Artificial intelligence in Medical Parasitology diagnosis and drug discovery: A systematic review (2014–2024)

Review Article

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ABSTRACT

Artificial Intelligence (AI) was introduced to the field of Medical Parasitology with many applications including predicting epidemics, diagnosis, therapeutic approaches, and diseases control. The current systematic review was conducted to retrieve published articles in the last decade related to AI applications in Medical Parasitology aiming to provide comprehensive data for more advancement in field diagnosis, and drug development. The PubMed, Scopus and Web of Science databases were screened systematically for articles covering AI in Parasitology published from 2014 to 2024, and SWOT analysis was conducted. In diagnosis, results revealed plenty of AI modalities including mobile applications, machine learning (ML) or deep learning (DL) based methods, neural network image models, convolutional neural network (CNN), digital microscopy, helminth egg analysis platform (HEAP), and transfer learning-based techniques. In addition, screening drug libraries opens new avenues for identification of new drug targets, and drug repurposing or combinations for better therapeutic regimens. It was concluded that AI modalities can help in making decisions and diagnosing parasites in various samples. Moreover, AI represents a crucial step for repurposing available drugs, and discovering drug targets for de novo drug development.

Keywords: AI; deep learning; diagnosis; drug discovery; drug repurposing; drug target; machine learning; parasitic diseases; therapeutic approach.

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Abbreviations: AI: Artificial intelligence; **ANNs:** Artificial neural networks; **C2Bnet:** Composite backbone network; **CNN:** Convolutional neural network; **CoSynE:** Combination synergy estimation; **DL:** Deep learning; **FA:** Fecal analyzer; **FCGAN:** Fuzzy cycle generative adversarial network; **HEAP:** Helminth egg analysis platform; **MALDI-TOF:** Matrix assisted laser desorption ionization time of flight; **ML:** Machine learning; **NTDs:** Neglected tropical diseases; **PDDGCN:** Parasitic disease-drug association predictor; **RT-DETR:** Real time detection transformer; **SWOT:** Strengths, weaknesses, opportunities and threats; **VS:** Virtual screening.

INTRODUCTION

Medical Parasitology is the field in medicine dealing with globally distributed chronic, serious and even deadly parasitic infections affecting humans[1]. Parasites are major etiological agents of neglected tropical diseases (NTDs) that are affecting mainly rural localities in low-income countries. Among them, the WHO recognized Chagas' disease, African sleeping sickness, leishmaniasis, onchocerciasis, lymphatic filariasis, echinococcosis, neurocysticercosis and schistosomiasis. They predominate in Africa, Asia and South America especially with poor sanitation and animal contact[2,3].

Artificial intelligence (AI) has been introduced to serve the aiding of diagnosis, management, and control of parasitic diseases. The AI concept goes back to Alan Turing (1950) and was first described in 1956 by John McCarthy as "The Science of Making Intelligent Machines"[4]. In medicine, AI dramatically evolved over the last 50 years, with many subtypes that include machine learning (ML), deep learning (DL), computer vision, and natural language processing. In fact, AI opened new avenues in various fields in medicine, helping to personalize management, provide predictive models for diagnosis and treatment responses, serve preventative medicine, enhance accuracy of diagnostic modalities and improve overall health outcomes[4].

Classic ML predictive models segment extracted photos, and identify regions of interest, *e.g.*, normal tissues versus tumor, the process that is called "radiomics". The goal of radiomics is extraction, and analysis of a large number of morphological features from medical images, *e.g.*, size, shape or diameter, to generate imaging biomarkers that can be used to improve clinical decision-making, particularly in fields of oncology, neurology, and cardiology[5].

On the other hand, DL represents a specific ML subfield using data algorithms. Artificial neural networks (ANNs) and convolutional neural networks (CNNs) are types of DL models serving different purposes based on their structure and strengths. In

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fact, ANNs are simple fully connected networks used for tasks involving structured data, like financial modeling, or classification tasks with non-image data. On the other hand, CNNs are designed for image processing tasks. They include convolutional layers that apply filters to sections of the image, capturing spatial and hierarchical features like edges, textures, and complex patterns. This makes CNNs highly effective for applications in medical imaging, radiomics, and where spatial relationships in data are crucial. Compared to ANNs, CNNs use fewer trainable parameters to process image data that improve computational efficiency[6]. Generally speaking, the idea of those networks is using convolutional layers among neuronal layers to translate image processing task to specific nuclear function[7].

For AI applications in the field of developing novel drug regimens, a computational model was designed to predict the associations between parasitic diseases and drugs using graph convolutional networks (GCNs), *i.e.*, termed PDDGCN. The molecular descriptions of anti-parasitic drugs are introduced with the genetic markers of the parasitic diseases to be analyzed. The predicted outcomes of possible associations are investigated or explored in clinical researches to reach better therapeutic efficacy[8].

