



## Integrating Semantic Literature Review and Simple Experiments: Comparison of AI Algorithms in Tropical Disease Case Studies

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### Abstract

Tropical diseases represent a global health challenge requiring innovative approaches for diagnosis and prediction. This study integrates semantic literature review with comparative experiments of artificial intelligence algorithms to analyze the effectiveness of various AI methods in handling tropical disease case studies. Through systematic analysis of 127 scientific publications from 2018-2025, we identified trends in using machine learning, deep learning, and natural language processing algorithms in tropical health domains. Comparative experiments were conducted on five main algorithms: Support Vector Machine (SVM), Random Forest, Neural Network, Convolutional Neural Network (CNN), and Long Short-Term Memory (LSTM) using datasets of malaria, dengue, and tuberculosis. Results show that CNN achieved the highest accuracy of 94.7% for malaria microscopic image classification, while LSTM performed best for dengue outbreak prediction with an F1-score of 0.89 using temporal data. Random Forest showed the most consistent performance across different diseases with an average accuracy of 87.3%. Semantic analysis revealed research gaps in multi-modal data integration and personalized medicine for tropical diseases. This study provides a comprehensive roadmap for AI implementation in tropical countries' healthcare systems.

*Keywords: semantic literature review, artificial intelligence, tropical diseases, machine learning, healthcare AI, comparative study*

### 1. Introduction

This Tropical diseases affect over one billion people worldwide, primarily in developing countries with tropical and subtropical climates [1]. The World Health Organization (WHO) identifies 20 neglected tropical diseases requiring special attention in prevention and treatment efforts [2]. The complexity of diagnosis, limited medical resources, and clinical symptom variability make tropical diseases a challenging domain for modern health technology applications [3]. Artificial intelligence (AI) has demonstrated transformative potential in healthcare, from computer-aided diagnosis to predictive analytics for outbreak detection [4]. However, AI applications in tropical disease contexts remain relatively limited and scattered across various methodological approaches without a comprehensive integrating framework [5]. Traditional literature reviews often fail to capture semantic relationships between studies, making deep insights about research evolution and gaps difficult to obtain [6]. Semantic literature review uses natural language processing and knowledge graphs to analyze not only textual content but also semantic relationships between concepts in research corpora [7]. This approach enables identification of hidden patterns, emerging trends, and research gaps undetected by conventional systematic reviews [8]. Integrating semantic analysis with empirical experiments provides a dual perspective combining theoretical insights with practical validation [9]. Previous research shows various AI algorithms have different performance characteristics depending on data type, problem complexity, and application domain [10]. For tropical diseases, factors like data scarcity, class imbalance, and population heterogeneity add complexity to optimal algorithm selection [11]. Systematic comparative studies are needed to provide evidence-based recommendations for AI implementation in tropical disease management [12]. This study's main contributions include: (1) comprehensive semantic literature review of AI publications for tropical diseases (2018-2025), (2) comparative experimental analysis of five state-of-the-art AI algorithms using real-world tropical disease datasets, (3) identification of research gaps and future directions in AI for tropical diseases, and (4) practical guidelines for AI implementation in tropical countries' healthcare systems.

## 2. The Proposed Method/Algorithm

### 2.1. Semantic Literature Review Framework

Our semantic literature review framework comprises five main stages: data acquisition, preprocessing, semantic analysis, knowledge extraction, and insight synthesis [13]. The data acquisition stage involves systematic searches of major academic databases including PubMed, IEEE Xplore, ACM Digital Library, and Scopus using validated query strings:

("artificial intelligence" OR "machine learning" OR "deep learning")  
 AND ("tropical disease" OR "malaria" OR "dengue" OR "tuberculosis")  
 AND ("diagnosis" OR "prediction" OR "classification")

[14]  
 The preprocessing stage includes document filtering based on inclusion/exclusion criteria, full-text extraction, and quality assessment using modified PRISMA guidelines [15]. Each document was evaluated for methodological rigor, dataset quality, experimental design, and reproducibility score. Only publications with quality scores  $\geq 7.0$  (scale 1-10) were included [16].

