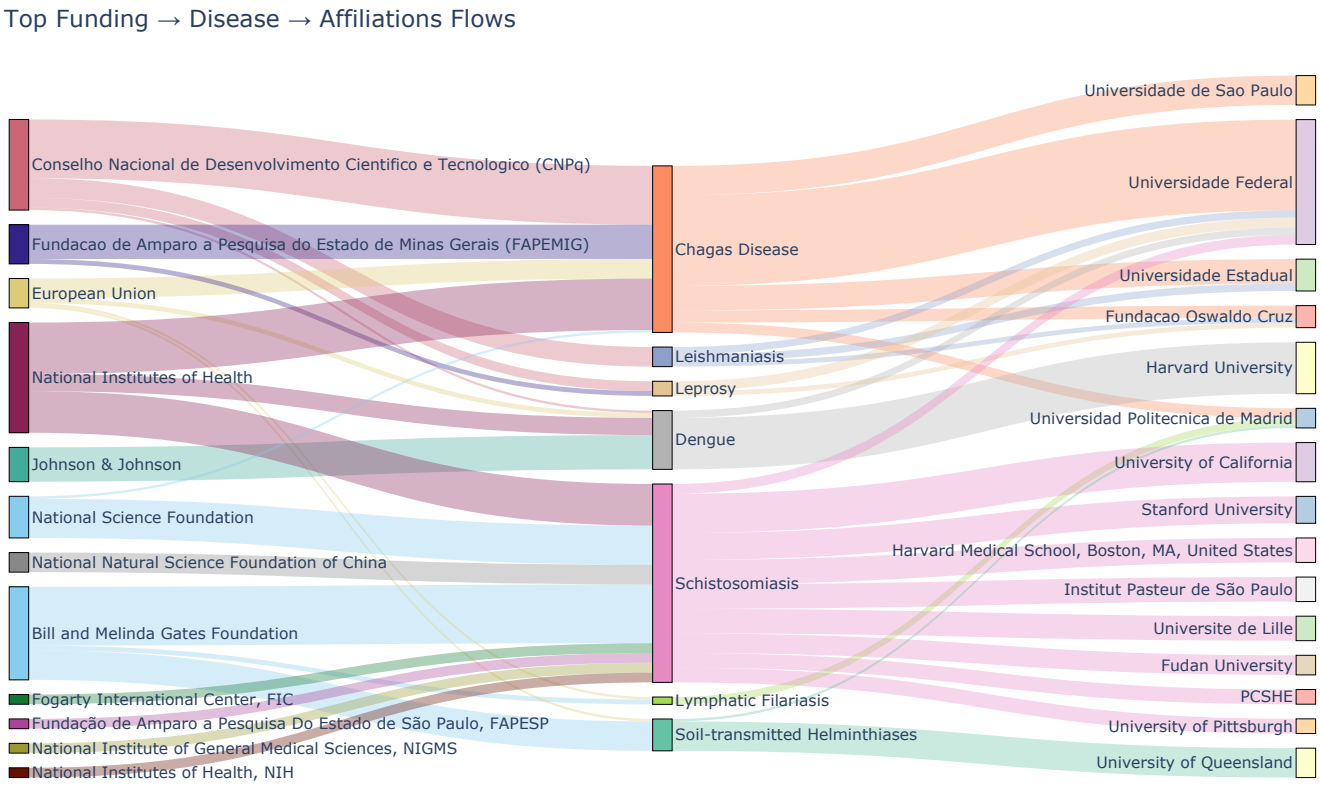
Together, these patterns show that national investment in middle-income endemic countries can substantially drive leadership in disease-specific AI research, while global funders and high-income country universities continue to anchor multi-disease collaborations. This reveals both the opportunities where local investment aligns with local burden and the gaps, where endemic regions remain underfunded and underrepresented in shaping research agendas.

Looking across the various analytical lenses, a consistent theme emerges: the field is growing but remains uneven across multiple dimensions. Growth has accelerated in recent years, yet activity is clustered around a limited set of diseases, applications, countries, and funders. This concentration highlights that, although AI is gaining traction in NTD research, its benefits are not evenly distributed across the disease portfolio or the regions most affected.