In the field of Medical Parasitology, AI facilitated remote Parasitology teaching and training using virtual microscopy, virtual libraries and telemedicine[9]. Based on epidemic prediction, genetic, and clinical factors, AI modalities are applied in decision formulation for diagnostic applications (Fig. 1), and discovering novel therapeutic regimens (Fig. 2). Therefore, the current systematic review was conducted to retrieve published articles related to AI applications in Medical Parasitology in the last decade, aiming to provide comprehensive data for more advancement in the field of AI in Medical Parasitology diagnosis and drug development.

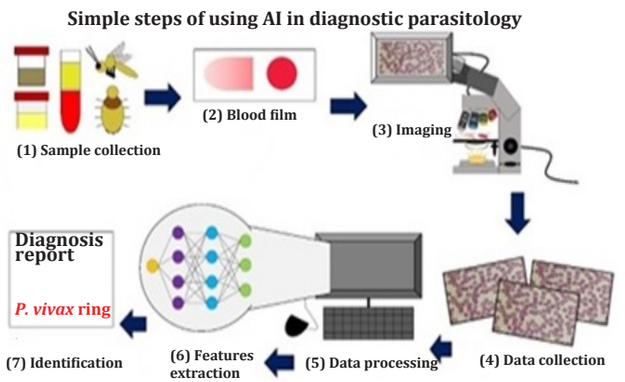

Fig. 1. A simplified diagram for AI application in the diagnosis of parasitic diseases. Data from patient samples is gathered, and digitized. The AI modality assists in identifying, and extracting key features of parasites to enable accurate and rapid analyses. In the data processing, AI models analyze patterns and predict infection types. Illustrated by Taha NM.

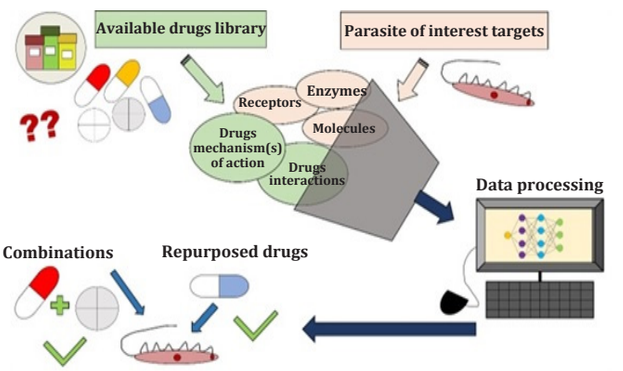

Fig. 2. A simplified diagram for AI application in drug discovery of parasitic diseases. The AI machines screen available drug libraries and the elaborated data are analyzed using parasite target molecules, receptors, enzymes, to find the best matched compound. Illustrated by Taha NM.

Screening and selection of literature studies: The guidelines of preferred reporting items for systematic reviews and meta-analyses (PRISMA) were followed[10]. Published articles on the use of AI in Parasitology were collected from databases of PubMed, Scopus and Web of Science covering the period from 2014 to 2024. All studies evaluating AI modalities in diagnosis, and drug discovery in Medical Parasitology were included. The used keywords included artificial, diagnosis, drug repurposing, drug targets, intelligence, parasite, parasitic diseases, parasitology, and treatment. Exclusion criteria included: 1) grey literature; 2) studies that are unavailable in English; 3) articles concerned with parasites not pathogenic to human; and 4) articles searching for vaccines. Figure (3) represents the PRISMA flow diagram for the search process.

Strengths, weaknesses, opportunities, threats (SWOT analysis): Following data collection, a SWOT analysis was done to explore areas related to

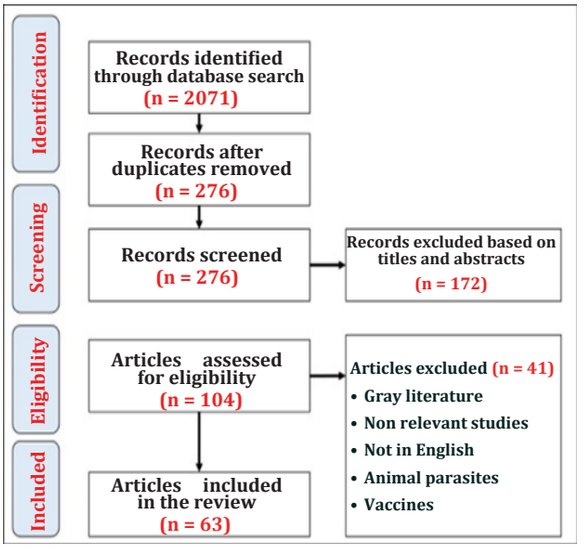

Fig. 3. PRISMA flow diagram representing the search process for AI articles in Parasitology.

AI application in Parasitology. The main concept of SWOT analysis is to help giving practical orientation to strategic management. It helps the pinpointing of strengths and opportunities associated with AI application in Parasitology fields. On the other hand, identifying weaknesses and threats at this early stage when AI models are progressively attracting medical field interests; thus benefiting from its positive points and preventing negative outcome[11].

A total of 2071 papers documented AI in Medical Parasitology: 63 articles (51 studies for diagnostic modalities, and 12 studies for screening drug libraries) published from 2014 to 2024 were included in the current study.