Semantic analysis employs a combination of pre-trained language models (BERT, BioBERT) and domain-specific ontologies to extract semantic embeddings from each document [17]. Knowledge graph construction uses Neo4j with nodes representing concepts (algorithms, diseases, metrics) and edges representing relationships (applies\_to, outperforms, correlates\_with) [18]. Graph algorithms like PageRank and community detection identify central concepts and research clusters [19].

### 2.2. Comparative Experimental Design

The comparative experiment was designed using a standardized evaluation framework with five-fold cross-validation for robust results [20]. Five algorithms representing different AI paradigms were selected: SVM (classical machine learning), Random Forest (ensemble methods), Neural Network (basic deep learning), CNN (image-based analysis), and LSTM (sequential data processing) [21].

Datasets covered three major tropical diseases with different data characteristics:

1. Malaria dataset: 27,558 microscopic blood cell images labeled parasitized/uninfected [22]
2. Dengue dataset: 15,000 epidemiological time series with 12 climatological/demographic features [23]
3. Tuberculosis dataset: 10,847 chest X-ray images annotated by radiologists [24]

Standardized preprocessing was applied algorithm-specifically: image normalization/augmentation for CNN, feature scaling/selection for SVM/Random Forest, and sequence padding/embedding for LSTM [25]. Hyperparameter optimization used grid search with Bayesian optimization for fair comparison [26].

## 3. Method

### 3.1. Data Collection and Preprocessing

Systematic literature searches were conducted on June 15, 2025 using advanced search strategies validated by information specialists [32]. Search strings were developed through iterative processes with pilot searches and expert consultation to ensure comprehensive coverage [33]. From 2,847 initial publications, 127 relevant papers remained after screening and quality assessment [34].

Inclusion criteria:

1. Peer-reviewed English publications
2. Focus on AI applications for tropical diseases
3. Use of real-world/clinical datasets
4. Presentation of quantitative results
5. Published 2018-2025 [35]

Exclusion criteria:

Review articles without original contributions

Conference abstracts

Publications with unclear methodologies

Studies with sample sizes  $< 100$  [36]

Full-text analysis used automated information extraction tools combined with manual verification [37]. Each publication was coded by 25 variables including algorithm type, disease category, dataset characteristics,

performance metrics, and methodological quality indicators [38]. Inter-rater reliability for coding reached Cohen's kappa = 0.89, indicating excellent agreement [39].

### 3.2. Semantic Analysis Implementation

Semantic analysis was implemented using state-of-the-art NLP techniques focused on biomedical domains [40]. Text preprocessing included tokenization, medical term named entity recognition, and concept normalization using UMLS [41]. Document representation combined TF-IDF, word embeddings, and BioBERT contextual embeddings [42].

Knowledge graph construction used a multi-step process of entity extraction, relation identification, and graph refinement . Entities were extracted using rule-based methods and ML models (precision=0.92, recall=0.87). Relations were identified via supervised learning with 5,000 manually annotated entity pairs [43].

Graph analysis employed network techniques including centrality measures, community detection, and temporal analysis . PageRank identified influential concepts while Louvain algorithm detected communities. Temporal analysis used sliding windows to identify evolving trends in tropical disease AI research .

### 3.3. Experimental Setup and Implementation

The experimental environment was configured using a high-performance computing cluster with:

1. 8 NVIDIA Tesla V100 GPUs
2. 256GB RAM
3. Intel Xeon Gold 6248 processors

All experiments used Python 3.9 with:

1. scikit-learn 1.0.2
2. TensorFlow 2.8.0
3. PyTorch 1.11.0
4. CUDA 11.6 for GPU acceleration

A standardized pipeline ensured reproducibility and fair algorithm comparisons, including:

1. Data loading
2. Preprocessing
3. Model training
4. Hyperparameter tuning
5. Evaluation
6. Result logging with versioning

Each experiment was run 10 times with different random seeds to compute statistical measures and confidence intervals .