A closer examination of the thematic landscape reinforces several key patterns. First, despite overall growth, research activity remains unevenly distributed, with a strong concentration in a small subset of NTDs and geographic regions. Second, diagnostic applications dominate the literature, while critical system-level use cases such as surveillance, treatment monitoring, and policy planning remain comparatively underexplored. Third, research leadership is concentrated in a handful of countries, notably Brazil, India, the United States, and China, reflecting both strong national investments and persistent gaps in representation from other endemic regions. Fourth, funding structures play a defining role in shaping research priorities, with a limited number of agencies and philanthropic organizations driving the agenda, often positioning endemic-country institutions as collaborators rather than primary leaders.

We interpret these findings as evidence that technical feasibility and available funding have thus far played a larger role in directing research efforts than local health priorities. This imbalance risks reinforcing existing inequities of neglect within NTD research if not actively addressed.

To address these gaps, we propose several priorities. First, investment should be diversified beyond diagnostics to include system-level applications such as surveillance, policy planning, and treatment monitoring, which are essential for strengthening



health systems. Second, funding mechanisms must become more equitable by supporting endemic-country institutions as primary recipients and leaders of research initiatives, thereby aligning scientific agendas with local needs. Third, the development and curation of open, well-annotated datasets should be prioritized to enable reproducibility, lower barriers to entry, and broaden participation across regions.

Taken together, these measures would allow AI research in NTDs to transition from opportunistic and uneven growth toward a more deliberate, inclusive, and impact-oriented trajectory. Such a shift is essential if AI is to contribute meaningfully to WHO 2030 roadmap and to address the structural inequities that continue to define the global burden of NTDs.

3 Discussion

This section synthesizes the findings of the review within equity-focused and policy-oriented frameworks relevant to NTD prevention and control. We contextualize the evidence within the broader socio-technical and socio-economic forces that shape the design, development, evaluation, and deployment of AI systems in global health contexts. A recurring theme across these dimensions is the profound influence of structural constraints, of which data scarcity and geographic bias are among the most consequential.

Data scarcity defined here as the limited availability of large, high-quality, and representative training and validation datasets, and geographic bias represent fundamental bottlenecks. Datasets overwhelmingly originate from Brazil, India, China, and high-income research hubs (Supplementary Table S9), while deeply endemic regions in sub-Saharan Africa and Southeast Asia remain substantially underrepresented[149–151].

AI models trained on geographically narrow datasets frequently exhibit degraded generalizability when deployed in high-burden, low-resource settings, risking the reinforcement of existing inequities rather than their reduction[152–154]. Disease-specific data availability further skews innovation: dengue, leishmaniasis, and schistosomiasis dominate the literature, while conditions such as Buruli ulcer, mycetoma, and dracunculiasis remain nearly absent from public repositories[155–157], partly because some, such as dracunculiasis, are nearing eradication, with only 54 human cases reported across four countries in 2019 compared with over

500 in 2012[158].

A key limitation across included studies is the general absence of uncertainty quantification (UQ) and explicit calibration assessment. Most models report only point estimates of predictive performance (e.g., accuracy or AUC), while comparatively few evaluate whether predicted probabilities are well calibrated against observed outcomes. This distinction is particularly important in the context of NTDs, where AI outputs may influence clinical triage, outbreak preparedness, and the allocation of scarce public-health resources under conditions of sparse, noisy, or incomplete data. High discrimination performance alone may therefore be misleading: a model can achieve strong apparent accuracy while systematically over- or under-estimating real-world risk, thereby limiting clinical and public-health utility. A small subset of studies in our review moved beyond accuracy-only reporting toward probabilistic or calibrated outputs. For example, Keshavamurthy et al.[159] combined data-balancing approaches with isotonic regression in rabies epidemiology to improve probability estimates in low-surveillance settings, while Su et al.[104] reported a Continuous Ranked Probability Score (CRPS = 0.19) for schistosomiasis forecasting. Several additional studies, including de Andrade Rodrigues et al.[108], Gerardo et al.[75], and Auerswald et al.[84], employed Bayesian modelling frameworks that inherently provide uncertainty-aware probabilistic outputs. Together, these examples highlight an important calibration gap across the current evidence base: although reliable probabilistic outputs are essential for trustworthy decision-making in endemic settings, calibration and uncertainty-aware modelling remain the exception rather than the norm. Future work should therefore place greater emphasis on predictive uncertainty estimation, calibration reporting, and probabilistic modelling approaches, including Bayesian and ensemble-based methods.