Modalities used in diagnosis of parasitic diseases

In the current review, 51 articles investigating different AI modalities were included to assist in classification, identification, and risk prediction of parasites in different samples and microscopic slides (Tables 1–4). The modalities included mobile applications, ML- or DL-based methods, neural network image models (artificial and deep), CNN, digital microscopy, HEAP, and transfer learning-based techniques.

***Plasmodium* spp.** (Table 1)

Several articles illustrated the use of AI models in diagnosis of malaria parasites. The most described approach was ML-based models that used image analysis (*e.g.*, EasyScan Go) technique connected to a microscope screening Giemsa-stained blood films. According to pre-trained faster region based CNNs for blood examination, differentiation between infected/uninfected red blood cells and parasitic stage specification from unprocessed heterogenous smear images were achieved with average precision of 0.99[12]. Examination of Giemsa-stained blood smears using EasyScan Go yielded 91.1% sensitivity and 75.6% specificity[13]. Based on malaria microscopy image data from NIH national library of medicine, malaria diagnosis of large number of cases was done by applying CNN algorithm with accuracy of ~ 97.81%[14]. In the 'AI-based object detection system' for malaria diagnosis (AIDMAN), the Yolov5 model was used for detection of plasmodial stages in thin blood smear followed by cellular classification. Finally, a CNN classifier was applied for diagnosis using blood smear images. It resulted in clinical validation accuracy of 98.44%[15]. A DL-based approach was used for detection of the parasite's stages in blood smear utilizing positive and negative images. Data augmentation was done to increase size of database. Then YOLOv8 algorithm was used for model training, and parasites were counted using a counting formula. This model showed accuracy 95% in parasite detection[16]. EfficientNet is another DL-based approach implemented for malaria detection using red blood cell images. This approach showed 97.57% accuracy in malaria detection[17].

Additionally, various algorithms were described that allowed discrimination of different *Plasmodium* spp. (*P. falciparum*, *P. malariae, P. knowlesi, P. cynomolgi,* and *P. ovale/vivax*) with average sensitivity and specificity that exceeded 96.8% and 99.3%, respectively with best results observed for merozoites[18]. In that study, an automated robotized light microscope allowed detection of *Plasmodium* infection and the stage of infection through auto-focusing the sample, and tracking the entire slide. Akcakır *et al*.[19] used another technique that allowed them to visualize a quantitative phase image of infected erythrocytes in a whole blood sample, enabling them to capture thousands of RBCs in a single field. The study recorded 91% specificity and 72% sensitivity.

Using a mobile application based on AI modalities for malaria diagnosis was described by Oliveira *et al*.[20]. In addition, using mid-infrared spectra to detect different species of malaria even in anemic conditions was described in a field study in rural Tanzania[21]. Moreover, an AI-based model that utilized the whole genome sequence data of malaria parasite was used for diagnosis of malaria and detection of the geographic origin of infections[22].

On the other hand, Picot *et al*.[23] developed an automated hematology analyzer for diagnosis and follow up of imported malaria in non-endemic areas, with reported sensitivity of 100% and specificity of 98.39% compared to the microscope. Additionally, this model provided accurate differentiation between *falciparum* and non-*falciparum* parasitemia and represented a reliable modality for follow up of patients on days 3, 7, and 28. Interestingly, another study that was conducted in Paris on imported cases of *P. falciparum* formulated a novel CNN model (MALARIS) to accurately estimate parasitemia in blood and help the successful management[24].

Tissue parasites (Table 2)

For *T. cruzi*; a motion-based counting system is used to quantify motile *Trypanosome*s in culture samples[34]. Another modality, hybrid DL-based AI platform (CiRA CORE) utilizes pattern recognition highlighting the nucleus and kinetoplast using an attention map to diagnose *T. cruzi*, *T. evansi* and *T. brucei*[35]. Additionally, an AI program was designed to use a hybrid DL technique of object identification and classification, and NN backbones on the in-house low-code AI platform (CiRA CORE). This model can identify and classify *Trypanosoma* species from microscopic images[36]. Leishmaniasis was also diagnosed using an AI modality that included automated identification using AlexNet, a DL algorithm to identify lesions photos[37]. Other techniques included ML-based systems using the Viola-Jones algorithms[38], LeishFuNet (a DL framework)[39] and DeepLeish modality[40]. The FCGAN, a transfer learning-based microscopic image recognition method, was assessed

Table 1. Different AI based methods used in the identification of malaria.

