Review

The Use of Artificial Intelligence in Tuberculosis Care: A Scoping Review

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Abstract

Tuberculosis (TB) is a subacute to chronic respiratory infection with insidious onset and protean symptoms. Treatment is complex and requires a multi-drug, multi-month regimen in which adherence is critical. Artificial intelligence (AI) offers promising solutions to challenges across the TB care cascade including screening, diagnosis and treatment. We conduct a scoping review of the literature published from 2017 to 2025 on the use of AI in TB screening, diagnosis, drug resistance diagnosis, treatment monitoring, and regimen design. We then extract data on study characteristics, AI methodology, input data, and sample size and describe AI tool performance and technology readiness level (TRL). Ninety studies are included, representing 803,383 study participants across 24 countries. Most studies (n=46) focus on radiological imaging for TB screening or diagnosis, but a burgeoning number of studies address drug resistance diagnosis (n=11), regimen design (n=4), treatment monitoring (n=12), and treatment adherence (n=8). Reported accuracy of AI interpretation of chest imaging for TB diagnosis was high at a median Area Under the receiver operating Curve (AUC) of 0.94 [IQR 0.12, range 0.81-0.99] for internal validation and 0.89 [IQR 0.14, range 0.66-0.98] for external validation, and a median TRL of 5 (IQR 1, range 4-7). AI demonstrates promise for advancing TB care towards World Health Organization (WHO) End TB targets, but several gaps remain, including AI-ready fit-for-task data availability, limited external validation and challenges in clinical integration. Closing these gaps will be critical for realizing the full potential of AI in TB care towards WHO End TB targets.

Keywords: tuberculosis; artificial intelligence; machine learning; statistical learning; deep learning; AI platform; neural network; automatic; diagnosis; screening; regimen design; treatment monitoring; drug resistance

1. Introduction

Tuberculosis (TB) is the top infectious disease killer globally, causing more than 10.5 million new cases of disease in 2023 (1). TB demonstrates stark regional variation in incidence ranging from 2 to >800 per 100,000 population by country (2). The World Health Organization (WHO) has proposed the End TB Strategy which aims to reduce global TB incidence to <10 per 100,000 by 2035, however, modelling has projected that even with maximal deployment of currently available treatment and preventative strategies for TB, this degree of reduction will not be possible (3). Further, the sustainability of current TB interventions is at risk given the dependence of TB control programs on non-governmental funding and international aid (4). More than ever before, innovations that

improve delivery of TB screening, diagnosis, and treatment are needed. AI is at the forefront of such innovations as it offers cross-cutting data processing and interpretation capability promising to increase access to healthcare, increase healthcare reliability, and reduce costs. Here, we review AI innovations in TB care with the aim of charting an AI research agenda that can support achievement of WHO End TB targets (5). Given the rapidly evolving and heterogeneous nature of AI applications in TB care, a scoping review is an appropriate approach to map existing evidence, identify knowledge gaps, and classify AI tools across the care cascade.

The TB care cascade comprises four main steps: screening, diagnosis, treatment regimen design, and treatment monitoring, with the goal of TB cure (Figure 1). Many gaps currently exist along this care cascade (6). Gaps in screening include the lack of low cost, high sensitivity tools for early detection of TB prior to symptom onset (*i.e.*, subclinical or asymptomatic TB) which is increasingly recognized as a critical step in interrupting transmission to reduce disease incidence (7,8). Prompt and accurate TB diagnosis in symptomatic patients presenting to healthcare facilities is crucial for the timely initiation of TB therapy needed not only for cure but also for the reduction of long-term disease complications (9). Diagnosis classically relies on microbiological detection of TB bacilli. Yet, the low burden of bacilli in relevant human samples like sputum, and gastric aspirate (especially for children and those with HIV) requires improvements in sensitivity (10). Tests that leverage new sample types such as tongue swabs are expected to be recommended by WHO soon, and exhaled breath condensates also hold promise. Other adjunctive non-microbiological diagnostics have the potential to expedite diagnosis or boost accuracy. These include a variety of novel assays, such as assays of the host immune response, ultrasound manifestations of disease, and audio recordings of breath sounds and/or cough. Several of these approaches are in early-stage development and/or have faced challenges in implementation due to cost or complexity.

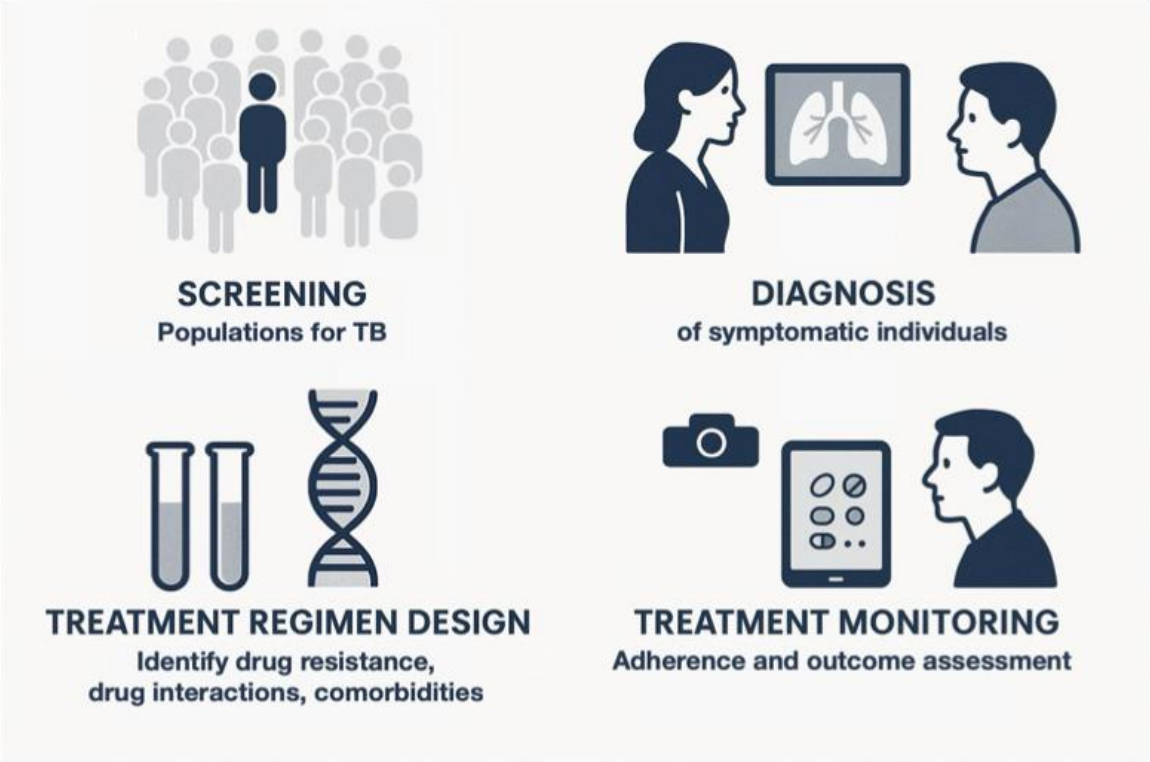


Figure 1. The TB care cascade comprises four main steps: screening, diagnosis, treatment regimen design, and treatment monitoring with the goal of TB cure. Source: Authors' schematic of the tuberculosis care cascade.

Challenges in regimen design include effectiveness of the regimen, drug resistance, drug interactions, and comorbidities. Globally, 10% of TB is resistant to the drug isoniazid, with 3% resistant to both isoniazid and rifampicin, i.e., multidrug resistant (MDR) (1). Recent reports on MDR-TB describe over 10% resistance to bedaquiline in some countries (11,12). Rapid and comprehensive drug resistance detection is critical for the design of an effective treatment regimen, but this has been difficult to achieve using traditional microbiological tools. In the last decade, pathogen sequencing has emerged as a viable rapid and low biohazard approach to comprehensive resistance diagnosis, but cost, output complexity, and interpretability are still major barriers.

After regimen design, treatment monitoring for adherence, side effects, and adequate microbiological and symptom response is needed. Monitoring is highly resource-intensive and limited by availability and accuracy of sputum testing including culture as well as human resources needed for outreach (14). Lastly, innovation around patient support, counseling, and education can facilitate adherence, management of side effects, and patient-centered care across the entire cascade.

In this study, we define AI broadly as encompassing statistical learning, machine learning, deep learning, and Large Language Models (15). Through automation and advanced analytical capabilities, AI can support interpretation of complex clinical data streams such as radiological images and genome sequencing data (16,17). AI tools can also integrate with compact medical or personal devices such as handheld ultrasound machines to support clinical decision-making, and smartphones to provide direct patient counselling or record medication adherence, bridging gaps in healthcare delivery in resource-limited settings.

This scoping review aims to map and characterize AI applications across the TB care cascade, describing their data inputs, reported performance, and technological readiness level for clinical use on a standardized scale. We also highlight key research and implementation gaps to inform future development and deployment of AI in global TB control.

2. Methods

The review protocol was registered on the Open Science Framework (OSF) and is available at https://osf.io/wah6d/overview (OSF registration number: wah6d).

2.1. Search Strategy and Study Identification

A literature search was conducted in PubMed for English-language studies published between January 1, 2017 and August 1, 2025. We limited inclusion to studies published from 2017 onward to reflect contemporary AI methodologies and clinical applications relevant to current TB care. Only English-language, peer-reviewed original research articles were included to ensure methodological transparency and feasibility of review. Reviews and non-original publications were excluded to avoid duplication of evidence. PubMed was chosen as it is known to be the largest indexed database of biomedical, peer-reviewed publications.

The search strategy targeted titles containing the following terms: ("tuberculosis," or "TB") and ("artificial intelligence," or "machine learning," or "deep learning," or "neural network," or "AI platform," or "automatic," or "smart pillbox," or "statistical learning," or "machine-learning"). This search yielded 380 unique records. The final search was conducted on August 1, 2025. The full PubMed search strategy, including field tags and limits, is provided in Table S1.

Articles were included if they met all the following criteria:

1) Original research article

2) Describing the development and testing of AI or a related method (as detailed by the search terms above)

3) The AI is intended to improve screening, active case finding, diagnosis, drug resistance diagnosis, treatment monitoring, drug regimen design, or resistance prediction of TB

4) The AI is applied to data derived from human subjects with active tuberculosis (clinical or subclinical, pulmonary with or without extrapulmonary) and an appropriate control population (e.g.

for TB screening: healthy individuals, for TB diagnosis: patients meeting criteria for TB testing but do not have TB, etc.).

Articles were excluded if they met any of the following criteria:

1) Any of the following type of articles: systematic review, scoping review, meta-analysis, editorial, commentary, letter, opinion piece, policy-focused paper

2) Focused primarily on population level incidence or forecasting and did not address individual and direct patient care

3) Analyzed data exclusively from animal or *in vitro* experiments that are not directly derived from human subjects

4) Studied proxy measures without explicit or direct clinical application in one of the four care categories, for example, predicted specific radiographic abnormalities (e.g., pleural effusion) rather than TB/ no-TB diagnosis

5) Focused on a disease other than pulmonary tuberculosis (including studies that focused solely on extrapulmonary TB) or if they compared tuberculosis to a specific other disease rather than the desired general non-TB control group e.g., COPD, pneumonia, HIV-only cohorts, or other non-TB comparator diseases.

2.2. Screening and Selection

Study selection was performed in stages in accordance with PRISMA guidelines (Figure 2). First, duplicates, retracted papers, author corrections, letters to the editor, resource articles, and comments were removed (n=23), resulting in 357 records for title screening. Then two reviewers (ASR and KRVH) independently reviewed titles and abstracts. ASR reviewed abstracts with the support of ChatGPT-4 and a standardized prompt detailing the relevant inclusion and exclusion criteria (Figure S1). The inclusion and exclusion rationale for each paper was manually reviewed and categorized by ASR.