Technical barriers compound these challenges further. Large DL models require high-performance computing infrastructure, including graphics processing units and tensor processing units, stable electricity, and reliable connectivity, resources that are frequently unavailable in low- and middle-income countries (LMICs)[160–162]. Many endemic-country health systems also lack personnel trained in ML and data engineering, increasing the risk that AI tools remain unsustainable pilot projects dependent on external expertise[163,164]. Reproducibility presents an additional concern: non-deterministic model behavior, heavy dependence on preprocessing pipelines, and inadequate reporting collectively impair independent validation and limit trust in published results[165,166].

Socioeconomic and ethical concerns further complicate implementation. Privacy risks, unclear data ownership, and the potential for data extraction without reciprocal benefit threaten community trust and raise concerns about digital colonialism, which refers to the modern practice where large, dominant tech corporations (mostly based in the Global North) extract data, control digital infrastructure, and exploit the markets of developing nations (the Global South), where endemic regions supply data while AI development and governance remain concentrated in high-income settings[167,168]. Algorithmic bias arising from non-representative training data may widen health disparities when tools are deployed in underrepresented populations. Chronic underfunding, infrastructure gaps, and the migration of AI expertise away from endemic regions further constrain sustainable local implementation.

Addressing these barriers requires coordinated investment in federated data networks aligned with FAIR (Findable, Accessible, Interoperable, and Reusable) principles[169], digital infrastructure, transparent governance frameworks, and capacity-building initiatives that position endemic-country institutions as equal partners rather than data suppliers. Without such safeguards, AI risks reinforcing the inequities it aims to alleviate (see Supplementary Information M for extended discussion). Beyond infrastructure and governance, these structural realities also raise deeper ethical imperatives that must be addressed if AI is to serve the populations most affected by NTDs.

For AI to contribute meaningfully to NTD control, its development and deployment must be explicitly equity-centered. Ensuring fairness requires more than technical innovation: it demands inclusive governance, local data sovereignty, and sustained investment in endemic-country institutions. Without local ownership and capacity, the benefits of AI tools are unlikely to reach the populations most affected. Embedding ethical design, participatory implementation, and transparent benefit-sharing into AI programs will be essential to meeting the WHO 2030 roadmap goals of elimination, universal health coverage, and sustainable health innovation. Realizing these ethical commitments in practice also depends on the rigor and transparency with which AI research is conducted and reported.

Strengthening the transparency, reproducibility, and real-world applicability of AI research in NTDs requires consistent adoption of established reporting frameworks. For clinical prediction models, the TRIPOD-AI[170] and PROBAST-AI[171] extensions provide guidance on dataset description, model development, calibration, and external validation. Image-based diagnostic studies should follow the Checklist for AI in Medical Imaging (CLAIM)[172], which specifies requirements for data acquisition, annotation, and evaluation workflows. Interventional or deployment studies should use the Consolidated Standards of Reporting Trials for AI (CONSORT-AI)[173] to ensure comprehensive reporting of AI behavior in clinical and field settings. Systematic reviews of diagnostic model performance should adhere to the PRISMA guidelines[174]. Our analysis indicates that current

literature seldom aligns with these standards, underscoring the need for wider adoption to improve methodological quality and support the safe translation of AI tools into NTD programmes. Rigorous reporting, however, is only one piece of the multiplicity of considerations; translating methodological quality into real-world impact ultimately depends on how well different disciplines and sectors work together.

Translating AI research into effective and sustainable NTD control requires both interdisciplinary integration and coordinated cross-sector collaboration. Interdisciplinary integration ensures that AI solutions are epidemiologically sound, clinically actionable, and contextually feasible, while cross-sector collaboration aligns technical innovation with institutional capacity, implementation expertise, and policy frameworks.