Applied technology	Results	Ref.
ML that detects infected/uninfected RBCs.	Precision 0.99	[12]
ML using EasyScan Go model*	Sensitivity 91.1%, Specificity 75.6%, Species identification accuracy: *P. falciparum* (93%), *P. vivax* (92%).	[13]
CNN algorithm based on microscopy image data from the National Library of Medicine	Accuracy 97.81%.	[14]
AIDMAN using YOLOv5 model@	Clinical validation accuracy 98.44%.	[15]
DL for accurate detection of parasitaemia.	Accuracy 95% with significantly less time spent by malaria experts.	[16]
DL for malaria detection	Accuracy 97.57%.	[17]
Imaging smartphone application and robotization of conventional optical microscopy	Precision 92.10%, Recall 93.50% recall.	[18]
DL using VGG16 model#	Specificity 98% Sensitivity 57%.	[19]
MicroApp mobile system	Accuracy 91%.	[20]
ML using mid-infrared spectroscopy	Accuracy 90%, Performance unaffected by various levels of anemia.	[21]
ML using whole genome data for geo-classification	Accuracy > 90% at a country level.	[22]
ML using flow cytometry model and Sysmex XN-31 for imported malaria diagnosis	Sensitivity 100% Specificity 98.39%.	[23]
CNN: Top-classifier CNN (MALARIS)	Strong correlation with a coefficient between 0.87 and 0.92.	[24]
CNN: Computer aided diagnostic algorithm	Promising outcomes. Manual verification of performance	[25]
CNN: Channel squeezed$ and boosted CNN image model	Accuracy 97.98%	[26]
DL algorithm for diagnosis and classification	Average analysis time 0.01 seconds. Recall 96%, Precision 94.9%, Sensitivity 96.8%, Specificity 99.3%.	[27]
ML/DL algorithms	Classification accuracy 99%.	[28]
DL: A real time detection transformer (RT-DETR) algorithm^ for patient level detection (positive or negative)	Accuracy 79.4% Recall 81.9%.	[29]
CNN model	Batch size decreased F1-score accuracy and average training time.	[30]
MALBoost& using gene regulatory network analysis	First approach to easily and efficiently allow gene regulation network construction.	[31]
NN model: Risk prediction with back propagation (BP)	Performance of the BP neural network model Sensitivity 71% Specificity 73.61%.	[32]
ML to predict liver stage development *in vitro* using microscopic images	Sensitivity 84.6%, Specificity 83.3%.	[33]

***:** EasyScan Go is a ML-based digital microscope developed to facilitate malaria diagnosis through automated image analysis of blood smears. The model combines with microscopy to improve the accuracy, and speed of malaria detection, even in resource-limited settings; **@:** YOLOv5 model is a state-of-the-art DL model specifically designed for object detection tasks. It is part of the YOLO family, known for its speed and accuracy in detecting objects in images or videos; **#:** Visual geometry group 16 is a CNN with 16 weight layers used to detect *Plasmodium* spp. by analyzing blood smear images, or classifying medical images; **$:** Channel-squeezed is an advanced CNN variation designed to optimize computational efficiency and improve performance in image recognition tasks; **^:** ML model based on transformers architectures, designed for real-time detection of objects to identify and classify objects in images and videos, and to determine its exact location; **&:** MALBoost is a computational tool designed for gene regulatory network analysis to focus on integrating ML to study regulatory mechanisms in *Plasmodium* biological systems.

for identification of *T. gondii* using Fuzzy Cycle Generative Adversarial network with accuracy of 94%[41]. Additionally, microfilariae of *L. loa, M. perstans, W. bancrofti* and *B. malayi* were detected using real time quantification[42].

***Schistosoma* spp.** (Table 3)

Meulah *et al*.[43] reported an innovative semi and fully automated Schistoscope 5.0 for optically identifying and quantifying *S. haematobium* eggs in urine samples. Through AI algorithms for images analysis, comparable sensitivities of 80.1% and 87.3% were recorded in semi and full automation respectively. Notably, specificity elevated from 48.9% in semi-automated to 95.3% in fully automated. Similarly, Oyibo *et al*.[44] developed a trained DNN model using dataset with over 5000 photos of *S. haematobium* eggs captured from biological samples. In addition, Makau-Barasa *et al*.[45] tested automated modalities based on AiDx NTDx multi-diagnostic Assist. Microscopy for determination and

Table 2. Different AI based methods used in the diagnosis of tissue parasites.

Disease	Applied technology	Results	Ref.
Trypanosomiasis	**ML:** A motion based counting system*	Good correlation of cell counts.	[34]
	DL-based Tryp dataset for box annotations of microscopy images	Advance research in diagnosing sleeping sickness.	[35]
	Hybrid **DL**-based AI platform (CiRA CORE)@	Effective AI algorithm.	[36]
Leishmaniasis	Automated identification using AlexNet#, a **DL** algorithm, to identify lesions photos	Average accuracy: 95.04%.	[37]
	ML-based system using the Viola-Jones algorithm$	**Macrophages containing *Leishmania*:** Recall 65%, Precision 50%, **Amastigotes outside macrophages:** Recall 52%, Precision 71%.	[38]
	LeishFuNet&, a **DL** framework	Accuracy 98.95 Specificity 98%, Sensitivity 100%; Precision 97.91%; F1-score 98.92%.	[39]
	DL method (DeepLeish)^	MAP score: Fine-tuned YOLOV5 73%, Faster RCNN: 54%; SSD: 57%.	[40]
Toxoplasmosis	**Transfer learning-based method** (FCGAN) (Cycle GAN)	Accuracy: 93.1-94%.	[41]
Filariasis Microfilariae of *W. bancrofti, B. malayi, L. loa, M. perstans*	**CNN:** Real-time quantification using mobile microscopy.	**Screening algorithm:** Precision (94.14%), Recall (91.90%), F1 score (93.01%); **Species differentiation algorithm:** Precision (95.46%), Recall (97.81%), F1 score (96.62%)	[42]