Hyperparameter optimization used Optuna framework with Tree-structured Parzen Estimator (TPE) . Search space was defined via literature review and preliminary experiments (150 hyperparameter combinations tested per algorithm). Early stopping and checkpointing prevented overfitting and optimized computational efficiency.

### 3.4. Data Augmentation and Validation Strategies

Algorithm-specific data augmentation techniques improved generalization:

1. CNN: rotation, flip, zoom, brightness adjustment, elastic deformation
2. LSTM: time warping, noise injection, SMOTE

Cross-validation used stratified k-fold (k=5) maintaining class distribution . Temporal splitting for time series data used:

1. 70% training
2. 15% validation
3. 15% testing

Independent test sets from different geographical regions evaluated generalizability. Model validation included:

1. Internal cross-validation
2. Temporal validation for time series
3. External validation with independent datasets

Calibration analysis evaluated probability reliability using Platt scaling and isotonic regression . Uncertainty quantification used Monte Carlo dropout and ensemble methods to measure prediction confidence

## 4. Results and Discussion

### 4.1. Semantic Literature Review Findings

This Analysis of 127 publications revealed key trends in tropical disease AI applications. Temporal distribution showed exponential growth from 8 papers (2018) to 34 (2024), with 40+ projected for 2025 - a 47% average annual growth rate.

Algorithm distribution showed:

1. Deep learning: 48%
2. Traditional ML: 31%
3. Hybrid approaches: 15%
4. Reinforcement learning: 6%

CNN was most used (28 publications), especially for image-based diagnosis, followed by Random Forest (19) and SVM (15)

Disease-specific analysis showed:

1. Malaria: 42 publications (33%)
2. Dengue: 28 (22%)
3. Tuberculosis: 24 (19%)
4. Other tropical diseases: 33 (26%)

Geographic distribution showed concentrations in:

1. Southeast Asia: 35%
2. Sub-Saharan Africa: 28%
3. South America: 22%
4. Other regions: 15%

Semantic network analysis revealed strong connections between:

1. "Image classification" and "malaria diagnosis"
2. "Time series prediction" and "dengue outbreak"
3. "Feature selection" and "tuberculosis screening"

Highest PageRank scores went to:

1. "Accuracy"
2. "Deep learning"
3. "Feature extraction"
4. "Clinical validation"

template was designed for two affiliations.

### 4.2. Performance Comparison Results

Standardized dataset evaluation provided detailed algorithm comparisons. For malaria classification:

1. CNN achieved best performance:
  - Accuracy:  $94.7\% \pm 1.2\%$
  - Precision:  $0.943 \pm 0.018$
  - Recall:  $0.951 \pm 0.015$
  - F1-score:  $0.947 \pm 0.012$
2. Random Forest:  $89.3\% \pm 2.1\%$  accuracy
3. SVM:  $85.7\% \pm 1.8\%$  accuracy

For dengue outbreak prediction:

1. LSTM showed superior performance:
  - F1-score:  $0.89 \pm 0.03$
  - AUC:  $0.94 \pm 0.02$
  - RMSE:  $12.4 \pm 1.8$  (4-week horizon)
2. Neural Network: F1-score  $0.84 \pm 0.04$
3. Random Forest/SVM: comparable F1-scores  $\sim 0.80$

Tuberculosis screening showed balanced performance:

1. CNN:
  - Accuracy:  $91.2\% \pm 1.7\%$
  - AUC:  $0.96 \pm 0.01$

2. Random Forest:
  - Accuracy:  $87.8\% \pm 2.3\%$
  - AUC:  $0.93 \pm 0.02$
3. Neural Network:
  - Accuracy:  $86.4\% \pm 2.0\%$
  - AUC:  $0.91 \pm 0.03$
4. SVM showed surprisingly competitive accuracy:  $84.9\% \pm 2.1\%$

Cross-dataset validation revealed:

1. CNN models trained on malaria data showed 8-15% accuracy drops when tested on different geographical regions, suggesting overfitting
2. Random Forest showed better generalizability with only 3-7% performance drops across regions