In epidemiology and public health, epidemiologists define transmission dynamics, outcome variables, and confounding factors, while AI researchers develop models capable of handling high-dimensional, sparse, and non-linear relationships[23,139,141]. Hybrid models integrating mechanistic and ML components can provide outputs that are both interpretable and predictive, supporting interventions such as targeted mass drug administration and vector control. In clinical diagnostics, pathologists and microbiologists establish gold-standard criteria and curate annotated datasets, while AI specialists design automated detection and quantification pipelines[21,22,58]. Co-designed validation studies are essential to ensure that these tools perform under real-world field conditions rather than only in laboratory settings.

For population-level policy planning and outbreak preparedness, interdisciplinary collaboration must also extend beyond model development toward operational readiness. In this context, operational readiness refers to whether an AI/ML system can be reliably integrated into real-world decision-making workflows, including timely updating with new surveillance data, external validation across endemic settings, interoperability with existing health information systems, and outputs that are interpretable and actionable for ministries of health and disease-control programmes. Established infectious-disease preparedness frameworks increasingly emphasize this broader deployment perspective, particularly through One Health approaches that integrate ecological, entomological, environmental, and climate signals with clinical and surveillance data to support early warning and coordinated response. Compared with these broader infectious-disease applications, AI/ML studies for NTD policy planning remain relatively limited and are still evaluated predominantly as proof-of-concept models rather than as deployable decision-support systems[175]. Aligning future NTD-focused work with operational-readiness frameworks can therefore strengthen the translation of predictive models into impact-oriented public-health action.

Drug discovery benefits similarly from collaboration between pharmacologists and parasitologists, who identify targets and validate compounds, and AI researchers who apply graph neural networks, DL, and natural language processing to screen compound libraries and optimize leads[26,28,87,88]. A curated overview of the key AI/ML frameworks, digital health platforms, and explainability tools supporting these workflows is provided in Supplementary Information K.2, Table K.10. This iterative loop has been demonstrated in schistosomiasis and leishmaniasis drug discovery programmes[176,177]. Equity and ethical considerations must be embedded throughout these collaborations, with social scientists and ethicists addressing data sovereignty, informed consent, algorithmic bias, and socio-economic impacts to ensure that tools are co-designed with communities and do not exacerbate stigma or health disparities[153,178–180].

At the cross-sector level, academic institutions provide research capacity and field access, while industry partners contribute engineering expertise, regulatory knowledge, and manufacturing capabilities[89,90,95]. Structured frameworks such as the Drugs for Neglected Diseases initiative (DNDi) model demonstrate how intellectual property agreements can be aligned with public health objectives[181]. Non-governmental organizations (NGOs), ministries of health, and disease control programmes connect innovations to endemic communities, ensuring tools are adapted to field conditions and integrated into existing workflows[182,183]. The WHO Roadmap 2021–2030[33] and the EU Integration of Heterogeneous Data and Evidence towards Regulatory and HTA Acceptance (IDERHA) project[184] exemplify federated, multi-stakeholder approaches that facilitate data sharing, policy adoption, and long-term sustainability. These collaborative frameworks take on particular significance when viewed against the targets set by the WHO Roadmap 2021–2030, which define the policy horizon within which AI tools must ultimately demonstrate impact.

The WHO Roadmap 2021–2030 sets targets including a 75% reduction in NTD-related disability-adjusted life years (DALYs), elimination of one or more NTDs in at least 100 countries, and global eradication of at least two NTDs[33,185,186]. The evidence reviewed here suggests that AI can contribute to several of these goals, though the extent of that contribution will depend on how well current methodological and equity gaps are addressed.

In diagnostics and surveillance, AI tools have demonstrated the potential to enhance disease detection, support point-of-care decision-making, and enable early outbreak identification[32]. Mobile phone-based microscopy platforms have shown particular promise for expanding diagnostic access in resource-limited endemic settings[32,167,187]. In therapeutics, computational approaches to drug discovery and repurposing have generated candidate compounds for underfunded NTDs including Chagas

disease and leishmaniasis, offering pathways that conventional laboratory-only pipelines could not support at equivalent cost or speed[188].