***:** Motion-based counting system for *T. cruzi* refers to a technological setup designed to quantify motile parasites in a sample; **@:** CiRA CORE is a hybrid DL-based AI platform that is designed for complex biological data analysis; **#:** AlexNet architecture is a deep CNN for image classification and identification tasks; **$:** Viola-Jones algorithm is a ML-based framework primarily used for object detection in images and videos; **&:** LeishFuNet is a DL framework designed specifically for the detection and classification of *Leishmania* (FuNet is derived from "fusion network); **^:** DeepLeish is a DL method specifically designed for automated detection and classification of *Leishmania* in microscopic images of blood smears; **%:** FCGAN refers to the uses of fully convolutional layers in both the generator and the discriminator networks (this structure allows FCGAN to be efficient, particularly for tasks involving image generation); **F1** score measures predictive performance, and it is calculated from the precision and recall of the test; **MAP score:** Mean average precision**; SSD:** Support system for detection; **RCNN:** Region-based CNN.

quantification of *S. haematobium* recorded sensitivities and specificities of 90.3%-98%, and 89%-99% in semi and fully automated modalities, respectively. Meulah *et al*.[43] also supported the role of the Schistoscope, as a promising diagnostic modality in detecting and quantifying *S. haematobium* eggs in urine samples with a special role in preserved slides and retrospective analysis in low-resource settings. Compared to conventional microscopy, the Schsitoscope showed 87.3%[43] and 98%[45] sensitivities in 2 studies, with a lower specificity (48.9%) in one study[43]. While the second study showed 99% specificity[45], the conventional microscopy showed 96.4%. Moreover, Schsitoscope revealed 62.9% and 78% sensitivities in comparison to composite reference standard (CRS) consisting of real time PCR and lateral flow testing.

Intestinal parasites (Table 3)

Accurate diagnosis of intestinal parasites is highly crucial, as they represent one of the main etiological risk factors of malnutrition, underdevelopment and anemia, especially in children living in developing countries. However, many limitations are encountered in conventional microscopic examination including time consuming, lack of equipment and expertise. Therefore, the need for time saving and convenient approaches in diagnosis would be of great value, and updated AI can provide better services to patients in remote underdeveloped areas[46,47].

Koydemir *et al*.[48] investigated a field portable system for *G. lamblia* cysts identification and quantification in water samples. The system was composed of a smartphone connected to handheld fluorescent microscope. Sample cassettes used 5 µm filters to capture cysts followed by rapid algorithmic analysis. This platform showed 79% efficiency and 84% sensitivity with a promising role in monitoring water quality in low resource and remote areas. Additionally, Mathison *et al*.[49] used a CNN that could screen negative trichrome slides, with reported positive agreement 98.88% and negative agreement 98.11% based on slide level.

Naing *et al*.[46] proposed a YOLOv4-tiny model, as an automated diagnostic tool for detection of stages of intestinal protozoan cysts in stool with sensitivity of 95.08%. Similarly, Boonyong *et al*.[47] developed a convenient, time saver, fully automated feces analyzer, Orienter Model FA280 (People's Republic of China). Reported limitations included high cost and low sensitivity.

Three Yolo approaches Yolov4-tiny, Yolov3, Yolov3-tiny were designed to recognize 34 intestinal parasitic classes including helminthic eggs in human feces. It gave 96.25% precision and 95.08% sensitivity for Yolov4-tiny[46]. The performance of fully automated feces analyzer Oriental model 280 (FA 280) was compared to formalin-ethyl acetate concentration (FECT). Although FA 280 is safe, simple, rapid and convenient for stool examination for parasitic detection, it is of high coast per sample and low sensitivity compared to FECT[47]. Ward *et al*.[50] developed a DL-based detection model for soil-transmitted helminths detection. The model identifies eggs of *A. lumbricoides, T. trichiura, S. mansoni* and hookworms in Kato-Katz prepared stool smears with average precision and recall of 94.9% and 96.1% respectively. Almost the same as previous models; a study by Lundin *et al*.[51] used an image-based AI to diagnose soil-transmitted helminths and compared the results with manual microscope-diagnosed stool samples, collected in 2020 from school children in Kwale and Kenya. The sensitivity of the DL system reached 80%, 92% and 76% and specificity of 98%, 90%, 95% in diagnosing *A. lumbricoides, T. trichiura* and hookworms respectively, with 10% more detection of eggs in lightly infected samples compared to conventional microscopy.

Table 3. Different AI based methods used in the diagnosis of schistosomiasis and intestinal parasites.