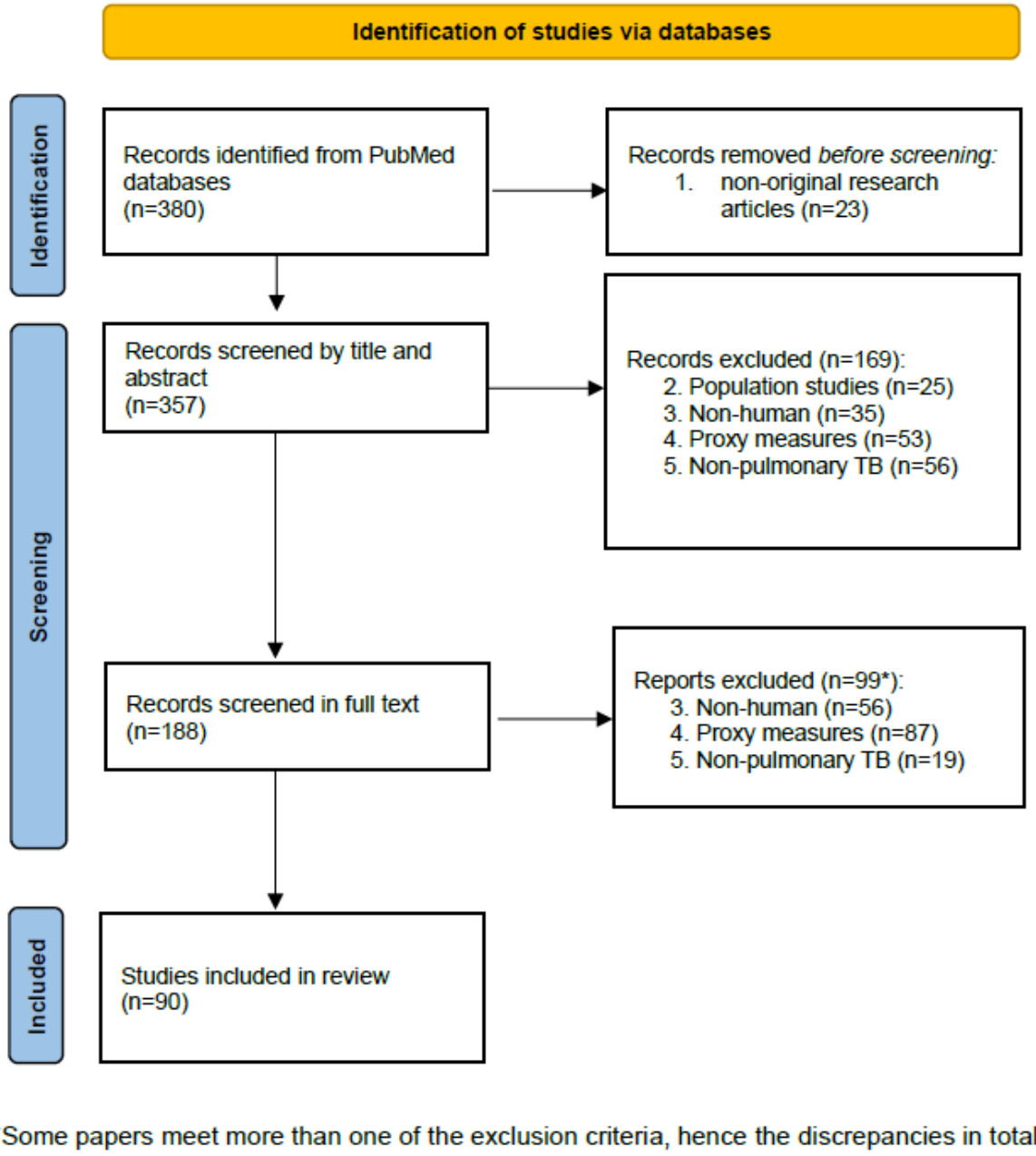


Figure 2. PRISMA flow diagram outlining the number of records identified, screened, excluded (with reasons), and included at each stage. Source: Authors' PRISMA diagram for this scoping review.

2.3. Study Data Extraction

Two reviewers (ASR, KRVH) independently extracted data from each included study. Data extraction forms were piloted on a subset of studies then refined prior to full extraction to ensure consistency and completeness. We captured the following variables: clinical application (screening, diagnosis, treatment monitoring or adherence, regimen design), AI methodology, type and source of input data, patient population and validation setting, sample size (and key subgroups, where relevant), training and/or external validation performance (such as sensitivity, specificity, accuracy, and Area Under the receiver operating characteristic Curve [AUC]), reference standard, stage of AI development, and study identifiers (year, country, setting). Any discrepancies were resolved by consensus. Extracted data were compiled into structured tables to enable comparison of clinical application, performance, and readiness for implementation across studies.

In addition to the metrics extracted above, we assessed each AI based on a standardized Technology Readiness Level (TRL). The TRL enables a semi-quantitative assessment of technological maturity and enables comparison of AI across studies and care categories. We adapted the US Department of Defense biomedical and digital health 8-level TRL scale (18) that ranges from initial scientific discovery (TRL 1) to clinical trial or advanced real-world evidence with full clinical implementation (TRL 8) (Table S2). For summarization and descriptive purposes only, we aggregated internal model performance, external model performance, or TRL across data input types and care categories (Table S3). These aggregates are not meant for clinical use or as endorsement of the accuracy or readiness of the AI tools, but rather as a description of the reported literature. We used Wilcoxon rank-sum tests to compare TRL distributions between groups. Consistent with scoping review methodology, no formal critical appraisal of study quality or risk of bias was conducted; instead, we extracted several quality-related metrics such as sample size, the gold standard metric the AI was compared to, study setting including multi-site setting, whether external validation was performed, and the reported difference in performance between training and external validation (Table S3).

3. Results

3.1. Overview of AI Applications in TB Care

The literature search identified 380 total studies of which 90 met inclusion criteria and from which we extracted study characteristics (Table 1). By care category, studies most commonly focused on the use of AI for TB diagnosis (n=33) and TB screening (n=23) (Table 2A, Table S3). We identified 20 studies focused on treatment monitoring, 11 on drug resistance diagnosis and four on regimen design; one study focused on a combination of care categories (diagnosis and regimen design) (Table 2B, Table S3). By data type, most AI tools interpreted imaging data (n=46; 38 (82%) chest X-ray [CXR]). Fewer studies analyzed other clinical or demographic data, including blood-based laboratory data, or symptom data collected from electronic health records or registries (n=17). Seven studies evaluated microbiological images or markers, six evaluated host or pathogen omic/molecular data, three clinical audio recordings, and in three there was direct patient interaction. Eight other studies used multimodal data sources, with some combining imaging with clinical variables. The cumulative sample size across all studies was 803,383, with a median sample size per study of 898.5 (IQR: 2,045, range 50-243,726) (Table S3). Technology readiness levels (TRLs) were used as a descriptive proxy for the maturity of AI tools. Across TB care categories, TRLs ranged from 4 to 8, with the most mature tools being concentrated in screening and diagnosis (Figure 3), whereas drug resistance diagnosis, regimen design, and monitoring applications showed greater variability and lower TRLs. Imaging-based tools for screening and diagnosis have higher median and upper-range TRLs than models relying on other input data types (Wilcoxon rank sum test, p=0.02, Figure 3).

Table 1. Summary of included studies evaluating AI tools for TB care. For each study, the table details the clinical category (screening, diagnosis, drug resistance diagnosis, treatment monitoring or adherence, and regimen design), and the type of input data. Source: Authors' compilation based on the 90 studies included in the scoping review.

Study category	**Study Count**	**Input Data Type**							References
		Imaging	Clinical Variables*	Micro	Pathogen or host Omics	Audio	Patient Facing	Multi-modal**	
Screening	**23**	17	2	-	-	3	-	1	(20,27–29,48–66)
Diagnosis	**33**	24	2	6	1	-	-		(19,26,45,67–96)
Drug Resistance Diagnosis	**11**	3	2	1	2	-	-	3	(16,46,97–107)

Monitoring (Outcome)	**12**	1	6	-	2	-	-	3	(17,47,106–115)
Monitoring (Adherence)	**8**	-	5	-	-	-	3	-	(42–44,116–120)
Regimen Design	**4**	2	-	-	1	-	-	1	(95,121–123)
Total Studies	**90*** **	46	17	7	6	3	3	8	

* Symptom data, electronic health record data, blood-based laboratory testing data. **Multimodal indicates studies that combined two or more data types (e.g. imaging and clinical variables). ***Sums for categories and data types exceed total studies due to overlapping classifications of study categories (one study classified as diagnosis and regimen design).

Table 2. AI Tools summarized by care category, data input, AI model, country, performance (AUC, external AUC), and technology readiness level (TRL). (A) AI Tools for TB screening and diagnosis. (B) AI Tools for TB drug resistance diagnosis, monitoring, and regimen design.

(A)								
Category	**Data Input**	**Specific Input**	**AI Tool Name**	**Country**	**AUC**	**Ext AUC**	**TRL**	**Ref**
Diagnosis	Clinical variables	Demographic + blood data	RF + ANN	Multi-country	1	0.946	6	(67)
		Blood data	RF (conditional)	China	0.978	0.963	6	(68)
	Imaging	CXR	JF CXR-1 v2	China	-	0.98	7	(26)
			qXR v3.2	India	0.944	-	5	(82)
			U-Net (DL)	-	-	0.91	6	(96)
			DL (custom, Google)	Multi-country	-	0.89	7	(72)
			CNN	China, USA	0.87	-	5	(70)
			EfficientNetV2 CAD	Taiwan, China, USA	0.878	0.806	6	(75)
			qXR v2	India	0.81	-	5	(78)
			CheXaid	South Africa	0.83	0.71	6	(93)
			HaMLET	Multi-country	0.97	0.94	6	(81)
			DLAD	Multi-country	0.988	0.977	6	(77)
			ResNet50 (DL)	South Korea	0.98	0.815	6	(92)
			LUNIT INSIGHT v3.1	Pakistan	0.85	-	7	(69)

			Lunit INSIGHT CXR v3	South Korea	0.924	-	5 (83)
			TB-CAD	South Korea	0.85	-	5 (80)
			EfficientNetB4	India	-	-	5 (76)
			EfficientNetB3	Multi-country	-	-	5 (73)
			EfficientNet-DNN	South Korea	-	0.82	6 (90)
			EfficientNetB4-CNN	India	0.975	0.665	6 (89)
		CT	SVM (GA-optimized)	Multi-country	-	-	5 (71)
			Attention-ResNet	China	0.97	-	5 (74)
			3D ResNet-50	China	0.992	0.946	6 (91)
			U-Net (DL)	China	0.98	-	5 (79)
			DL (custom pipeline)	China	0.971	-	6.5 (94)
			DeepTB	China	0.943	-	5 (95)
	Micro-biological	Sputum	MiniLab TB assay	China	-	-	5 (88)
		Microscopy images	ANN	Mexico	1	-	4 (86)
			Depth-wise CNN	Brazil	-	-	5 (84)
		Digital pathology	TB-AI	China	-	-	4 (45)
			Modified EfficientNet	Taiwan	-	-	6 (87)
		Histopathology	HALO AI	Japan	-	-	5 (85)
	Omics data	Metabolomics + clinical data	RF, SVM, MLP	China	-	-	5 (19)
Screening	Clinical (audio)	Cough sound	LR (MFCC-based)	South Africa	0.94	-	6.5 (50)
			CNN	South Africa	0.95	-	4 (48)
			Swaasa AI	India	0.94	0.9	7 (49)
	Clinical variables	Symptoms + demographics	CDSS	Brazil	0.79	-	5 (51)

		EHR	RF (risk model)	Switzerland, Austria	0.72	0.67	5.5	(52)
	Imaging	CXR	DL (Google Teachable Machine)	Taiwan	-	0.951	5	(61)
			qXR v3/v4	Peru	-	0.78	7	(59)
			ResNet (normalization-free)	Multi-country	0.993	-	5.5	(55)
			F-CAD	Cambodia	-	0.86	7	(56)
			Genki (DeepTek)	India	-	-	7	(65)
			ResNet- DCNN	China	0.994	-	6.5	(54)
			CAD4TB v5	Zambia	-	0.87	7	(64)
			qXR v2; CAD4TB v6	Pakistan	-	0.92	8	(27)
			XmarTB	Public/China	-	-	5	(62)
			qXR v3	Nigeria	-	-	7	(58)
			DLAD	South Korea	-	0.999	6.5	(60)
			qXR-based AI	Nepal	-	-	6.5	(57)
			JF CXR-1 v2	China	-	0.978	7	(28)
			CAD4TB v6/ v7	South Africa, Lesotho	-	0.865	7	(63)
			Multiple CAD tools	Bangladesh	-	0.908	7	(29)
			Multiple CAD tools	Nepal, Cameroon	-	0.94	6.5	(66)
			AI4TB	Nepal	0.72	-	5.5	(53)
	Imaging + clinical	CXR + clinical data	CNN (demographic)	South Korea	-	0.971	5	(20)