Realizing these opportunities requires deliberate investment in local capacity. Integrating scientists, clinicians, and community representatives from endemic regions into AI development ensures tools are contextually appropriate and aligned with local priorities[32]. Funding initiatives should prioritize AI expertise development, routine data collection infrastructure, epidemiological modelling capacity, and frontline diagnostic applications in the settings where NTD burden is highest[32,189].

In conclusion, this review documents meaningful growth in the application of AI to NTDs, particularly in diagnostic imaging, disease classification, and outbreak prediction. That growth, however, is uneven. Research activity is concentrated in a small number of diseases, data modalities, and institutions, with most studies originating from middle- and high-income countries despite the highest disease burden falling on other endemic regions. Many models are developed on limited or non-representative datasets, raising legitimate concerns about generalizability, bias, and fairness in deployment.

The current evidence base carries several methodological limitations that temper these findings. Most studies remain at a proof-of-concept stage, with limited external validation, inconsistent reporting of model development and evaluation procedures, and few prospective or real-world assessments. Considerations critical to implementation, including model interpretability, integration within health systems, data governance, and local capacity building, are rarely addressed. Heterogeneity in methods and performance metrics further limits direct comparison across studies, pointing to an urgent need for disease-specific benchmarks that can anchor future evaluations and facilitate cumulative progress.

A further limitation is that we did not perform a formal study-level risk-of-bias assessment. Given the substantial heterogeneity across included studies in disease focus, study design, data modality, and reported outcomes, our aim was to provide a structured synthesis of the current evidence base rather than a comparative appraisal of methodological quality. This should be considered when interpreting individual study findings and the overall strength of the evidence summarized in this review.

Future research should prioritize equity-centered AI development, grounded in partnerships with endemic-country institutions, adherence to AI-specific reporting guidelines, and robust external and prospective validation. Sustained investment in data infrastructure, governance frameworks, and workforce capacity will be essential to move beyond isolated demonstrations toward sustainable deployment. Achieving this will require not only technical advances but also deliberate efforts to align research priorities with the needs of the populations most affected by NTDs.