Disease	Applied technology	Results	Ref.
Schistosomiasis	**Schistoscope**[!] 5.0 for optical digital detection and quantification.	Sensitivity and specificity: Semi- automated 80.1%, 95.3%, Fully- automated 87.3%, 48.9%.	[43]
	Automated microscope (**Schistoscope**) with AI.	Robust, stable optical performance of the device.	[44]
	AiDx NTDx[@] multi diagnostic assisted microscopy.	Semi-automated: Sensitivity: 90.3% Specificity 89% Fully automated: Sensitivity 98%, Specificity 99%.	[45]
Intestinal parasites	**Automatic object detection** of protozoan cysts and helminthic eggs.	Precision 96.25%, Sensitivity 95.08%.	[46]
	Fully automatic fecal analyzer, Orienter Model **FA280**[**]	Fair overall agreement for the species identification.	[47]
	A field portable system[#] for identification and quantification of *G. lamblia*.	Sensitivity 84%.	[48]
	AI and digital slide scanning using a **CNN** model.	Accuracy 98.88%.	[49]
	Digital pathology device[&] for automated scanning and detection[%]	Precision 94.9%, Recall 96.1%, Inference time 1.58 sec/image.	[50]
	Digital mobile microscopy	Sensitivity for *A. lumbricoides* 80%, *T. trichiura* 92%, Hookworm 76%, Specificity for *A. lumbricides* 98%, *T. trichiura* 90%, Hookworm 95%.	[51]
	HEAP–DL based	Increased efficiency of manual validation, adapt to low-cost computers.	[52]
	Digitalization of microscopic analysis[^]	Precision 98.44%, Recall 80.94%.	[53]
	DL architecture + Composite Back-bone Network (C2BNet)[*]	C2BNet showed satisfactory performance, with more precise detection of eggs from 2D microscopic image.	[54]
	CNN based model.	Sensitivity 92.2%, Specificity 91.1%, Accuracy 91.2%.	[55]
	VETSCAN IMAGYST[$] screening.	Sensitivity 75.8–100%, Specificity 91.8–100%, Time 10–14 min.	[56]
	Morphometric and ecological data analysis using ML% for taxonomic identification.	A novel procedure for taxonomic species identification supporting future research.	[57]

!: A diagnostic device designed for the detection and quantification of *S. haematobium* eggs in urine samples using optical digital microscopy; **@:** An intelligence integration that focuses on NTDs; **#:** Refers to an analytical device designed for use outside laboratory settings; **$:** A diagnostic platform designed for veterinary use. It integrates digital imaging and AI to facilitate the identification of parasites, bacteria, and other pathogens in animal samples; **%:** A ML application for processing, and interpretation of data related to the physical characteristics and ecological patterns of organisms used for identification and classification; **^:** Digitalization of microscopic analysis for converting traditional, manual microscopic examination into a digital format using advanced imaging and computational technologies; **&:** A device used for automated scanning and detection that digitizes tissue slides for automated examination, analysis, and diagnosis; ***:** A DL architecture designed to enhance object detection by utilizing multiple backbone networks, instead of relying on a single, larger backbone; ****:** A fully automatic digital fecal analyzer designed for parasite detection. It uses advanced automation and AI to perform multiple tasks, such as sample mixing, imaging, and analysis.

Lee *et al*.[52] created the helminth egg analysis platform (HEAP) for diagnosing and quantifying helminth eggs for medical technicians' assistance, as a good education and training resource. Similarly, Dacal *et al*.[53] used AI for detecting soil-transmitted helminths and Wan *et al*.[54] used a DL-based object detection model for parasitic egg detection with improvement in the performance of their models regarding motion blurring, zooming and focusing failure. Utilizing a novel approach, Gan *et al*.[55] developed a CNN for hookworms' detection in capsule endoscopy photos with sensitivity 92.2%, specificity 91.1% and accuracy 91.2%. The VETSCAN IMGYST system which consist mainly of three components: a simple preparation device, a scanner and an analysis software was compared as a fecal preparation method to conventional fecal flotation techniques and assessd as screening system for parasitic detection. It showed a diagnostic sensitivity 75.8-100% and specificity 91.8-100%[56]. Besides, ML was used as a new approach for taxonomic identification via egg characterization of capillariid species deposited in institutional helminth collection. This approach provided a novel technique for taxonomic species identification, data integration from central biological collections and the logic of AI techniques[57].

Characterization of medically important arthropods and snails (Table 4)

Similarly, several AI modalities have been described for identification of medically important arthropods, and snails. The major health problem of malaria control was a target for improvement by applying AI models. Nabet *et al*.[58] developed an AI model that can recognize spectral patterns associated with laboratory-reared *A. stephensi* mosquito (aged 0-10 days, 11-20 days and 21-28 days), with best prediction accuracies of 73%, 89% and 78% respectively. This method allowed predicting *Anopheles* mosquito drivers for infection such as mosquito age, blood feeding state and detecting the possibility of *P. berghei* infection.