(B)

Category	**Data Input**	**Specific Input**	**AI Tool Name**	**Country**	**AUC**	**Ext AUC**	**TRL**	**Ref**
Drug resistance diagnosis	Clinical variables	EHR	XGB, RF, SVM, Adaboost, LR, kM	Brazil	0.888	-	5.5	(98)
		Epidemiological data	ANN	Moldova	0.87	-	4	(97)
	Imaging	CXR	Ens- DL	Multi-country	0.951	-	5	(99)
			Ens-DL (AMIS)	Multi-country	0.889	-	5.5	(100)
		CT	Patch-CNN + SVM	Multi-country	-	-	4	(46)
	Imaging + clinical	CXR + clinical data	SVM	Multi-country	0.784	-	5	(102)
		CT scan + demographics	Radiomics	China	0.881	0.834	6	(101)
			Multimodal fusion	China	0.899	-	5.5	(103)

	Micro-biological	Xpert Ultra (Tm profiles)	Tm-Dist	Multi-country	-	-	5	(104)
	Omics	WGS-derived resistance	GenTB	Multi-country	-	0.94	6	(16)
	Omics + clinical	WGS SNPs + clinical data	LR, GBC, XGB	Uganda	0.95	0.63	5	(105)
Monitoring (Outcome)	Clinical variables	Symptoms + demographics	ANN, SVM, kNN, RF, DT	Multi-country	-	-	5	(111)
		Demographics + blood data	RF, SGB, CART, MARS	Multi-country	0.808	-	5.5	(112)
		Registry data	Landmark+ RF	Moldova	-	-	5	(109)
		Clinical trial data	DT, RF, SVM, NB	India	0.909	-	5	(110)
		EHR	DT	South Africa	-	-	5	(113)
			XGB, RF, MLP, LGBM, LR, SVM	Taiwan	0.834	-	5	(108)
	Imaging	CT	PM1-3	China	0.815	0.735	6	(106)
	Imaging + clinical	Chest X-ray + clinical data	DL (DeepCatch-X-TB v1)	South Korea	-	-	5	(114)
			Ens- DL (DenseNet121)	Multi-country	0.86	0.714	5.5	(17)
		CT + demographics	RF	China	0.913	0.815	6	(107)
	Omics data	Metabolomics + clinical data	kNN	China	0.87	-	4	(115)
		Proteomics	SVM- MMC	China	-	-	4	(47)
Monitoring (Treatment adherence)	Clinical variables	Registry data	SVM, AdaBoost, RF, ANN, LR	Uganda	0.87	-	5	(117)
		Epidemiological data	LGBM	Brazil	0.72	-	5	(116)
		Demographic + blood data	RF, SVM, ANN	Pakistan	-	-	5	(118)
		EHR	RF, ANN, NB, kNN, LR	Indonesia	0.808	-	5.5	(120)
			LR (risk model)	Ethiopia	0.78	-	5	(119)
	Patient-facing	Video- based ingestion	3D-ResNet	Uganda	0.87	-	4	(42)
		Dispensation events	STAMP	India	-	-	6.5	(43)
		Device datalog	EvriMED	Ethiopia	-	-	7	(44)
Regimen Design	Imaging	CT	DeepTB	China	0.943	-	5	(95)
		CXR	TB- DR CDSS	Multi-country	0.947	-	6	(121)
	Imaging + clinical	CXR + clinical data	DL-Risk	China	0.7	0.77	5	(95)
	Omics data	WGS-derived resistance	TR- CDSS	South Africa	-	-	6	(123)

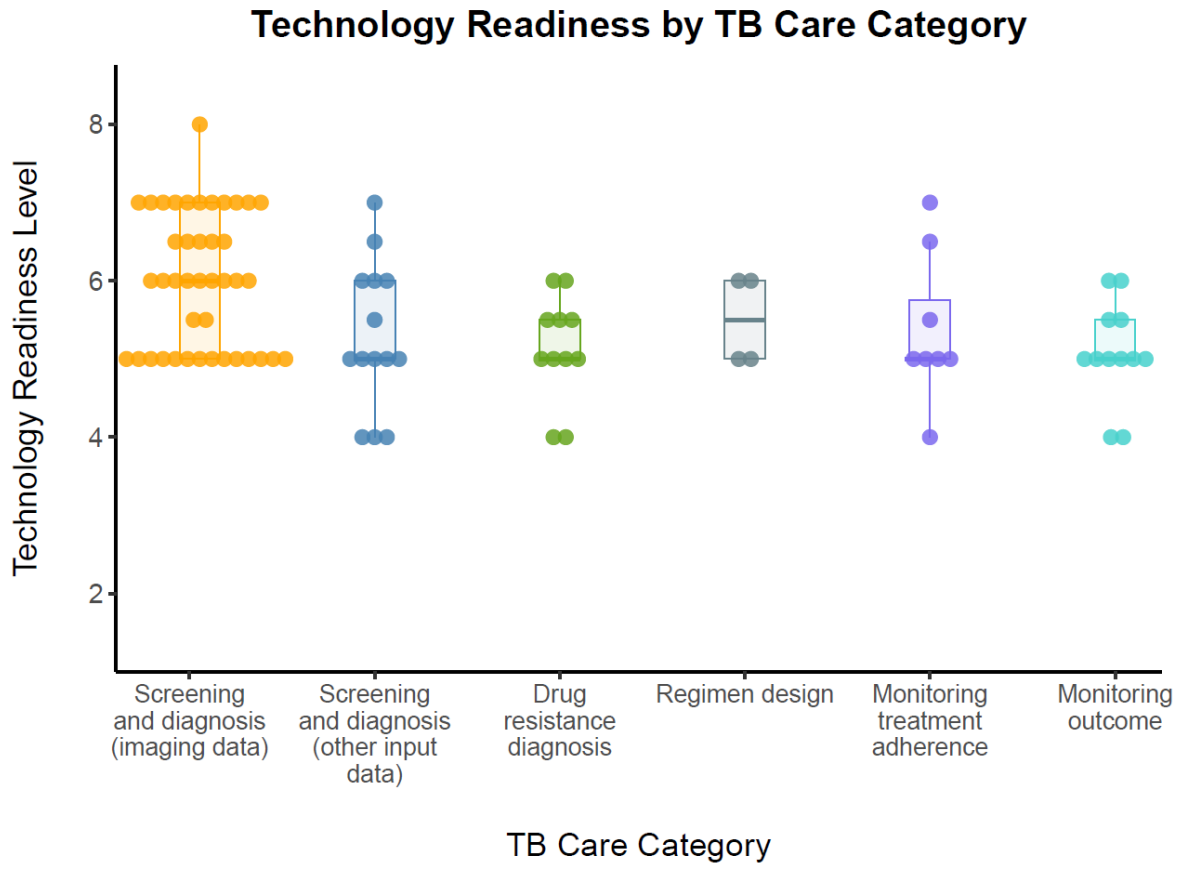


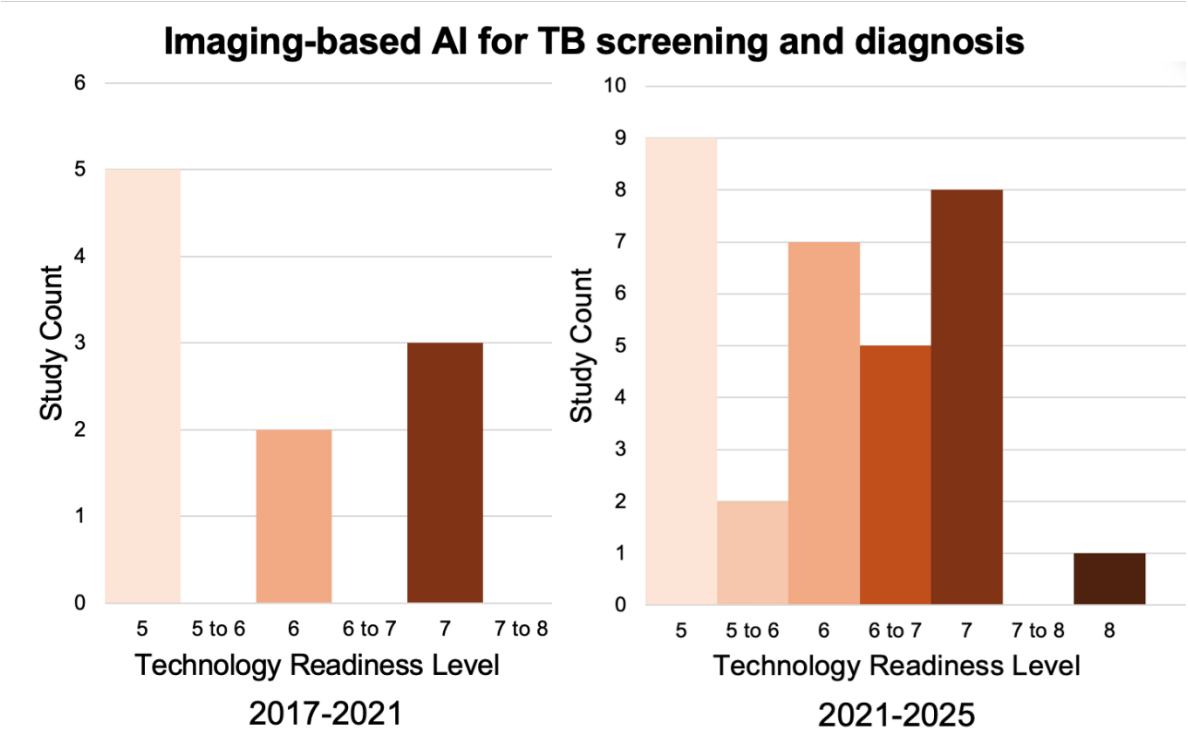
Figure 3. Technology readiness level by TB care category. Swarm plot of technology readiness levels for individual AI tools, grouped by TB care category. Each dot represents a single tool; vertical position indicates its technology readiness level, and horizontal jitter is added to reduce overlap of points within each category. Source: Authors' analysis of technology readiness levels for 90 AI tools identified in the scoping review.

3.2. Screening and Diagnosis

Overview and input data: Studies of AI-based screening and diagnosis (n=56) primarily analyzed CXR images (n=35) and, less commonly, computed tomography (CT) scan images (n=6). Other data input types included microbiological data (n=6), clinical variables (n=4), and cough/audio recordings (n=3); one study utilized patient omics data (19) and one study integrated clinical variables with imaging to boost accuracy (20). AI TB diagnosis and screening are benchmarked against microbiology (culture and/or GeneXpert, n= 19), expert clinician assessment (including radiologists or pathologists, n=18) or a predefined composite microbiological and clinical criterion (n=19). Imaging-based studies typically report large sample sizes, some exceeding 150,000 participants, with a median study size of 1,780 (IQR 8,828, range 100-168,012) for internal training and validation, and 1,173 (IQR 5,528, range 36-25,598) for external validation (Table S3).

Performance and external validation: Reported accuracy, sensitivity, and specificity were high for diagnostic imaging studies on internal training and validation (AUC 0.94 [IQR 0.12, range 0.81-0.99], sensitivity 92% [IQR 10.2, range 67-100], and specificity 93% [IQR 17.1, range 64.3-98.7]). 58.5% of diagnostic or screening imaging studies reported model external validation (Figure 4A). Performance for diagnostic imaging studies on external validation was lower but still high (AUC 0.89 [IQR 0.14, range 0.66-0.98], sensitivity 90% [IQR 7, range 19-100], and specificity 85% [IQR 29, range 26-100]). A similar trend is noted for all screening studies (all data modalities), where the median AUC for training data was 0.94 (IQR 0.21, range 0.72-0.99), compared with 0.91 (IQR 0.10, range 0.67-1.00) for external validation.