4 Methods

4.1 Search Strategy

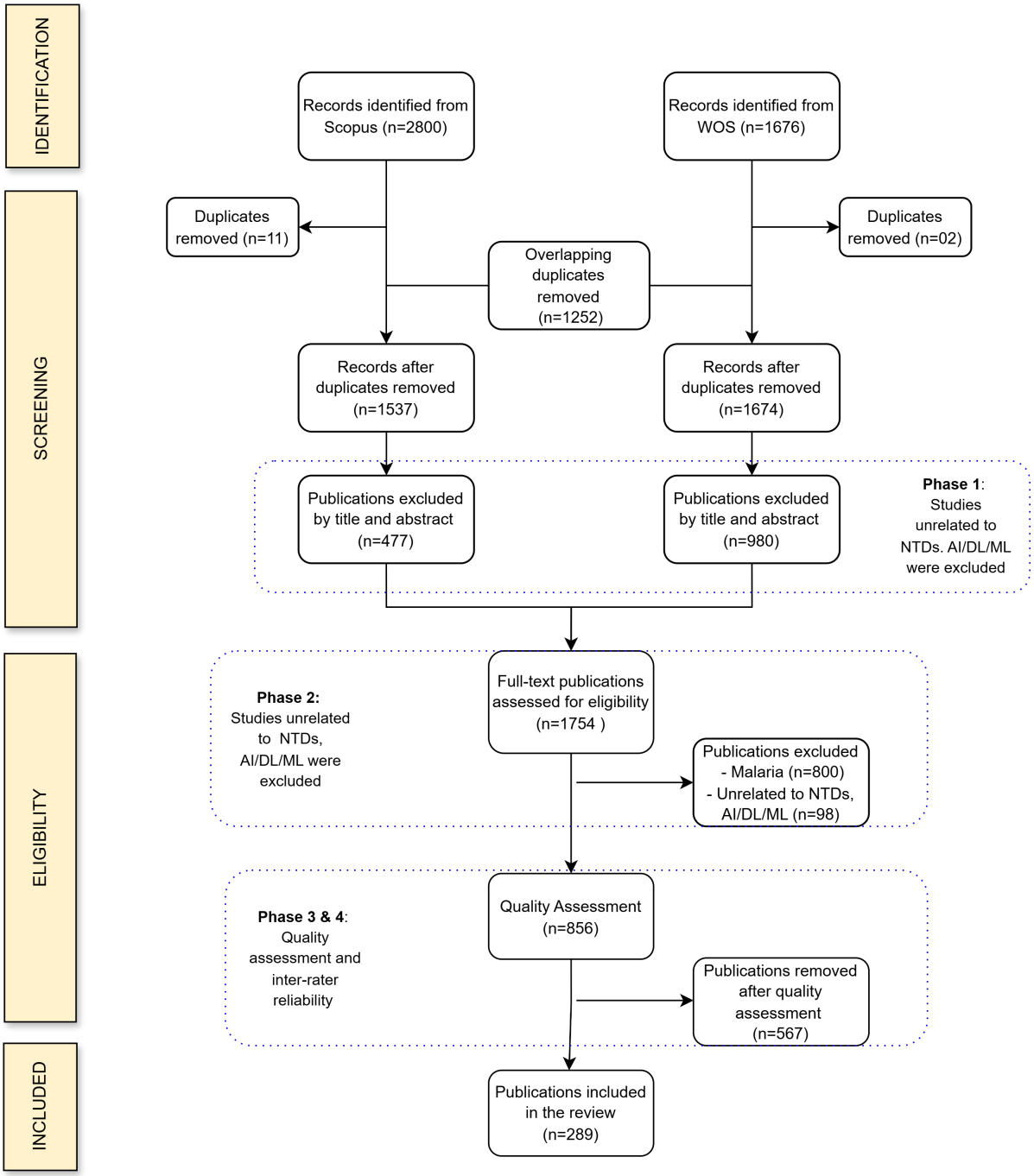
We conducted a systematic review following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA)[190] guidelines to ensure methodological rigor and transparency. A literature search was performed across two major academic databases: Scopus and Web of Science (WoS). The search covered the period 2015 to 2025 and used a broad combination of keywords to capture relevant studies at the intersection of AI and NTDs. AI was considered the broader field encompassing ML methods, while DL, defined as ML approaches based on multilayer neural network architectures[20,191], was treated as a subset of ML[19]. The search strategy was structured around three key concepts: (i) AI or ML methods, (ii) NTDs, and (iii) application domains in healthcare and public health. The exact search string applied in both databases is in Supplementary Information C.

4.2 Eligibility Criteria

The inclusion criteria were limited to peer-reviewed research articles published in English between 2015 and 2025. Articles were required to directly address the application of AI or ML methods to WHO-recognized NTDs, with direct relevance to areas such as diagnosis, prognosis, surveillance, treatment monitoring, drug discovery, or other public health applications.

Studies were included if they applied AI, ML, or DL approaches to develop or evaluate models addressing any of the tasks investigated herein. A substantive ML component was defined as the application, development, or evaluation of data-driven predictive or pattern-recognition algorithms (i.e., AI or ML) beyond rule-based or purely statistical analyses. Articles were excluded for the following reasons: publication outside the 2015–2025 cutoff window; being a non-original-research article type (e.g., reviews, editorials, commentaries); not being written in English; or having a retracted status.

The study selection and quality assurance followed four sequential phases designed to refine the retrieved records into a final corpus of methodologically robust and topically relevant studies. The initial database search retrieved a total of 4,476 publications, comprising 2,800 records from Scopus and 1,676 records from WoS. After removing 13 intra-database duplicates



(Scopus: 11; WoS: 2) and 1,252 overlapping duplicates across databases, 3,211 unique records (Scopus: 1,537; WoS: 1,674) were retained for title and abstract screening.

4.3 Study Selection

In the first phase, the 3,211 records were divided among 4 annotators without overlap for screening at the title and abstract level to determine whether a study engaged with AI, ML, or DL methodologies to WHO-recognized NTDs listed in Table A.1 (see Supplementary Information A.3) and malaria. Following this screening, 477 records from Scopus and 980 records from WoS were excluded, and the remaining 1,754 studies (Scopus: 1,060; WoS: 694) advanced to full-text screening.