#### 4.3. Computational Efficiency Analysis

Significant accuracy-computation trade-offs emerged:

1. CNN:
  - Training time:  $4.2 \pm 0.8$  hours (GPU)
  - Inference:  $23 \pm 5$  ms/image
  - Suitable for batch processing
2. LSTM:
  - Training:  $2.1 \pm 0.4$  hours
  - Inference:  $8 \pm 2$  ms/sequence

Traditional algorithms showed computational advantages:

1. Random Forest:
  - Training:  $15 \pm 3$  minutes
  - Inference:  $<1$  ms/sample
  - Ideal for resource-constrained environments
2. SVM:
  - Training:  $8 \pm 2$  minutes
  - Inference:  $2 \pm 1$  ms/sample

Memory requirements:

1. CNN: 2-8GB GPU memory
2. LSTM: 1-4GB
3. Random Forest: 100-500MB
4. SVM: 50-200MB

Energy consumption analysis revealed deep learning models consumed 15-50× more energy than traditional algorithms during training.

#### 4.4. Clinical Validation and Real-world Performance

Independent hospital dataset validation revealed performance gaps between controlled experiments and real applications:

1. Malaria diagnosis accuracy dropped 6-12% on clinical samples with varying image quality/staining
2. CNN showed better robustness to image quality variations than traditional approaches

Dengue outbreak prediction validation showed:

1. LSTM models provided 2-4 week early warnings before official outbreaks:
  - Sensitivity: 0.78
  - Specificity: 0.85
2. Relatively high false positive rate (15%) suggested need for calibration/threshold optimization

Tuberculosis screening pilot study (500 patients) showed:

1. AI-assisted diagnosis improved:
  - Screening efficiency: +40%
  - Reduced missed cases: 23%
2. AI-radiologist agreement:  $\kappa = 0.72$  (substantial)

User acceptance study (45 healthcare professionals) revealed:

1. 78% considered AI tools valuable assistance

2. 65% expressed concerns about over-reliance on automated diagnosis
3. Training requirements and integration challenges were major adoption barriers

#### 4.5. Research Gaps and Future Directions

Semantic analysis identified significant research gaps:

1. Multi-modal data integration: only 12% publications combined different data types
2. Personalized medicine: only 3 publications considered individual patient characteristics
3. Explainable AI (XAI): only 18% included interpretability analysis
4. Clinical decision support systems: only 8 publications
5. Algorithmic fairness: only 5 publications explicitly addressed fairness
6. Federated learning: only 2 publications in tropical diseases
7. Edge computing/mobile health: only 9 focused on low-resource environments

Future research directions:

1. Multi-modal AI frameworks integrating diverse data sources
2. Personalized treatment recommendation systems
3. Explainable AI models to increase clinician trust
4. Federated learning frameworks for collaborative research
5. Edge computing solutions for remote areas

## 5. Conclusion

This study successfully integrated semantic literature review with comparative experimental analysis to provide comprehensive understanding of AI applications for tropical diseases. Semantic analysis of 127 publications revealed rapid research growth with strong deep learning focus, particularly CNN for image diagnosis and LSTM for temporal prediction.

Comparative results showed algorithm selection should match specific problem characteristics and available resources:

1. CNN excelled for image-based tasks but required significant computation
2. LSTM performed best for time series prediction
3. Random Forest emerged as balanced choice with good performance and generalizability

Clinical validations confirmed AI's potential value but revealed implementation challenges. User studies showed cautious optimism from healthcare professionals, emphasizing training and workflow integration needs.

Research gap analysis identified opportunities in:

1. Multi-modal data integration
2. Personalized medicine
3. Explainable AI
4. Resource-limited deployment solutions

Practical implications include evidence-based algorithm selection guidelines, implementation recommendations for different resource settings, and a roadmap addressing current limitations through targeted research. These findings can inform tropical countries' healthcare AI adoption policies and guide future research investments for maximum global health impact.

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