(A)



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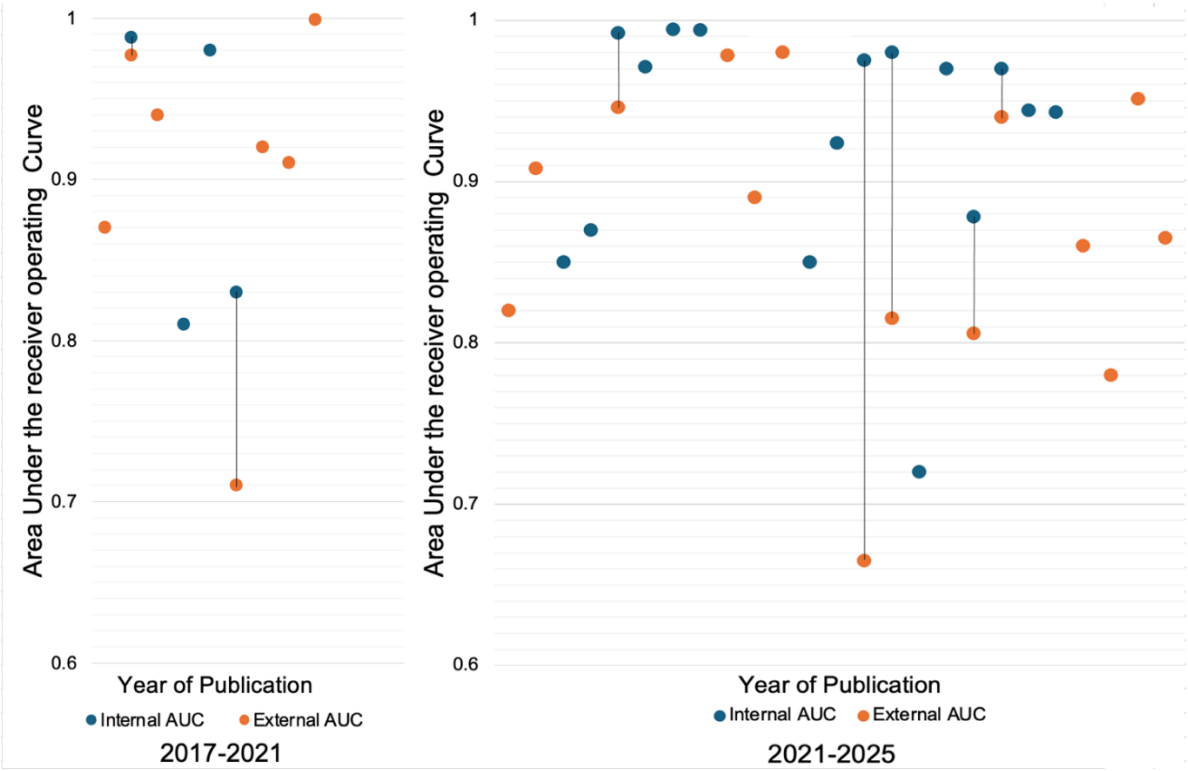

Figure 4. Imaging-based AI Tools for TB screening and diagnosis. Panel A shows technology readiness level (TRL) by publication year for AI tools interpreting imaging data. **Panel B** shows reported area under the curve (AUC) by year of publication; internal validation AUCs are in blue and external validation AUCs in orange. Vertical lines connect internal-external pairs from the same study, illustrating changes in performance between internal and external evaluation over time.

Technology readiness: The median TRL for screening and diagnostic imaging studies is 6 (IQR 1.5, range 5-8), with several commercial CXR AI platforms (e.g., CAD4TB, qXR, Lunit INSIGHT CXR) reaching TRL 7-8 and being prospectively evaluated and implemented in high-burden, real-world

settings. In contrast, clinical, omics, and microbiological AI screening and diagnostic studies are relatively immature (median TRL = 5, IQR 1.25, range 4-7). Median TRLs for imaging studies increased between the early publication period (January 2017-June 2021) and the later period (July 2021-August 2025) (Wilcoxon rank-sum test, p=0.003, Figure 4B).

Key gaps: The studies identified in the review report training of AI for TB diagnosis and screening in a limited number of countries (20 distinct countries), raising concerns about the generalizability to other contexts. Deployment of imaging AI relies on digital capture of chest radiography, which is currently limited in very low resource settings.

3.3. Regimen Design: Drug Resistance Diagnosis

Overview and input data: The 11 studies in this domain aim to diagnose resistance either to individual drugs (n=4) or classify the patient's presentation into one of several drug resistance classes e.g., drug-susceptible (DS), MDR or extensively drug-resistant (XDR) (n=7). The tools use pathogen whole-genome-sequencing (WGS) (n=2) or PCR probe melting temperatures (n=1) that detect pathogen DNA mutations as input for predicting individual drug resistance profiles. Other studies used radiography: CXR (n=3) and CT scan (n=3), of which three studies combined imaging with clinical data to classify presentation into resistance classes; two studies used only clinical variables at presentation (n=2). The reference standard is phenotypic drug susceptibility testing (DST) (n=11), with others also using Sanger sequencing (n=1) or comparison with other tools (TB-Profiler and Mykrobe) (n=1). The median study sample size for training was 540 (IQR 2,050, range 33-5,039).

Performance and external validation: Performance metrics indicate moderate to good accuracy in internal validation, with median AUC of 0.89 (IQR 0.04, range 0.78-0.95). For the three of the 11 models with external validation, the median AUC was 0.83 (IQR 0.31, range 0.63-0.94).

Technology readiness: Most AI models for drug resistance diagnosis are in the clinical validation phase, with a median TRL of 5 (IQR 0.5, range 4-6). No tools have achieved regulatory approval or broad adoption, but some demonstrate high accuracy in large-scale external validation efforts (e.g., GenTB externally validated on 20,403 patient isolates with an AUC of 0.94 [**Table S3**]), indicating readiness for clinical deployment in select contexts.

Key gaps: Gaps include limited causal formulation of the AI tasks. This can limit the identification of fit-for-task data for building generalizable models (e.g., CXR alone is unlikely to be sufficiently discriminatory for drug resistance diagnosis given it can only capture lung disease severity). Drug-resistant TB bacteria differ from susceptible bacteria by a few mutations, and these mutations have very limited or subtle effects on pathogenesis (21). Another related gap is limited external validation, including across geographic settings where resistance frequencies and TB genotypes vary.

3.4. Regimen Design: Regimen Composition

Overview and input data: Only a handful of studies met criteria for inclusion into this care category (n=4) and all have been published since 2020. These studies aimed to use AI to synthesize clinical, microbiological, and genomic data (e.g., WGS-based resistance profiles) to propose individualized drug regimens, with two specifically for MDR-TB. Three of these tools benchmark against laboratory gold standards (DST, microbiological, or molecular confirmation), whilst clinical decision support systems (CDSS) benchmark AI recommendations against clinician-designed regimens to support expert decision-making, especially in resource-limited settings. Studies reported a wide range of sample sizes, with a median study size of 1,228 (IQR 3,546, range 20-7,008).

Performance and external validation: Median internal AUC was 0.94 (IQR 0.25, range 0.70-0.95), with external validation performed in two studies. Among these, only one study reported performance in external validation (AUC 0.77).

Technology readiness: Similar to drug resistance diagnosis, the median TRL is 5.5 (IQR 1, range 5-6) indicating that technology is still in the prototype phase and requires clinical validation.

Key gaps: The identified regimen design models are limited by predominantly retrospective or prototype evaluations with minimal multi-country prospective external validation, and reliance on specific imaging/genomic datasets that may not generalize to diverse or low resource clinical settings.

3.5. Treatment Monitoring (Outcome & Adherence)

Overview and input data: The identified AI tools (n=12) used clinical variables (n=6), omics data (n=2), imaging data (n=1), or multimodal inputs combining imaging and clinical variables (n=3) to estimate cure, failure, relapse, mortality, or adverse reactions. Adherence-focused tools (n=8) used baseline clinical characteristics (typically from registry data) or digital adherence technologies (e.g., smart pillboxes, video observed therapy) to predict or detect non-adherence, respectively. The goal is to improve adherence in a personalized way and improve treatment outcomes. Median sample size was 790 (IQR 1,650, range 114-17,958) and 678 (IQR 2,388, range 100-243,726) for outcome and adherence prediction studies, respectively. The largest study by Rodrigues et al. (2024) predicted low adherence using a large national TB registry cohort (243,726 cases) relying on 8 baseline predictors, primarily comprising basic sociodemographic and self-reported clinical variables.

Performance and external validation: For internal validation, outcome prediction AI tools had a median AUC of 0.86 (IQR 0.09, range 0.81-0.91), and a median sensitivity and specificity of 89% (IQR 20, range 69-96) and 83% (IQR 21, range 70-93), respectively. Three of these 12 models underwent external validation, and the median AUC for external validation was lower at 0.74 (IQR 0.05, range 0.71-0.82). Adherence prediction tools had a median AUC of 0.81 (IQR 0.12, range 0.72-0.87), with none of the tools externally validated.

Technology readiness: Outcome models had a median TRL of 5 (IQR 0.5, range 4-6), typically reflecting analytical or retrospective validation. Adherence-monitoring tools similarly had a median TRL of 5 (IQR 1, range 4-7), with some tools (e.g., EvriMED smart pillbox) piloted in operational settings (TRL 7).

Key gaps: In contrast to outcome models, no adherence models were externally validated. Adherence models are largely developed and evaluated retrospectively, with limited external generalizability; additional research is needed to assess real-world utility and integration into existing care pathways.

4. Discussion

This scoping review demonstrates that AI applications in TB care are advancing rapidly but unevenly across the care cascade. AI tools for TB screening and diagnosis, particularly CXR interpretation, are comparatively mature, while applications addressing drug resistance diagnosis, regimen design, treatment monitoring, and adherence remain at earlier stages of development. This pattern mirrors broader trends in clinical AI, where image-based diagnostic tasks have progressed more quickly than tools designed to support longitudinal care and complex clinical decision-making (22). The dominance of diagnostic imaging applications also reflects structural advantages common to radiology-focused AI: Imaging data are standardized, reference standards are well defined, and tasks such as disease classification or triage are narrowly scoped (23). This has led to faster performance gains, more external validation, and earlier clinical adoption than AI applications that aim to predict treatment outcomes, guide therapy selection, or support adherence. The latter require integration of heterogeneous and longitudinal data, which are capabilities that remain challenging for current AI approaches and implementation in practice (24,25).

Within TB care, and more generally within AI decision support in healthcare, AI-based CXR interpretation represents a notable success story. Several tools have achieved high performance, undergone external validation, and been deployed in real-world, high-burden settings (26–30). Importantly, this progress has been driven not only by algorithmic innovation but also by coordinated investments in data infrastructure and evaluation. The FIND-led AI4Health initiative, which created large, curated, and geographically diverse AI-ready datasets for CXR-based TB diagnosis, exemplifies how standardized, high-quality data can accelerate both development and

clinical validation (31). By enabling benchmarking, external validation, and regulatory engagement, this effort has helped move CXR AI from proof-of-concept to implementation.

Our findings also underscore the limitations of concentrating AI innovation primarily on diagnosis and screening. Improvements in case detection alone are unlikely to achieve substantial population-level impact if downstream challenges (such as inappropriate regimen selection, undetected drug resistance, poor adherence, or delayed recognition of treatment failure) persist (32). Many of the largest gaps in the TB care cascade occur after diagnosis, particularly in settings with constrained laboratory capacity and limited clinical follow-up resources (33).

This review has highlighted that the relative immaturity of AI tools outside diagnosis and screening is linked to the lack of benchmarks and AI-ready datasets for these tasks. We found the few models for regimen design or treatment monitoring were trained on small or single-center, context-specific datasets, and had limited external validation, modest technology readiness levels, and uncertain generalizability (34,35). This stands in contrast to diagnostic imaging, where purpose-built datasets and benchmarks have enabled rapid iteration and comparison across tools. The success of CXR AI suggests that similar investments in AI-ready datasets and benchmarks could substantially accelerate progress in other domains of TB care. For example, globally representative datasets, e.g., from clinical trials, linking pathogen whole-genome sequencing, phenotypic DST, treatment regimens, and outcomes would support more robust resistance prediction and regimen optimization models (36,37). Likewise, longitudinal datasets integrating clinical variables, microbiological results, digital adherence technologies, and patient-reported outcomes could enable more effective AI tools for treatment monitoring and adherence support (38). Without such coordinated data efforts, advances in model architecture alone are unlikely to overcome current translational barriers.