In the second phase, the full texts of the 1,754 papers were divided among 4 annotators without overlap to determine whether they applied AI, ML, or DL methodologies to WHO-recognized NTDs. This was done to capture papers whose eligibility could

not be determined from the title and abstract alone. The second phase excluded 98 papers not implementing AI, ML, or DL methodologies to WHO-recognized NTDs. To preserve the thematic specificity of the review, the 800 identified malaria-related studies were excluded at this stage. Although malaria is not formally classified as an NTD by the WHO, it was intentionally included in the initial search strategy to quantify the volume of malaria research supported by international organizations and to contextualize funding disparities relative to WHO-recognized NTDs. This phase confirmed 856 studies as NTD-relevant then progressed to the third phase.

4.4 Quality Assurance and Inter-Rater Reliability

In the third phase, all 856 papers underwent quality assessment, which involved screening the full texts for methodological limitations, inadequate reporting, or the absence of substantive AI, ML, or DL components applied to WHO-recognized NTDs. Key concerns included missing descriptions of data provenance, sample size, class balance, and label quality, as well as insufficient discussion of missing data handling and preprocessing procedures. We also noted superficial model descriptions, such as claims of using AI, ML, or DL without specifying the underlying architecture, hyperparameter tuning strategies, or training procedures. Additional methodological issues included improper validation practices, such as the absence of cross-validation or inappropriate train/validation/test splits. Furthermore, we assessed whether performance metrics were suitable for imbalanced classification tasks. We also examined the inclusion of baseline comparisons, and clinical relevance.

The 856 papers were divided into four equal blocs of 214 papers each, with every bloc independently assessed by three annotators. In total, 12 independent annotators evaluated whether each paper satisfied the quality assessment criteria. Each annotator was provided with a separate Excel sheet to independently record their ratings (1 for agreement and 0 for disagreement). This approach was adopted to minimize potential bias and prevent annotators from influencing one another's judgements. Each annotator was allocated a 30-day assessment period and instructed to evaluate approximately 54 papers per week, a pace chosen to balance efficiency with careful, fatigue-free assessment.

Upon completion of the annotation, the ratings from all annotators were consolidated and inter-rater reliability was assessed using Fleiss' kappa[192]. Fleiss' kappa is a statistical measure that quantifies the degree of agreement among three or more raters. We implemented Fleiss' kappa using Python 3 on Google Colab, which yielded $\kappa = 0.805$. This reflects an almost perfect agreement under the proposed interpretive framework proposed in[193].

In the fourth phase, all studies for which annotators disagreement was recorded were referred to four independent annotators for reassessment. Consensus discussions were conducted to determine the final inclusion or exclusion status of each contested paper, concluding the adjudication process. Following this arbitration 567 studies were excluded. Ultimately, 289 research articles were incorporated into the final systematic review. The complete screening and selection procedure is shown in Figure 7.

4.5 Metadata Extraction and Standardization of Study-Level Variables

Metadata extraction was conducted for all included studies during full-text review to support downstream quantitative and network-based analyses. This process included key study-level variables such as funding, author affiliations, country or countries of dataset origin, disease category, data modality, and reported AI/ML task type. All extracted metadata were standardized using a harmonization protocol to ensure consistency across heterogeneous reporting formats.

Funding information was recorded verbatim where reported in the included studies and subsequently normalized by mapping synonymous or hierarchically related entities to their parent funding organizations (e.g., institutional sub-units aggregated under their primary agency). Where multiple funding sources were declared, all funders were retained and equally represented in the analysis. In cases where funding was not reported, this was explicitly coded as "not reported."

This harmonized metadata framework enabled the construction of the cross-study analyses presented in the Results section, including geographic distribution visualizations and the Sankey diagram of funding and institutional collaboration patterns.