Besides, ANNs were coupled with matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry to predict drivers of *Anopheles* mosquito for malaria transmission[58]. The AI technology that involves well-trained algorithms for arthropods images analysis was established with 98.8-99.0% precision. In the same context, DL-based algorithms were used to identify *A. americanum, D. variabilis,* and *I. scapularis* ticks with 99.5% accuracy[59,60]. Additionally, *R. microplus* egg hatching prediction was done effectively using DL-based automatic method[61]. In addition, DL-based visual model was tested for intelligent *O. hupensis* snail recognition with precision 90.1%[62].

Modalities used in treatment of parasitic diseases (Table 5)

The present study discussed 12 articles dealing with drug targets screening for better treatment and combination modalities. Targeted parasites included

Table 4. Different AI based methods used in the identification of snails and arthropods.

	Applied technology	Results	Ref.
A. stephensi	**ANNs** + matrix assisted laser desorption ionization time of flight (MALDI-TOF)[@] mass spectrometry.	Prediction accuracy: Mosquito age 73%, blood feeding 89%, *P. berghei* infection 78%.	[58]
Arthropods	AI technology involving analysis of pictures using well-trained algorithms[#]	Precision 98.8-99.0%.	[59]
A. americanum, D. variabilis, I. scapularis.	Ticks identification tool using **DL** algorithms.	Accuracy 99.5%.	[60]
***R. microplus* larva**	**DL** based automatic method to predict hatching based on egg morphology of tick.	No statistical difference. Validated and proved method to be effective with considerable reduction in time to obtain results.	[61]
***Oncomelania hupensis* snail**	**DL**-based visual model[*] for intelligent snail recognition.	Precision 90.1%, Sensitivity 91%, Specificity 97.5%, Accuracy 96.2%, F1 score 90.51%.	[62]

@: A powerful analytical modality combined with ANNs to characterize biomolecules measuring their mass-to-charge ratio; **#:** Well-trained algorithms based on ML models used for accurate predictions or decisions based on a large amount of data for different arthropods identification; ***:** A DL-based visual model for intelligent snail recognition uses ML algorithms to automatically identify and classify different species of snails.

Plasmodium spp., *Trypanosoma* spp., and *Schistosoma* spp. Global morbidities and mortalities from parasitic diseases represent a major health concern. Most available anti-parasitic drugs are not 100% effective with potential development of drug resistance. In addition, the available anti-parasitic medications have many adverse effects and low safety margins. The proposal of new therapeutic targets using AI models would accelerate the process of drug discovery[63,64]. Utilizing Waikato environment for knowledge analysis (WEKA), a free software consisting of collection of ML and data analysis, Kumari and Chandra[63] created a predictive modality (random forest based model). The designed modality is suitble for classification, and regression tasks in ML. It constructs predictors used for classifying diseases, or identifying risk factors based on genetic data, medical images, and clinical records. The study recorded 97.94% specificity, and 97.3% accuracy. These models can suggest anti-malarial candidates from classified vast datasets of compounds.

They identified 18 non-toxic compounds out of the 59 bioactive anti-malarial candidates that inhibit aspartyl aminopeptidase (M18AAP) of *P. falciparum*.

In addition, Williams *et al*.[64] introduced 'eve', a robot scientist based on AI models that was designated to discover drugs economically. 'Eve' re-evaluated various available drugs against parasitic targets, and one of its validated discoveries was TNP-470, an anti-cancer with known dihydrofolate reductase inhibition activity. It showed a potential anti-plasmodial efficacy against *P. vivax*. Similarly, Mason *et al*.[65] applied a ML approach known as combination synergy estimation (CoSynE), to predict interactive combinations using data of previous studies and molecular compositions.

Additionally, new ML quantitative structure-activity relationship (ML-QSAR) models were validated by Borba *et al*.[66], to detect chemical targets against *Plasmodium* stages and provide explanations for the predicted efficacy using explainable AI (XAI). The experiment introduced 6 new compounds with dual efficacy against different stages. A CNN combined with BGRU model showed accuracy 0.9–0.98 in mapping *P. falciparum* mitochondrial proteins, helping identifying therapeutic targets[67].

In correlation, Lima *et al*.[68] applied n integrated AI approach assisted by a virtual screening (VS) method. Shape-based models and ML were used to detect new candidates and protein kinase 7 (PK7) inhibitors were proved to have *in vitro* anti-plasmodial efficacy. Eight virtual hits were evaluated and promising candidates were identified. LabMol-167 suppressed *P. falciparum* and *P. berghei* ookinete conversion and showed low cytotoxicity. Another PK (PK5) was also proposed as therapeutic target for *P. falciparum*. Zhang *et al*.[69] also presented a predicting model for artemisinin resistance using *P. falciparum* transcriptomic data representing a critical step in malaria therapy research. This platform set of rules presented a valid model that uses molecular biomarkers to predict resistance, and its validity was further supported by the first integration within Dream of Malaria (DREAM) challenge[70].