Several additional cross-cutting gaps emerged across the TB AI literature. External validation remains inconsistent outside imaging-based diagnosis, raising concerns about robustness across diverse epidemiological and health system contexts (34). Also, we note a measurable drop in performance between internal and external validation across all care domains. TB is a heterogeneous disease, with clinical presentation and risk profiles shaped by local epidemiologic and health system factors (39,40). This heterogeneity may underlie the performance drop in external validation (39,40). As such, future development and evaluation of tools should prioritize robust multi-country validation prior to broader implementation, to ensure that performance estimates are reliable and that tools are appropriately tailored to diverse contexts. Many models rely on correlational features with limited causal relevance, particularly for resistance and outcome prediction (41). Our search did not identify studies that yet leverage LLM- or chatbot-based tools for patient monitoring or support. Recently, such tools have appeared promising in other chronic illnesses, including mental health; we identify this as an area of potential growth for AI in TB care (42–44). In addition, few studies assess integration into clinical workflows or evaluate downstream effects on patient outcomes or health system performance (45–48). These limitations are well recognized in clinical AI more broadly but are particularly consequential for TB, where failures at any stage of care directly contribute to transmission, resistance amplification, and mortality.

This scoping review has several limitations. We focused our search on PubMed to efficiently capture a comprehensive set of high-quality, peer-reviewed biomedical studies; while this approach focused the search, it is possible that additional studies indexed in other databases were not identified. We included only English-language publications, which may have limited representation of non-English literature. Abstract screening was assisted by ChatGPT-4, which helped streamline the review process, although all final selections were carefully reviewed manually. Finally, consistent with scoping review methodology, no formal exclusion was made based on critical appraisal or risk-of-bias assessment. However, we do describe several key quality metrics including sample size, gold standard metric, setting of the study and the conduct of external validation, which helped assess gaps and future directions in this area.

5. Conclusions and Implications

In conclusion, this scoping review suggests that the next phase of AI innovation in TB should move towards tools that address the full care cascade. The experience of AI-based CXR interpretation demonstrates what is possible when high-quality data, rigorous validation, and implementation pathways are aligned. Extending this model, especially through the development of AI-ready datasets for non-diagnostic tasks, represents a promising opportunity to accelerate clinically meaningful AI applications and support progress towards WHO End TB goals.

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Abbreviations

Model types and methods: AI indicates artificial intelligence; ML, machine learning; DL, deep learning; ANN, artificial neural network; CNN, convolutional neural network; DNN, deep neural network; MLP, multilayer perceptron; RF, random forest; DT, decision tree; CART, classification and regression tree; LR, logistic regression; SVM, support vector machine; NB, naïve Bayes; kNN, k-nearest neighbor; GBM, gradient boosting machine; XGB, extreme gradient boosting (XGBoost); LGBM, light gradient boosting machine; AdaBoost, adaptive boosting; Ens-DL, ensemble deep learning.

Imaging: CXR, chest radiograph; CT, computed tomography; DLAD, deep-learning-based automatic detection; U-Net, U-shaped convolutional neural network; ResNet, residual neural network; DenseNet, densely connected convolutional neural network; EfficientNet, efficient convolutional neural network family.

Data types: EHR, electronic health record; WGS, whole-genome sequencing; SNP, single-nucleotide polymorphism.

Performance and development: AUC, area under the receiver-operating-characteristic curve; Ext AUC, external-validation AUC; TRL, technology readiness level.

Clinical systems: CDSS, clinical decision support system; TB-DR, tuberculosis drug resistance.

References

1. World Health Organization. Global Tuberculosis Report 2023. 1st ed. Geneva: World Health Organization; 2023. 1 p.
2. Okhovat-Isfahani B, Bitaraf S, Mansournia MA, Doosti-Irani A. Inequality in the global incidence and prevalence of tuberculosis (TB) and TB/HIV according to the human development index. Med J Islam Repub Iran. 2019 May 22;33:45. https://doi.org/10.34171/mjiri.33.45 PubMed PMID: 31456969; PubMed Central PMCID: PMC6708111.
3. Menzies NA, Gomez GB, Bozzani F, Chatterjee S, Foster N, Baena IG, et al. Cost-effectiveness and resource implications of aggressive action on tuberculosis in China, India, and South Africa: a combined analysis of nine models. Lancet Glob Health. 2016 Nov 1;4(11):e816–26. https://doi.org/10.1016/S2214-109X(16)30265-0
4. Menzies NA, Brown TS, Imai-Eaton JW, Dodd PJ, Cohen T, Martinez L. Potential paediatric tuberculosis incidence and deaths resulting from interruption in programmes supported by international health aid, 2025-34: a mathematical modelling study. Lancet Child Adolesc Health. 2025 Nov;9(11):787–95. https://doi.org/10.1016/S2352-4642(25)00218-4 PubMed PMID: 40953585.
5. WHO. Implementing the end TB strategy: the essentials [Internet]. Geneva: World Health Organization; 2015 [cited 2025 Jul 11]. 113 p. Available from: https://iris.who.int/handle/10665/206499
6. Marley G, Zou X, Nie J, Cheng W, Xie Y, Liao H, et al. Improving cascade outcomes for active TB: A global systematic review and meta-analysis of TB interventions. PLOS Med. 2023 Jan 3;20(1):e1004091. https://doi.org/10.1371/journal.pmed.1004091 PubMed PMID: 36595536; PubMed Central PMCID: PMC9847969.
7. van Zyl C, Badenhorst M, Hanekom S, Heine M. Unravelling 'low-resource settings': a systematic scoping review with qualitative content analysis. BMJ Glob Health. 2021 Jun 3;6(6):e005190.

https://doi.org/10.1136/bmjgh-2021-005190 PubMed PMID: 34083239; PubMed Central PMCID: PMC8183220.

8. Yayan J, Franke KJ, Berger M, Windisch W, Rasche K. Early detection of tuberculosis: a systematic review. Pneumonia Nathan Qld. 2024 Jul 5;16(1):11. https://doi.org/10.1186/s41479-024-00133-z PubMed PMID: 38965640; PubMed Central PMCID: PMC11225244.
9. Halabi JE, Palmer N, McDuffie M, Golub JJ, Fox K, Kohane I, et al. Measuring health-care delays among privately insured patients with tuberculosis in the USA: an observational cohort study. Lancet Infect Dis. 2021 Aug 1;21(8):1175–83. https://doi.org/10.1016/S1473-3099(20)30732-5 PubMed PMID: 33770534.
10. Parsons LM, Somoskövi Á, Gutierrez C, Lee E, Paramasivan CN, Abimiku A, et al. Laboratory Diagnosis of Tuberculosis in Resource-Poor Countries: Challenges and Opportunities. Clin Microbiol Rev. 2011 Apr;24(2):314–50. https://doi.org/10.1128/CMR.00059-10 PubMed PMID: 21482728; PubMed Central PMCID: PMC3122496.
11. Khoshnood S, Goudarzi M, Taki E, Darbandi A, Kouhsari E, Heidary M, et al. Bedaquiline: Current status and future perspectives. J Glob Antimicrob Resist. 2021 Jun 1;25:48–59. https://doi.org/10.1016/j.jgar.2021.02.017
12. Barilar I, Fernando T, Utpatel C, Abujate C, Madeira CM, José B, et al. Emergence of bedaquiline-resistant tuberculosis and of multidrug-resistant and extensively drug-resistant Mycobacterium tuberculosis strains with rpoB Ile491Phe mutation not detected by Xpert MTB/RIF in Mozambique: a retrospective observational study. Lancet Infect Dis. 2024 Mar;24(3):297–307. https://doi.org/10.1016/S1473-3099(23)00498-X PubMed PMID: 37956677.
13. Auer C, Gupta A, Malbacius C, Ghafoor A, Kock Y, Medvedieva O, et al. Savings from the introduction of BPaL and BPaLM regimens at the country level. IJTLD OPEN. 2024 Jul 1;1(7):314–9. https://doi.org/10.5588/ijtldopen.24.0213 PubMed PMID: 39035434; PubMed Central PMCID: PMC11257096.
14. Horne DJ, Royce SE, Gooze L, Narita M, Hopewell PC, Nahid P, et al. Sputum Monitoring during Tuberculosis Treatment for Predicting Outcome: A Systematic Review and Meta-analysis. Lancet Infect Dis. 2010 Jun;10(6):387–94. https://doi.org/10.1016/S1473-3099(10)70071-2 PubMed PMID: 20510279; PubMed Central PMCID: PMC3046810.
15. Harshit B, Shailaja N. The Role of Artificial Intelligence in Enhancing Decision-Making Across Industries. 2025.
16. Gröschel MI, Owens M, Freschi L, Vargas R, Marin MG, Phelan J, et al. GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. Genome Med. 2021 Aug 30;13(1):138. https://doi.org/10.1186/s13073-021-00953-4
17. Ghanem M, Srivastava R, Ektefaie Y, Hoppes D, Rosenfeld G, Yaniv Z, et al. Tuberculosis disease severity assessment using clinical variables and radiology enabled by artificial intelligence. medRxiv : the preprint server for health sciences. United States; 2025. p. 2024.08.19.24311411. https://doi.org/10.1101/2024.08.19.24311411 PubMed PMID: 39228708; PubMed Central PMCID: PMC11370523.
18. Medical Countermeasures | TECHNOLOGY READINESS LEVELS (TRLs) FOR MEDICAL COUNTERMEASURE PRODUCTS (DIAGNOSTICS AND MEDICAL DEVICES) [Internet]. [cited 2025 Dec 9]. Available from: https://medicalcountermeasures.gov/trl/trls-for-medical-devices
19. Hu X, Wang J, Ju Y, Zhang X, Qimanguli W, Li C, et al. Combining metabolome and clinical indicators with machine learning provides some promising diagnostic markers to precisely detect smear-positive/negative pulmonary tuberculosis. BMC Infect Dis. 2022 Aug 25;22(1):707. https://doi.org/10.1186/s12879-022-07694-8 PubMed PMID: 36008772; PubMed Central PMCID: PMC9403968.
20. Heo SJ, Kim Y, Yun S, Lim SS, Kim J, Nam CM, et al. Deep Learning Algorithms with Demographic Information Help to Detect Tuberculosis in Chest Radiographs in Annual Workers' Health Examination Data. Int J Environ Res Public Health. 2019 Jan 16;16(2). https://doi.org/10.3390/ijerph16020250 PubMed PMID: 30654560; PubMed Central PMCID: PMC6352082.