Data Availability

All data supporting for this study are openly available at: https://github.com/yusufbrima/MLNTD/tree/main/data

Code Availability

All code supporting for this study are openly available at: https://github.com/yusufbrima/MLNTD

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Author Contribution Statement

YB and MA conceptualized the study. YB, MA, YN, MKN, ANF, TB, DGC, SGF, JLEKF, SL, NO, BR, CFN, LPS, NS, BAW, MJ, and XSN contributed to the methodology. YB, MA, MKN, YN, NB, DNNT, EMM, JLEKF, LSK, AK, LDK, HTL, PM, SM, LSM, SS, BGLS, HMT, SZ, and XSN performed the formal analysis. YB, MA, ANF, TB, DGC, SGF, JLEKF, SL, NO, BR, CFN, LPS, NS, BAW, and XSN contributed to the investigation. YN and MKN were responsible for data curation. MKN, YN, NB, DNNT, EMM, JLEKF, LSK, AK, LDK, HTL, PM, SM, LSM, SS, BGLS, HMT, SZ, and MJ conducted the paper screening. YN and MKN prepared the PRISMA diagram. YB and MA performed the coding and visualization. YB, MA, MKN, YN, ANF, NB, TB, DGC, DNNT, EMM, SGF, JLEKF, MJ, LSK, LHK, AK, LDK, HTL, SL, PAM, SM, LSM, ONO, BR, CFN, LPS, SS, NS, BGLS, HMT, BAW, SZ, and XSN contributed to writing the original draft and to reviewing and editing the manuscript. YB, MA, and XSN provided supervision. YB and MA handled project administration. MA, DGC, NO, BR, and XSN were responsible for funding acquisition. All authors read and approved the final manuscript.

Competing Interests

The authors declare no competing financial or non-financial interests.

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Figure Legends

Figure 1. Conceptual taxonomy of AI applications in NTDs. Applications are organized into individual-level domains, encompassing patient-centric tasks such as diagnosis, prognosis, and treatment monitoring, and population-level domains, encompassing public health functions such as surveillance, outbreak prediction, drug discovery, and policy planning.

Figure 2. Annual publication trends by disease type, 2015–February 2025. (**A**) Annual NTD publication counts, with dengue and chikungunya and leishmaniasis showing the most pronounced growth. (**B**) Annual non-NTD publication counts included as a comparator. 2025* data represent a partial year (search concluded 20 February 2025).

Figure 3. Distribution of AI research across application categories in NTDs. (**A**) Total publication counts by application category across the full study period, with percentages indicating each category's share of the overall NTD literature. (**B**) Annual publication counts per application category from 2015 to February 2025. Diagnostics represent the largest share (120 publications, 41.5%), followed by surveillance (49, 17.0%) and prognostics (41, 14.2%). 2025* data represent a partial year (search concluded 20 February 2025).

Figure 4. Geographic distribution of AI publications on NTDs by country of affiliation. Countries are shaded according to the total number of included publications contributed by authors affiliated with institutions in each country, with darker color intensity indicating a higher publication count. The map highlights the concentration of research output in a small number of middle and high-income countries and the relative underrepresentation of many NTD-endemic regions.

Figure 5. Top 20 countries by number of datasets used in AI for NTD studies. Bar length reflects the number of studies sourcing data from each country. Brazil, India, and China contribute the largest share of datasets, while many NTD-endemic countries in sub-Saharan Africa remain underrepresented.

Figure 6. Funding, disease focus, and author affiliation networks in AI for NTD research. Sankey diagram illustrating the relationships between funding organizations (left), the NTD investigated (centre), and the institutional affiliations of study authors (right) across the included studies. Each node represents a funding body, disease, or affiliated institution, whereas each connecting band represents one or more studies linking these entities. The width of each band is proportional to the number of publications represented, with wider flows indicating more frequent funding–disease or disease–affiliation connections. The figure highlights patterns in disease-specific funding and the concentration of affiliated research institutions.

Figure 7. PRISMA flow diagram of study selection. Study selection followed the PRISMA framework. Records were identified through systematic database searches in WoS and Scopus, duplicates were removed, and remaining records were screened by title and abstract. Full-text articles were then assessed for eligibility according to the predefined inclusion and exclusion criteria, yielding the final set of studies included in this review.

Supplementary Files

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