Moreover, Kwofie *et al*.[71] examined the use of ML in predicting novel anti-schistosomal compounds. The DL and ML systems based on deep neural networks acting through dual classifications, were proposed. Moreira-Filho *et al*.[72] also focused on innovative methodologies to identify anti-schistosomal drug candidates. Described approaches included automated techniques, fragmented base screening, computer aided, and AI-based methods. In the same context, Villalta and Rachakonda[73] reported applying structure-based designs for discovering new drug candidates for Chagas disease, accelerating drug discovery process and introducing new promising candidates. Additionally, Landaburu *et al*.[74] discussed the value of using genomics and integrating chemical and genomic data on *Trypanosoma* and other organisms to enhance the process of introducing new therapeutic targets for trypanosomiasis treatment.

Finally, the discovery of the relationships between diseases and drugs is crucial for understanding the pathogenesis of underlying parasitic diseases. The computational methods showed high efficiency in identifying and illustrating disease-drug associations, however, most of AI methods are based on link-based techniques within biomedical, bi-partite networks. Parasitic disease-drug association predictor (PDDGCN) is a suggested model that can facilitate new drug discovery for parasitic diseases. It has been reorganized as a central dataset of disease-drug associations of parasitic diseases utilizing the most updated databases, based on a multi-view graph convolutional network. The PDDGCN platform performs 5 state-of-the-art techniques as well as 4 ML procedures[8].

Table 5. Articles discussing AI assisted drug libraries screening.

Disease	Applied technology	Ref.
PDDGCN	The PDDGCN platform performs 5 state-of-the-art techniques as well as 4 ML procedures.	[8]
Malaria	ML model to discover potential synergistic combinations.	[63]
	Screening drug libraries for drug repurposing. Validated discovery is TNP-470 (Anti-cancer); a potent inhibitor of dihydrofolate reductase.	[64]
	ML model to discover potential synergistic combinations.	[65]
	ML quantitative structure-activity relationship (ML-QSAR).	[66]
	CNN and bidirectional gated recurrent unit (BGRU) to classify mitochondrial proteins.	[67]
	Integrative AI assisted virtual screening (VS) for new anti-plasmodial targets.	[68]
	ML for predicting artemisinin resistance.	[69]
Schistosomiasis	ML using big data for predicting anti-schistosomal compounds.	[71]
	Drug candidates' identification using automated assays, fragment base screening, computer and AI based modalities.	[72]
Trypanosomiasis	AI in Chagas disease drug discovery.	[73]
	Chemo-genomic screens for susceptibility or resistance.	[74]

SWOT analysis following data collection: Results of SWOT analysis regarding strengths, weaknesses, opportunities and threats to AI application in parasitology were summarized in table (6). Application of AI to the field of Parasitology created a revolutionary shift in many aspects. Analysis of associated strengths revealed improved diagnostic sensitivity of parasitological stages, saving time, ability to predict epidemiology of parasitic diseases and efficient prediction of therapeutic targets[8,16,64]. On the other hand, many weaknesses were reported like the huge cost, the need for large data, issues in specificity, sensitivity and accuracy, need for extensive training and technical expertise, and ethical considerations[9]. However, other prospects like increased accessibility of service into remote areas and improved patient care were discovered[22]. Threats reported were the unavailability of accurate or inadequate data for training, system bias, poor infrastructure, the threat to substituting jobs of parasitologists and data security issues[4].

Table 6. The SWOT analysis for AI utilization in Parasitology research.

Strengths	Weaknesses	Opportunities	Threats
•Improved diagnosis sensitivity •Predicting diseases epidemiology •Efficient image acquisition and processing •Time saving •Efficient prediction of therapeutic targets	•Huge cost •Vast data needed •Inadequate specificity, sensitivity and accuracy •Extensive training required •Inadequate technical expertise •Ethical considerations •Data security issues	•Accessibility of service in remote areas •Improved patient care •Availability of information technology support •Expert personnel not required	•Lack of accurate data •Inadequate data for training •Poor infrastructure •System bias •Ethical and accountability issues •Loss of parasitologists jobs •Security issues and hacking

CONCLUDING REMARKS

- The AI divisions like ML and DL can help in making decisions and diagnosing parasitic diseases in various samples, that would save time and efforts and is especially beneficial in settings where there is lack of expertise.
- The AI represented a crucial step for repurposing available drug libraries and discovering drug targets for de novo drug development.
- Modalities of ML-based, and CNN-based models are widely applied in diagnosis of malaria with high sensitivity, and accuracy.
- Satisfactory results were obtained in using DL-based modalities in diagnosis of trypanosomiasis and leishmaniasis.
- Several AI modalities were used for intestinal parasites screening in stool samples and fixed smears, however, main limitations included high cost and low sensitivity.
- Schistoscope-based AI modality was used to identify and quantify *S. haematobium* eggs in urine samples and tissue slides with promising results.
- The ML-based models opened new avenues in drug discovery in malaria, schistosomiasis and trypanosomiasis, through predicting therapeutic targets and drug combinations.

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