21. Farhat M, Cox H, Ghanem M, Denkinger CM, Rodrigues C, Abd El Aziz MS, et al. Drug-resistant tuberculosis: a persistent global health concern. Nat Rev Microbiol. 2024 Oct;22(10):617–35. https://doi.org/10.1038/s41579-024-01025-1
22. Ogut E. Artificial Intelligence in Clinical Medicine: Challenges Across Diagnostic Imaging, Clinical Decision Support, Surgery, Pathology, and Drug Discovery. Clin Pract. 2025 Sep;15(9):169. https://doi.org/10.3390/clinpract15090169
23. Pesapane F, Codari M, Sardanelli F. Artificial intelligence in medical imaging: threat or opportunity? Radiologists again at the forefront of innovation in medicine. Eur Radiol Exp. 2018 Oct 24;2(1):35. https://doi.org/10.1186/s41747-018-0061-6
24. Bajwa J, Munir U, Nori A, Williams B. Artificial intelligence in healthcare: transforming the practice of medicine. Future Healthc J. 2021 Jul;8(2):e188–94. https://doi.org/10.7861/fhj.2021-0095 PubMed PMID: 34286183; PubMed Central PMCID: PMC8285156.
25. Curth A, Peck RW, McKinney E, Weatherall J, van der Schaar M. Using Machine Learning to Individualize Treatment Effect Estimation: Challenges and Opportunities. Clin Pharmacol Ther. 2024 Apr;115(4):710–9. https://doi.org/10.1002/cpt.3159 PubMed PMID: 38124482.
26. Yang Y, Xia L, Liu P, Yang F, Wu Y, Pan H, et al. A prospective multicenter clinical research study validating the effectiveness and safety of a chest X-ray-based pulmonary tuberculosis screening software JF CXR-1 built on a convolutional neural network algorithm. Front Med. 2023;10:1195451. https://doi.org/10.3389/fmed.2023.1195451 PubMed PMID: 37649977; PubMed Central PMCID: PMC10463041.
27. Khan FA, Majidulla A, Tavaziva G, Nazish A, Abidi SK, Benedetti A, et al. Chest x-ray analysis with deep learning-based software as a triage test for pulmonary tuberculosis: a prospective study of diagnostic accuracy for culture-confirmed disease. Lancet Digit Health. 2020 Nov 1;2(11):e573–81. https://doi.org/10.1016/S2589-7500(20)30221-1 PubMed PMID: 33328086.
28. Liao Q, Feng H, Li Y, Lai X, Pan J, Zhou F, et al. Evaluation of an artificial intelligence (AI) system to detect tuberculosis on chest X-ray at a pilot active screening project in Guangdong, China in 2019. J X-Ray Sci Technol. 2022;30(2):221–30. https://doi.org/10.3233/XST-211019 PubMed PMID: 34924433; PubMed Central PMCID: PMC9028657.
29. Qin ZZ, Ahmed S, Sarker MS, Paul K, Adel ASS, Naheyan T, et al. Tuberculosis detection from chest x-rays for triaging in a high tuberculosis-burden setting: an evaluation of five artificial intelligence algorithms. Lancet Digit Health. 2021 Sep;3(9):e543–54. https://doi.org/10.1016/S2589-7500(21)00116-3 PubMed PMID: 34446265.
30. Use of computer-aided detection software for tuberculosis screening: WHO policy statement [Internet]. [cited 2026 Feb 12]. Available from: https://www.who.int/publications/i/item/9789240110373
31. Validation Platform for AI-based diagnostic evaluation. FIND [Internet]. [cited 2025 Dec 29]. Available from: https://www.finddx.org/what-we-do/projects/validation-platform-for-ai-based-diagnostic-evaluation/
32. Subbaraman R, Jhaveri T, Nathavitharana RR. Closing gaps in the tuberculosis care cascade: an action-oriented research agenda. J Clin Tuberc Mycobact Dis. 2020 May 1;19:100144. https://doi.org/10.1016/j.jctube.2020.100144
33. Faust L, Naidoo P, Caceres-Cardenas G, Ugarte-Gil C, Muyoyeta M, Kerkhoff AD, et al. Improving measurement of tuberculosis care cascades to enhance people-centred care. Lancet Infect Dis. 2023 Dec 1;23(12):e547–57. https://doi.org/10.1016/S1473-3099(23)00375-4 PubMed PMID: 37652066.
34. Peetluk LS, Ridolfi FM, Rebeiro PF, Liu D, Rolla VC, Sterling TR. Systematic review of prediction models for pulmonary tuberculosis treatment outcomes in adults. BMJ Open. 2021 Mar 2;11(3):e044687. https://doi.org/10.1136/bmjopen-2020-044687 PubMed PMID: 33653759; PubMed Central PMCID: PMC7929865.
35. Liang S, Ma J, Wang G, Shao J, Li J, Deng H, et al. The Application of Artificial Intelligence in the Diagnosis and Drug Resistance Prediction of Pulmonary Tuberculosis. Front Med. 2022 Jul 28;9. https://doi.org/10.3389/fmed.2022.935080

36. Chen Y, Jiang Q, Peierdun M, Takiff HE, Gao Q. The mutational signatures of poor treatment outcomes on the drug-susceptible Mycobacterium tuberculosis genome. eLife. 2023 May 3;12:e84815. https://doi.org/10.7554/eLife.84815 PubMed PMID: 37133242; PubMed Central PMCID: PMC10188106.
37. A data compendium associating the genomes of 12,289 Mycobacterium tuberculosis isolates with quantitative resistance phenotypes to 13 antibiotics. PLoS Biol. 2022 Aug 9;20(8):e3001721. https://doi.org/10.1371/journal.pbio.3001721 PubMed PMID: 35944069; PubMed Central PMCID: PMC9363010.
38. Mohamed MS, Zary M, Kafie C, Chilala CI, Bahukudumbi S, Foster N, et al. The impact of digital adherence technologies on treatment outcomes, adherence, and patient-reported outcomes in tuberculosis: a systematic review and meta-analysis. BMC Infect Dis. 2025 Oct 14;25(1):1314. https://doi.org/10.1186/s12879-025-11503-3
39. Cadena AM, Fortune SM, Flynn JL. Heterogeneity in tuberculosis. Nat Rev Immunol. 2017 Nov;17(11):691–702. https://doi.org/10.1038/nri.2017.69 PubMed PMID: 28736436; PubMed Central PMCID: PMC6247113.
40. Stein CM, Baker AR. Tuberculosis as a complex trait: impact of genetic epidemiological study design. Mamm Genome Off J Int Mamm Genome Soc. 2011 Feb;22(1–2):91–9. https://doi.org/10.1007/s00335-010-9301-7 PubMed PMID: 21104256; PubMed Central PMCID: PMC3043369.
41. Xu Y, Mao Y, Hua X, Jiang Y, Zou Y, Wang Z, et al. Machine learning-based prediction of antimicrobial resistance and identification of AMR-related SNPs in Mycobacterium tuberculosis. BMC Genomic Data. 2025 Jul 12;26(1):48. https://doi.org/10.1186/s12863-025-01338-x
42. Sekandi JN, Shi W, Zhu R, Kaggwa P, Mwebaze E, Li S. Application of Artificial Intelligence to the Monitoring of Medication Adherence for Tuberculosis Treatment in Africa: Algorithm Development and Validation. Jmir Ai. 2023;2(1):e40167. https://doi.org/10.2196/40167 PubMed PMID: 38464947; PubMed Central PMCID: PMC10923555.
43. Jason Charles SC, Anusha K, Mahesh K, Ramasubramanian R, Kaliraj P, Selvaraj V. Enhancing Tuberculosis Treatment Adherence: Evaluating the Efficacy of the Support for Treatment Adherence and Medication Protocols (STAMP) Device for Automatic Dispensing and Real-Time Medication Monitoring. Cureus. 2024 Sep;16(9):e69611. https://doi.org/10.7759/cureus.69611 PubMed PMID: 39421074; PubMed Central PMCID: PMC11486486.
44. Tadesse AW, Cusinato M, Weldemichael GT, Abdurhman T, Assefa D, Yazew H, et al. Risk factors for poor engagement with a smart pillbox adherence intervention among persons on tuberculosis treatment in Ethiopia. BMC Public Health. 2023 Oct 14;23(1):2006. https://doi.org/10.1186/s12889-023-16905-z PubMed PMID: 37838677; PubMed Central PMCID: PMC10576388.
45. Xiong Y, Ba X, Hou A, Zhang K, Chen L, Li T. Automatic detection of mycobacterium tuberculosis using artificial intelligence. J Thorac Dis. 2018 Mar;10(3):1936–40. https://doi.org/10.21037/jtd.2018.01.91 PubMed PMID: 29707349; PubMed Central PMCID: PMC5906344.
46. Gao XW, Qian Y. Prediction of Multidrug-Resistant TB from CT Pulmonary Images Based on Deep Learning Techniques. Mol Pharm. 2018 Oct 1;15(10):4326–35. https://doi.org/10.1021/acs.molpharmaceut.7b00875 PubMed PMID: 29257894.
47. Yao F, Zhang R, Lin Q, Xu H, Li W, Ou M, et al. Plasma immune profiling combined with machine learning contributes to diagnosis and prognosis of active pulmonary tuberculosis. Emerg Microbes Infect. 2024 Dec;13(1):2370399. https://doi.org/10.1080/22221751.2024.2370399 PubMed PMID: 38888093; PubMed Central PMCID: PMC11225635.
48. Botha GHR, Theron G, Warren RM, Klopper M, Dheda K, van Helden PD, et al. Detection of tuberculosis by automatic cough sound analysis. Physiol Meas. 2018 Apr 26;39(4):045005. https://doi.org/10.1088/1361-6579/aab6d0 PubMed PMID: 29543189.
49. Yellapu GD, Rudraraju G, Sripada NR, Mamidgi B, Jalukuru C, Firmal P, et al. Development and clinical validation of Swaasa AI platform for screening and prioritization of pulmonary TB. Sci Rep. 2023 Mar 23;13(1):4740. https://doi.org/10.1038/s41598-023-31772-9
50. Pahar M, Klopper M, Reeve B, Warren R, Theron G, Niesler T. Automatic cough classification for tuberculosis screening in a real-world environment. Physiol Meas. 2021 Nov 26;42(10). https://doi.org/10.1088/1361-6579/ac2fb8 PubMed PMID: 34649231; PubMed Central PMCID: PMC8721487.

51. Souza Filho JB de OE, Sanchez M, Seixas JM de, Maidantchik C, Galliez R, Moreira A da SR, et al. Screening for active pulmonary tuberculosis: Development and applicability of artificial neural network models. Tuberc Edinb Scotl. 2018 Jul;111:94–101. https://doi.org/10.1016/j.tube.2018.05.012 PubMed PMID: 30029922.
52. Bartl L, Zeeb M, Kälin M, Loosli T, Notter J, Furrer H, et al. Machine Learning-Based Prediction of Active Tuberculosis in People with HIV using Clinical Data. Clin Infect Dis Off Publ Infect Dis Soc Am. 2025 Mar 25;ciaf149. https://doi.org/10.1093/cid/ciaf149 PubMed PMID: 40132061.
53. Adhikari DR, Kang YA, Gautam S, Dahal PK. Utilization of artificial intelligence for tuberculosis screening in Nepal. Indian J Tuberc. 2023 Jul;70(3):319–23. https://doi.org/10.1016/j.ijtb.2022.08.002 PubMed PMID: 37562907.
54. Nijiati M, Ma J, Hu C, Tuersun A, Abulizi A, Kelimu A, et al. Artificial Intelligence Assisting the Early Detection of Active Pulmonary Tuberculosis From Chest X-Rays: A Population-Based Study. Front Mol Biosci. 2022;9:874475. https://doi.org/10.3389/fmolb.2022.874475 PubMed PMID: 35463963; PubMed Central PMCID: PMC9023793.
55. Acharya V, Dhiman G, Prakasha K, Bahadur P, Choraria A, M S, et al. AI-Assisted Tuberculosis Detection and Classification from Chest X-Rays Using a Deep Learning Normalization-Free Network Model. Comput Intell Neurosci. 2022;2022:2399428. https://doi.org/10.1155/2022/2399428 PubMed PMID: 36225551; PubMed Central PMCID: PMC9550434.
56. Okada K, Yamada N, Takayanagi K, Hiasa Y, Kitamura Y, Hoshino Y, et al. Applicability of artificial intelligence-based computer-aided detection (AI-CAD) for pulmonary tuberculosis to community-based active case finding. Trop Med Health. 2024 Jan 2;52(1):2. https://doi.org/10.1186/s41182-023-00560-6 PubMed PMID: 38163868; PubMed Central PMCID: PMC10759734.
57. Maka Shrestha R, Paudel RC, Adhikari P, Ghimire RH, Gurung K, Shrestha R. Diagnostic Accuracy of Artificial Intelligence-Based Chest X-Ray reading for screening of Tuberculosis. J Nepal Health Res Counc. 2024 Dec 19;22(3):477–83. https://doi.org/10.33314/jnhrc.v22i03.4637 PubMed PMID: 39923159.
58. John S, Abdulkarim S, Usman S, Rahman MT, Creswell J. Comparing tuberculosis symptom screening to chest X-ray with artificial intelligence in an active case finding campaign in Northeast Nigeria. BMC Glob Public Health. 2023 Oct 6;1(1):17. https://doi.org/10.1186/s44263-023-00017-2 PubMed PMID: 39681894; PubMed Central PMCID: PMC11622919.
59. Biewer AM, Tzelios C, Tintaya K, Roman B, Hurwitz S, Yuen CM, et al. Accuracy of digital chest x-ray analysis with artificial intelligence software as a triage and screening tool in hospitalized patients being evaluated for tuberculosis in Lima, Peru. PLOS Glob Public Health. 2024;4(2):e0002031. https://doi.org/10.1371/journal.pgph.0002031 PubMed PMID: 38324610; PubMed Central PMCID: PMC10849246.
60. Lee JH, Park S, Hwang EJ, Goo JM, Lee WY, Lee S, et al. Deep learning-based automated detection algorithm for active pulmonary tuberculosis on chest radiographs: diagnostic performance in systematic screening of asymptomatic individuals. Eur Radiol. 2021 Feb;31(2):1069–80. https://doi.org/10.1007/s00330-020-07219-4 PubMed PMID: 32857202.
61. Chen CF, Hsu CH, Jiang YC, Lin WR, Hong WC, Chen IY, et al. A deep learning-based algorithm for pulmonary tuberculosis detection in chest radiography. Sci Rep. 2024 Jun 28;14(1):14917. https://doi.org/10.1038/s41598-024-65703-z PubMed PMID: 38942819; PubMed Central PMCID: PMC11213931.
62. Parreira PL, Fonseca AU, Soares F, Conte MB, Rabahi MF. Chest X-ray evaluation using machine learning to support the early diagnosis of pulmonary TB. Int J Tuberc Lung Dis Off J Int Union Tuberc Lung Dis. 2024 Apr 1;28(4):171–5. https://doi.org/10.5588/ijtld.23.0230 PubMed PMID: 38563343.
63. Nzimande N, Murphy K, Reither K, Bosman S, Ayakaka I, Glass TR, et al. Performance of CAD4TB artificial intelligence technology in TB screening programmes among the adult population in South Africa and Lesotho. J Clin Tuberc Mycobact Dis. 2025 Aug;40:100540. https://doi.org/10.1016/j.jctube.2025.100540 PubMed PMID: 40547074; PubMed Central PMCID: PMC12179731.
64. Melendez J, Philipsen RHHM, Chanda-Kapata P, Sunkutu V, Kapata N, van Ginneken B. Automatic versus human reading of chest X-rays in the Zambia National Tuberculosis Prevalence Survey. Int J Tuberc Lung

Dis Off J Int Union Tuberc Lung Dis. 2017 Aug 1;21(8):880–6. https://doi.org/10.5588/ijtld.16.0851 PubMed PMID: 28786796.

65. Jayaraman P, S S, Paul S, Pant R, Gupte T, Kulkarni V, et al. Artificial intelligence as a proficient tool in detecting pulmonary tuberculosis in massive population screening programs: a case study in Chennai, India. J Rural Med JRM. 2025 Jan;20(1):13–9. https://doi.org/10.2185/jrm.2024-015 PubMed PMID: 39781302; PubMed Central PMCID: PMC11704598.
66. Qin ZZ, Sander MS, Rai B, Titahong CN, Sudrungrot S, Laah SN, et al. Using artificial intelligence to read chest radiographs for tuberculosis detection: A multi-site evaluation of the diagnostic accuracy of three deep learning systems. Sci Rep. 2019 Oct 18;9(1):15000. https://doi.org/10.1038/s41598-019-51503-3 PubMed PMID: 31628424; PubMed Central PMCID: PMC6802077.
67. Zhu Q, Liu J. A united model for diagnosing pulmonary tuberculosis with random forest and artificial neural network. Front Genet. 2023;14:1094099. https://doi.org/10.3389/fgene.2023.1094099 PubMed PMID: 36968608; PubMed Central PMCID: PMC10033863.
68. Luo Y, Xue Y, Liu W, Song H, Huang Y, Tang G, et al. Development of diagnostic algorithm using machine learning for distinguishing between active tuberculosis and latent tuberculosis infection. BMC Infect Dis. 2022 Dec 29;22(1):965. https://doi.org/10.1186/s12879-022-07954-7 PubMed PMID: 36581808; PubMed Central PMCID: PMC9798640.
69. Tavaziva G, Majidulla A, Nazish A, Saeed S, Benedetti A, Khan AJ, et al. Diagnostic accuracy of a commercially available, deep learning-based chest X-ray interpretation software for detecting culture-confirmed pulmonary tuberculosis. Int J Infect Dis. 2022 Sep 1;122:15–20. https://doi.org/10.1016/j.ijid.2022.05.037 PubMed PMID: 35597555.
70. Showkatian E, Salehi M, Ghaffari H, Reiazi R, Sadighi N. Deep learning-based automatic detection of tuberculosis disease in chest X-ray images. Pol J Radiol. 2022;87:e118–24. https://doi.org/10.5114/pjr.2022.113435 PubMed PMID: 35280947; PubMed Central PMCID: PMC8906182.
71. Hrizi O, Gasmi K, Ben Ltaifa I, Alshammari H, Karamti H, Krichen M, et al. Tuberculosis Disease Diagnosis Based on an Optimized Machine Learning Model. J Healthc Eng. 2022;2022:8950243. https://doi.org/10.1155/2022/8950243 PubMed PMID: 35494520; PubMed Central PMCID: PMC9041161.
72. Kazemzadeh S, Yu J, Jamshy S, Pilgrim R, Nabulsi Z, Chen C, et al. Deep Learning Detection of Active Pulmonary Tuberculosis at Chest Radiography Matched the Clinical Performance of Radiologists. Radiology. 2023 Jan;306(1):124–37. https://doi.org/10.1148/radiol.212213 PubMed PMID: 36066366.
73. Nafisah SI, Muhammad G. Tuberculosis detection in chest radiograph using convolutional neural network architecture and explainable artificial intelligence. Neural Comput Appl. 2022 Apr 19;1–21. https://doi.org/10.1007/s00521-022-07258-6 PubMed PMID: 35462630; PubMed Central PMCID: PMC9016694.
74. Zhang S, He C, Wan Z, Shi N, Wang B, Liu X, et al. Diagnosis of pulmonary tuberculosis with 3D neural network based on multi-scale attention mechanism. Med Biol Eng Comput. 2024 May;62(5):1589–600. https://doi.org/10.1007/s11517-024-03022-1 PubMed PMID: 38319503.
75. Wang CH, Chang W, Lee MR, Tay J, Wu CY, Wu MC, et al. Deep Learning-based Diagnosis of Pulmonary Tuberculosis on Chest X-ray in the Emergency Department: A Retrospective Study. J Imaging Inform Med. 2024 Apr;37(2):589–600. https://doi.org/10.1007/s10278-023-00952-4 PubMed PMID: 38343228; PubMed Central PMCID: PMC11031502.
76. Devasia J, Goswami H, Lakshminarayanan S, Rajaram M, Adithan S. Observer Performance Evaluation of a Deep Learning Model for Multilabel Classification of Active Tuberculosis Lung Zone-Wise Manifestations. Cureus. 2023 Sep;15(9):e44954. https://doi.org/10.7759/cureus.44954 PubMed PMID: 37818499; PubMed Central PMCID: PMC10561790.
77. Hwang EJ, Park S, Jin KN, Kim JI, Choi SY, Lee JH, et al. Development and Validation of a Deep Learning-based Automatic Detection Algorithm for Active Pulmonary Tuberculosis on Chest Radiographs. Clin Infect Dis Off Publ Infect Dis Soc Am. 2019 Aug 16;69(5):739–47. https://doi.org/10.1093/cid/ciy967 PubMed PMID: 30418527; PubMed Central PMCID: PMC6695514.
78. Nash M, Kadavigere R, Andrade J, Sukumar CA, Chawla K, Shenoy VP, et al. Deep learning, computer-aided radiography reading for tuberculosis: a diagnostic accuracy study from a tertiary hospital in India.

Sci Rep. 2020 Jan 14;10(1):210. https://doi.org/10.1038/s41598-019-56589-3 PubMed PMID: 31937802; PubMed Central PMCID: PMC6959311.

79. Ma L, Wang Y, Guo L, Zhang Y, Wang P, Pei X, et al. Developing and verifying automatic detection of active pulmonary tuberculosis from multi-slice spiral CT images based on deep learning. J X-Ray Sci Technol. 2020;28(5):939–51. https://doi.org/10.3233/XST-200662 PubMed PMID: 32651351; PubMed Central PMCID: PMC12067939.
80. Park J, Hwang EJ, Lee JH, Hong W, Nam JG, Lim WH, et al. Identification of Active Pulmonary Tuberculosis Among Patients With Positive Interferon-Gamma Release Assay Results: Value of a Deep Learning-based Computer-aided Detection System in Different Scenarios of Implementation. J Thorac Imaging. 2023 May 1;38(3):145–53. https://doi.org/10.1097/RTI.0000000000000691 PubMed PMID: 36744946.
81. Lee SH, Fox S, Smith R, Skrobarcek KA, Keyserling H, Phares CR, et al. Development and validation of a deep learning model for detecting signs of tuberculosis on chest radiographs among US-bound immigrants and refugees. PLOS Digit Health. 2024 Sep;3(9):e0000612. https://doi.org/10.1371/journal.pdig.0000612 PubMed PMID: 39348377; PubMed Central PMCID: PMC11441656.
82. Ridhi S, Robert D, Soren P, Kumar M, Pawar S, Reddy B. Comparing the Output of an Artificial Intelligence Algorithm in Detecting Radiological Signs of Pulmonary Tuberculosis in Digital Chest X-Rays and Their Smartphone-Captured Photos of X-Ray Films: Retrospective Study. JMIR Form Res. 2024 Aug 21;8:e55641. https://doi.org/10.2196/55641 PubMed PMID: 39167435; PubMed Central PMCID: PMC11375380.
83. Choi SY, Choi A, Baek SE, Ahn JY, Roh YH, Kim JH. Effect of multimodal diagnostic approach using deep learning-based automated detection algorithm for active pulmonary tuberculosis. Sci Rep. 2023 Nov 13;13(1):19794. https://doi.org/10.1038/s41598-023-47146-0 PubMed PMID: 37957334; PubMed Central PMCID: PMC10643438.
84. Serrão MKM, Costa MGF, Fujimoto LBM, Ogusku MM, Costa Filho CFF. Automatic bright-field smear microscopy for diagnosis of pulmonary tuberculosis. Comput Biol Med. 2024 Apr;172:108167. https://doi.org/10.1016/j.compbiomed.2024.108167 PubMed PMID: 38461699.
85. Zaizen Y, Kanahori Y, Ishijima S, Kitamura Y, Yoon HS, Ozasa M, et al. Deep-Learning-Aided Detection of Mycobacteria in Pathology Specimens Increases the Sensitivity in Early Diagnosis of Pulmonary Tuberculosis Compared with Bacteriology Tests. Diagn Basel Switz. 2022 Mar 14;12(3). https://doi.org/10.3390/diagnostics12030709 PubMed PMID: 35328262; PubMed Central PMCID: PMC8946921.
86. Díaz-Huerta JL, Téllez-Anguiano AC, Gutiérrez-Gnecchi JA, Arellano-Calderón S, Olivares-Rojas JC. Analysis and comparison of image processing and artificial intelligence algorithms to detect AFB in pulmonary tuberculosis images. Tuberc Edinb Scotl. 2022 May;134:102196. https://doi.org/10.1016/j.tube.2022.102196 PubMed PMID: 35325761.
87. Wang HS, Liang WY. Combining Artificial Intelligence and Simplified Image Processing for the Automatic Detection of Mycobacterium tuberculosis in Acid-fast Stain : A Cross-institute Training and Validation Study. Am J Surg Pathol. 2024 Jul 1;48(7):866–73. https://doi.org/10.1097/PAS.0000000000002223 PubMed PMID: 38595262.
88. Li Q, Ou XC, Pang Y, Xia H, Huang HR, Zhao B, et al. A novel automatic molecular test for detection of multidrug resistance tuberculosis in sputum specimen: A case control study. Tuberc Edinb Scotl. 2017 Jul;105:9–12. https://doi.org/10.1016/j.tube.2017.03.008 PubMed PMID: 28610793.
89. Devasia J, Goswami H, Lakshminarayanan S, Rajaram M, Adithan S. Deep learning classification of active tuberculosis lung zones wise manifestations using chest X-rays: a multi label approach. Sci Rep. 2023 Jan 17;13(1):887. https://doi.org/10.1038/s41598-023-28079-0 PubMed PMID: 36650270; PubMed Central PMCID: PMC9845381.
90. Lee S, Yim JJ, Kwak N, Lee YJ, Lee JK, Lee JY, et al. Deep Learning to Determine the Activity of Pulmonary Tuberculosis on Chest Radiographs. Radiology. 2021 Nov;301(2):435–42. https://doi.org/10.1148/radiol.2021210063 PubMed PMID: 34342505.
91. Nijiati M, Zhou R, Damaola M, Hu C, Li L, Qian B, et al. Deep learning based CT images automatic analysis model for active/non-active pulmonary tuberculosis differential diagnosis. Front Mol Biosci.

2022;9:1086047. https://doi.org/10.3389/fmolb.2022.1086047 PubMed PMID: 36545511; PubMed Central PMCID: PMC9760807.

92. Choi YR, Yoon SH, Kim J, Yoo JY, Kim H, Jin KN. Chest Radiography of Tuberculosis: Determination of Activity Using Deep Learning Algorithm. Tuberc Respir Dis. 2023 Jul;86(3):226–33. https://doi.org/10.4046/trd.2023.0020 PubMed PMID: 37183400; PubMed Central PMCID: PMC10323207.
93. Rajpurkar P, O'Connell C, Schechter A, Asnani N, Li J, Kiani A, et al. CheXaid: deep learning assistance for physician diagnosis of tuberculosis using chest x-rays in patients with HIV. NPJ Digit Med. 2020 Sep 9;3:115. https://doi.org/10.1038/s41746-020-00322-2 PubMed PMID: 32964138.
94. Yan C, Wang L, Lin J, Xu J, Zhang T, Qi J, et al. A fully automatic artificial intelligence-based CT image analysis system for accurate detection, diagnosis, and quantitative severity evaluation of pulmonary tuberculosis. Eur Radiol. 2022 Apr;32(4):2188–99. https://doi.org/10.1007/s00330-021-08365-z PubMed PMID: 34842959; PubMed Central PMCID: PMC8628489.
95. Liang S, Xu X, Yang Z, Du Q, Zhou L, Shao J, et al. Deep learning for precise diagnosis and subtype triage of drug-resistant tuberculosis on chest computed tomography. MedComm. 2024 Mar;5(3):e487. https://doi.org/10.1002/mco2.487 PubMed PMID: 38469547; PubMed Central PMCID: PMC10925488.
96. Nijiati M, Zhang Z, Abulizi A, Miao H, Tuluhong A, Quan S, et al. Deep learning assistance for tuberculosis diagnosis with chest radiography in low-resource settings. J X-Ray Sci Technol. 2021;29(5):785–96. https://doi.org/10.3233/XST-210894 PubMed PMID: 34219703.
97. You S, Chitwood MH, Gunasekera KS, Crudu V, Codreanu A, Ciobanu N, et al. Predicting resistance to fluoroquinolones among patients with rifampicin-resistant tuberculosis using machine learning methods. PLOS Digit Health. 2022;1(6):e0000059. https://doi.org/10.1371/journal.pdig.0000059 PubMed PMID: 36177394; PubMed Central PMCID: PMC9518704.
98. Falcao IWS, Cardoso DL, Coutinho Dos Santos Santos AE, Paixao E, Costa FAR, Figueiredo K, et al. Model for predicting drug resistance based on the clinical profile of tuberculosis patients using machine learning techniques. PeerJ Comput Sci. 2024;10:e2246. https://doi.org/10.7717/peerj-cs.2246 PubMed PMID: 39650511; PubMed Central PMCID: PMC11623081.
99. Sethanan K, Pitakaso R, Srichok T, Khonjun S, Weerayuth N, Prasitpuriprecha C, et al. Computer-aided diagnosis using embedded ensemble deep learning for multiclass drug-resistant tuberculosis classification. Front Med. 2023;10:1122222. https://doi.org/10.3389/fmed.2023.1122222 PubMed PMID: 37441685; PubMed Central PMCID: PMC10333053.
100. Prasitpuriprecha C, Pitakaso R, Gonwirat S, Enkvetchakul P, Preeprem T, Jantama SS, et al. Embedded AMIS-Deep Learning with Dialog-Based Object Query System for Multi-Class Tuberculosis Drug Response Classification. Diagn Basel Switz. 2022 Nov 28;12(12). https://doi.org/10.3390/diagnostics12122980 PubMed PMID: 36552987; PubMed Central PMCID: PMC9777254.
101. Li Y, Wang B, Wen L, Li H, He F, Wu J, et al. Machine learning and radiomics for the prediction of multidrug resistance in cavitary pulmonary tuberculosis: a multicentre study. Eur Radiol. 2023 Jan;33(1):391–400. https://doi.org/10.1007/s00330-022-08997-9 PubMed PMID: 35852573; PubMed Central PMCID: PMC9294743.
102. Yang F, Yu H, Kantipudi K, Karki M, Kassim YM, Rosenthal A, et al. Differentiating between drug-sensitive and drug-resistant tuberculosis with machine learning for clinical and radiological features. Quant Imaging Med Surg. 2022 Jan;12(1):675–87. https://doi.org/10.21037/qims-21-290 PubMed PMID: 34993110; PubMed Central PMCID: PMC8666787.
103. Song C, Huang A, Zhao C, Wen L, Song S, Lin Y, et al. Multimodal radiomics integrating deep learning and clinical features for diagnosing multidrug-resistant tuberculosis in HIV/AIDS patients. J Glob Antimicrob Resist. 2025 Jun;43:134–42. https://doi.org/10.1016/j.jgar.2025.04.013 PubMed PMID: 40324593.
104. Cao Y, Parmar H, Simmons AM, Kale D, Tong K, Lieu D, et al. Automatic Identification of Individual rpoB Gene Mutations Responsible for Rifampin Resistance in Mycobacterium tuberculosis by Use of Melting Temperature Signatures Generated by the Xpert MTB/RIF Ultra Assay. J Clin Microbiol. 2019 Dec 23;58(1). https://doi.org/10.1128/JCM.00907-19 PubMed PMID: 31533985; PubMed Central PMCID: PMC6935902.
105. Babirye SR, Nsubuga M, Mboowa G, Batte C, Galiwango R, Kateete DP. Machine learning-based prediction of antibiotic resistance in Mycobacterium tuberculosis clinical isolates from Uganda. BMC Infect Dis. 2024

Dec 5;24(1):1391. https://doi.org/10.1186/s12879-024-10282-7 PubMed PMID: 39639222; PubMed Central PMCID: PMC11622658.

106. Nijiati M, Guo L, Tuersun A, Damola M, Abulizi A, Dong J, et al. Deep learning on longitudinal CT scans: automated prediction of treatment outcomes in hospitalized tuberculosis patients. iScience. 2023 Nov 17;26(11):108326. https://doi.org/10.1016/j.isci.2023.108326 PubMed PMID: 37965132; PubMed Central PMCID: PMC10641748.
107. Lv X, Li Y, Cai B, He W, Wang R, Chen M, et al. Utility of Machine Learning and Radiomics Based on Cavity for Predicting the Therapeutic Response of MDR-TB. Infect Drug Resist. 2023;16:6893–904. https://doi.org/10.2147/IDR.S435984 PubMed PMID: 37920476; PubMed Central PMCID: PMC10619461.
108. Liao KM, Liu CF, Chen CJ, Feng JY, Shu CC, Ma YS. Using an Artificial Intelligence Approach to Predict the Adverse Effects and Prognosis of Tuberculosis. Diagn Basel Switz. 2023 Mar 13;13(6). https://doi.org/10.3390/diagnostics13061075 PubMed PMID: 36980382; PubMed Central PMCID: PMC10047137.
109. Kheirandish M, Catanzaro D, Crudu V, Zhang S. Integrating landmark modeling framework and machine learning algorithms for dynamic prediction of tuberculosis treatment outcomes. J Am Med Inform Assoc JAMIA. 2022 Apr 13;29(5):900–8. https://doi.org/10.1093/jamia/ocac003 PubMed PMID: 35139541; PubMed Central PMCID: PMC9006704.
110. Ahamed Fayaz S, Babu L, Paridayal L, Vasantha M, Paramasivam P, Sundarakumar K, et al. Machine learning algorithms to predict treatment success for patients with pulmonary tuberculosis. PloS One. 2024;19(10):e0309151. https://doi.org/10.1371/journal.pone.0309151 PubMed PMID: 39413064; PubMed Central PMCID: PMC11482692.
111. Asad M, Mahmood A, Usman M. A machine learning-based framework for Predicting Treatment Failure in tuberculosis: A case study of six countries. Tuberc Edinb Scotl. 2020 Jul;123:101944. https://doi.org/10.1016/j.tube.2020.101944 PubMed PMID: 32741529.
112. Pasipanodya JG, Smythe W, Merle CS, Olliaro PL, Deshpande D, Magombedze G, et al. Artificial intelligence-derived 3-Way Concentration-dependent Antagonism of Gatifloxacin, Pyrazinamide, and Rifampicin During Treatment of Pulmonary Tuberculosis. Clin Infect Dis Off Publ Infect Dis Soc Am. 2018 Nov 28;67(suppl_3):S284–92. https://doi.org/10.1093/cid/ciy610 PubMed PMID: 30496458; PubMed Central PMCID: PMC6904294.
113. Hosu MC, Faye LM, Apalata T. Predicting Treatment Outcomes in Patients with Drug-Resistant Tuberculosis and Human Immunodeficiency Virus Coinfection, Using Supervised Machine Learning Algorithm. Pathog Basel Switz. 2024 Oct 24;13(11). https://doi.org/10.3390/pathogens13110923 PubMed PMID: 39599476; PubMed Central PMCID: PMC11597124.
114. Kim HJ, Kwak N, Yoon SH, Park N, Kim YR, Lee JH, et al. Artificial intelligence-based radiographic extent analysis to predict tuberculosis treatment outcomes: a multicenter cohort study. Sci Rep. 2024 Jun 7;14(1):13162. https://doi.org/10.1038/s41598-024-63885-0 PubMed PMID: 38849439; PubMed Central PMCID: PMC11161500.
115. Wang Z, Guo Z, Wang W, Zhang Q, Song S, Xue Y, et al. Prediction of tuberculosis treatment outcomes using biochemical makers with machine learning. BMC Infect Dis. 2025 Feb 17;25(1):229. https://doi.org/10.1186/s12879-025-10609-y PubMed PMID: 39962412; PubMed Central PMCID: PMC11834319.
116. Rodrigues MMS, Barreto-Duarte B, Vinhaes CL, Araújo-Pereira M, Fukutani ER, Bergamaschi KB, et al. Machine learning algorithms using national registry data to predict loss to follow-up during tuberculosis treatment. BMC Public Health. 2024 May 23;24(1):1385. https://doi.org/10.1186/s12889-024-18815-0 PubMed PMID: 38783264; PubMed Central PMCID: PMC11112756.
117. Gichuhi HW, Magumba M, Kumar M, Mayega RW. A machine learning approach to explore individual risk factors for tuberculosis treatment non-adherence in Mukono district. PLOS Glob Public Health. 2023;3(7):e0001466. https://doi.org/10.1371/journal.pgph.0001466 PubMed PMID: 37399173; PubMed Central PMCID: PMC10317231.

118. Hussain OA, Junejo KN. Predicting treatment outcome of drug-susceptible tuberculosis patients using machine-learning models. Inform Health Soc Care. 2019;44(2):135–51. https://doi.org/10.1080/17538157.2018.1433676 PubMed PMID: 29461901.
119. Anley DT, Akalu TY, Dessie AM, Anteneh RM, Zemene MA, Bayih WA, et al. Prognostication of treatment non-compliance among patients with multidrug-resistant tuberculosis in the course of their follow-up: a logistic regression-based machine learning algorithm. Front Digit Health. 2023;5:1165222. https://doi.org/10.3389/fdgth.2023.1165222 PubMed PMID: 37228302; PubMed Central PMCID: PMC10203954.
120. Perwitasari DA, Faridah IN, Dania H, Setiawan D, Safaria T. Machine learning model to predict the adherence of tuberculosis patients experiencing increased levels of liver enzymes in Indonesia. PloS One. 2025;20(1):e0315912. https://doi.org/10.1371/journal.pone.0315912 PubMed PMID: 39854377; PubMed Central PMCID: PMC11760577.
121. Prasitpuriprecha C, Jantama SS, Preeprem T, Pitakaso R, Srichok T, Khonjun S, et al. Drug-Resistant Tuberculosis Treatment Recommendation, and Multi-Class Tuberculosis Detection and Classification Using Ensemble Deep Learning-Based System. Pharm Basel Switz. 2022 Dec 22;16(1). https://doi.org/10.3390/ph16010013 PubMed PMID: 36678508; PubMed Central PMCID: PMC9864877.
122. Xu D, Zeng J, Xie F, Yang Q, Huang K, Xiao W, et al. Construction of a risk model and deep learning network based on patients with active pulmonary tuberculosis and pulmonary inflammation. Biomed Rep. 2023 May;18(5):34. https://doi.org/10.3892/br.2023.1616 PubMed PMID: 37034573; PubMed Central PMCID: PMC10079808.
123. Verboven L, Callens S, Black J, Maartens G, Dooley KE, Potgieter S, et al. A machine-learning based model for automated recommendation of individualized treatment of rifampicin-resistant tuberculosis. Res Sq. 2023 Feb 16;rs.3.rs-2525765. https://doi.org/10.21203/rs.3.rs-2525765/v1 PubMed PMID: 36824956; PubMed Central PMCID: PMC9949242.: