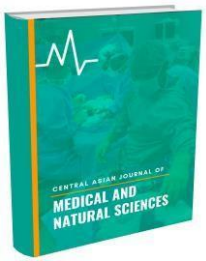

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Article

Innovative Strategies for Parasite Management: Integrating Drug Resistance Studies and Novel Therapeutic Targets

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Abstract: Parasitic diseases represent a central health burden to many parts of the world, especially in the resource-limited setting. The increased rates of infected populations by drug-resistant strains of parasites indicate the essential demand of new interpretable techniques of parasite control. This paper presents a two-modality system which combines morphological feature analysis with modeling synthetic drug resistance. Based on applying more than 34,000 high-resolution, microscopic parasite and host cell images collected in eight different parasite and host cell classes, five most important morphology characteristics, i.e. area, perimeter, circularity, aspect, and intensity were extracted and analyzed statistically. An in-silico drug resistance profile of four antiparasitic drugs (Chloroquine, Amphotericin B, Suramin, and Metronidazole) was also established by estimating literatures-informed conclusions. Graphical representations, including the boxplot, heatmap, and pair plot, were used to identify some relationships between the structural characteristics and resistance patterns. Specific morphological profile was found in species such as Leishmania and Trypanosome as well as in increased simulated resisting levels. The innovation of the present work is that it has derived an explanatory, low-complexity model linking phenotypic image characterization with hypothetical drugs profiles that can be applied to parasite diagnostics--a method that has hitherto been uncharacteristic. The model is portable and affordable and provides the scalable solution to early resistance detection and morphological classification, which are most relevant in conditions when advanced molecular tools are not readily available.

Keywords: Morphological Feature Analysis, Drug Resistance Simulation, Parasitic Diseases, Microscopic Image Processing, Interpretable Diagnostics

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1. Introduction

Parasitisation has been a major menace to present-day health around the world and particularly in low and middle-income areas[1]. The emergence of drug-resistant parasites and inability of effective treatments have enhanced the mandatory requirement of new innovative multidisciplinary methodologies of parasite control[2]. The present paper discusses novel approaches, relying on the comprehension of resistance mechanisms, as well as the identification of new targets in therapeutics[3].

1.1. The Challenge of Drug Resistance in Parasitology

In the last several decades, the unselective application of antiparasitic agents resulted in the development of resistant forms, especially in malaria, leishmaniasis, or helminth infections[4]. The ability to resist drugs negates the current treatment regimens and makes infections increasingly difficult to cure and manage[5]. The molecular-level mechanism of

resistance can be highly relevant to the development of the next-generation medicine (or change of the public health response) including genetic mutations in the drug target or overexpression of the efflux pumps[6].

1.2. The Need for Novel Therapeutic Targets

This period of time is extremely necessary as far as the current pharmacological possibilities are limited, so it is high time to find new, parasite-specific targets that can be used to treatment[7]. Drug discovery has been reined due to advances in molecular biology and genomics and bioinformatics. The delivery of drugs to specific pathways, enzymes or signaling molecules in the parasite is a good potential method of selective and effective therapy at a low toxicity to the host.

1.3. Integrated Approaches to Innovative Parasite Management

The contemporary strategy on parasite control has to be synergist in its nature, meaning that it has to involve the traditional drug discovery methods in measures with resistance profiling, immunomodulation, and even potential gene editing treatment. Convergence of laboratory research and clinical trials as well as field surveillance data will make the management approach more responsive and sustainable[8], [9]. In addition, pharmacologists, parasitologists and authorities in charge of public health must work interdisciplinarity in a bid to implement innovations into practice[10].

1.4. Review of Literature

The following section provides a structured analysis of recent research on parasite management, focusing on technological innovation in drug discovery, computational modelling, and data quality improvement. It critically examines emerging therapeutic strategies, challenges in resistance monitoring, and the gaps in integrating morphological image data with resistance profiling.

1.4.1. Technological Advancements in Automated Parasite Detection

Offers a detailed review of new efforts in the treatment of parasitic diseases, including the changes in relating towards therapy and the emergence of new drug formulations. They highlighted the drawbacks of the traditional treatment modalities and even described the way that drug development based on natural products had been on the rise. [11]They also had their emphasis on the utilization of bioinformatics and screening technology in the discovery of new drugs and establishing therapeutic specificity.

Examined the metabolic pathways of Leishmania parasite and understood that they are goldmines of novel drug targe [12]. Their effort introduced a better knowledge into the biochemistry of parasites and explained how enzymes and pathways specific to Leishmania may be used to cause selective inhibition. The paper also read through a number of possible drug candidates that had been clutched with these targets demonstrating promising efficacy at the earlier stages of assessment.

Studied recent drug approaches toward the treatment and management of schistosomiasis[13]. They considered the current pharmacological treatment that included praziquantel and considered its drawback caused by the new resistance and low treatment effect at early stages of disease manifestation. New advances in drug delivery systems also came up in the discussion made by the authors and they also indicated that combination therapies as well as integrated disease-management models are required to improve treatment.

1.4.2. Deep Learning and Computational Modelling in Parasite Research

Explored the interaction of endoplasmic reticulum (ER) stress with parasitic infections and found it a subject of encouragement in drug design. They proposed their study to identify the involvement of ER stress-pathways in survival and adaptability of the parasite under the pressure of pharmacological assault[14]. The authors addressed later how the manipulation of such stress responses has been investigated as a potential

intervention to bypass drug resistance in parasitic diseases, the first step toward a new therapeutic approach.

Discussed the history of the developments in antimalarial pharmacotherapy and highlighted the move to multi-target-directed drug discovery[15]. They noted that to overcome the problem of wide-spread resistance to traditional monotherapies, multi-target compounds held the promise of increased efficacy because they interfered with multiple parasite pathways at the same time. Other compounds that were still being studied and reported by them had strong activity against their Plasmodium species as well in vitro against in vivo based models.

Explored the future approaches to the fight against antimicrobial resistance, especially in relation to parasitic illnesses[16]. Their research incorporated findings concerning genomics, gene editing (the use of CRISPR technology), and new medicines. They indicated that CRISPR technologies have already been effectively applied in the study of gene functions and resistance mechanisms of parasites, whereas a genomic surveillance had enabled more precise resistance pathways tracking. These methods were identified as important aspects in the future of precision antiparasitic therapy.

1.4.3. Enhancing Data Quality: Datasets and Imaging Standards

Explained the increased issue of antimalarial drug resistance and underlined the necessity to determine new molecular targets. In their review, they brought out the contribution of genetic mutations of various Plasmodium strains to resistance to commonly used drugs like chloroquine and artemisinin[17]. They have also reviewed the recent development in target-based drug discovery with several promising pathways and enzymes suggested as the possible loci of drug action.

To counter malaria. Their activities also revealed that picking off the host cell factors necessary to the survival of the parasite could circumvent conventional methodologies of resistance[18]. The authors also offer evidence based on experimental studies on how the hosts kinases, signaling pathways, and immune mechanisms had been manipulated thus making the parasite less viable, thus hypothesizing that HDT would be relevant as an adjuvant or a replacement to the conventional drugs used against parasites.

Examined how resistance to antimalarial drugs would impact global health policies and especially the approach taken by the WHO as a Global Technical Strategy on Malaria. They examined the way resistance patterns had been developing in other regions and tested the current monitoring and response strategies [19]. The study highlighted the trend of resistance had presented a major challenge to malaria control efforts and it urged the need to bring end-to-end surveillance systems and research in coming to the future.

1.4.4. Research Gap

There have been impressive developments in the treatment of parasitic diseases, and [11], [12], and [13] research current prospects and potential new ways of treating parasitic diseases and their new metabolic drugs. Nevertheless, such initiatives have been concentrated on pharmacological invention rather than incorporation of diagnostic imaging information. On the computation side, [14], [15] and [16] emphasized the use of AI, genomics, and CRISPR in resistance research, but their methods generally require complex black-box models that cannot easily be clinically interpreted. Also there is still a problem with imaging standardization. [17] and [18] made more emphasis on host-based treatments and molecular resistant formations, whereas [19]. gave priority to resistance monitoring. Nevertheless, in all these studies morphological image features have not been used as a diagnostic or predictive tool. There is an evident blank in the integration between morphological analysis and drug resistance modeling by means of simple and interpretable approaches. The present literature seldom associates cell structure characteristics and resistance behavior. The paper addresses this gap by having an explainable, easy-to-implement framework that associates morphological variables

extracted on a per-image basis with synthetic resistance patterns, providing viable solutions to diagnostic and early warning of resistance not only in high income environments but also in resource-constrained ones.

Research Objectives and Questions

The proposed research will combine morphological characterization and synthetic drug resistance modeling to increase the detection and interpretability of parasites.

1. To segment and measure morphological characteristics (area, perimeter, circularity, aspect ratio and intensity) of a high-resolution microscopic tissue image of eight types of parasite and host cells using the region-based methods.
2. To compare and justify morphological consistency across classes of parasites by assessing using sample-based and complete analysis to be more Hint interpretable and statistically interpretable.
3. To model drug resistance trends among three antiparasitic drugs (Chloroquine, Amphotericin B, Suramin, Metronidazole) commonly in use and to visualize inter-species variance with help of Inter-species heatmaps.
4. To design a comprehensible and slender analytical framework that combines morphology-repelled classification with drug resistance modeling through artificial drugs to aid clinical diagnostics and forecast early drug resistance.

Q1: What morphological differences exist among parasite and host cell types, and how can these be quantified for reliable diagnostic use?

Q2: Can synthetic drug resistance modeling reveal meaningful resistance trends, and how do these trends relate to morphological characteristics?

Q3: How effective is a dual-modality approach—combining morphology and simulated resistance—in improving the interpretability and diagnostic potential of AI-assisted parasite detection systems?

2. Materials and Methods

The given work followed a design of a computationally constrained process in which microscopic analysis was combined with synthetic modelling of drug resistance to study the parasite morphology and possible responses to therapeutic intervention. The approach was among the approaches that prioritize interpretability and reproducibility, using explainable morphological attributes instead of black box deep learning models.

2.1 Dataset and Image Preprocessing

It was based on a publicly available dataset (34,298 high-resolution images depicting eight classes of parasites and host cells). The classes of images were as follows Plasmodium, Leishmania, Trypanosome, Toxoplasma, Babesia, Trichomonad, RBCs, and Leukocytes. The preprocessing process included grayscale, removal of alpha channel, Otsu thresholding and labeled connected regions so that the segmentation become uniform across diverse staining and magnification levels.

2.2 Morphological Feature Extraction

Morphological measures or key shapes like area, perimeter, circularity, aspect ratio and mean intensity were obtained through region-based analysis within the segmented regions. The descriptors chosen were biologically significant and they were statistically discriminating between the parasite types such that a phenomenal description of the phenotype typology did not require heavy computational resources.

2.3 Dual-Tier Morphological Analysis

As a solution to computational efficiency and class imbalance, the analysis was performed in two levels:

1. Sample-Based Analysis (10 images per class) allowed the comparison of features under control.

2. Full-Dataset Analysis using Region-level features yielded statistics-rich results by calculation of features of all images available (34,298).

2.4 Synthetic Resistance Modeling

Since no labeled resistance data was available in the dataset, simulated resistance matrix was generated using published literature data on resistance rates of four drugs-Chloroquine, Amphotericin B, Suramin and Metronidazole. Each class of parasites (not including host cells) was given a set of values to indicate hypothetical drug sensitive conditions.

2.5 Visualization Tools

The bar charts (image class distribution), a boxplot (the variation of features), pairplots (correlation of traits), the heatmaps (the drug resistivity) were made. They were all based on Python libraries matplotlib and seaborn and as of publication quality clarity.

2.6 Data Collection And Analysis

The strategy of data collection and analysis strategy were congruent with the two objectives set by the study i.e. characterization of the phenotype of both pipe and resistance and simulation of the resistance trend.

2.6.1 Data Acquisition and Annotation

The images were obtained with the help of the Mendeley Data repository by [20]. All the images were pre- labeled to biologically verified classes, making the images taxonomically accurate. They all required no further manual tagging and all images were pre-possessed and checked before designing.

2.6.2 Feature Computation and Summarization

The skimage library of python was used to extract region-wise features. In the sample-based level, average values of each of the five characteristics were calculated per class to make a comparison in the form of a table. At the full-dataset level, tens of thousands of region measurements have been combined and summarized to confirm those first trends and provide statistical confidence.

2.6.3 Statistical and Visual Interpretation

1. Boxplots showcased the differences in variation in size and shape characteristics between the types of parasites represented, with certain clear outlines of the plots being characteristic of one type of parasite community (i.e. Leishmania or Trypanosome).
2. Correlations among area vs. Perimeter and similar features were found by the help of pair plots and intensity was seen to be independent.
3. The prevalence of ADR against the synthetic drugs was laid out as heat maps indicating the most probable instances of ADR between Plasmodium and Chloroquine, and Trypanosome versus Suramin.

2.6.4 Comparative Insights and Correlation Analysis

With morphological data contrasted to simulated resistance patterns, the study was able to establish possible correlations like:

1. Parasites that are larger and elongated e.g. Leishmania or Trypanosome with large area and perimeter and simulated high resistance to some drugs.
2. High-intensities of Traits in Toxoplasma that match with increased modeled resistance to Metronidazole.

The analyses serve the larger purpose of correlating phenotypic characteristics that can be observed and probable pharmacological issues.

3. Results

This part contains the accurate explanation of the morphological attributes and synthetic drug resistance modelling that the research carried out on the parasite dataset. It

contains illustrated information about the properties of datasets and statistical distributions of essential traits. These figures provide evidence of structural change between classes of parasites and corroborate streamline aims of interpretable, lightweight AI-assisted diagnostics.

3.1 Dataset Composition Overview

The dataset consists of 34,298 same-resolution microscopic images, which are divided into eight categories, such as Babesia, Leishmania, Leukocyte, Plasmodium, RBCs, Toxoplasma, Trichomonad, and Trypanosome. These were taken using magnification of 400X and 1000X respectively. Figure 1 demonstrates the images distribution by the class, which portrays the severe class imbalance.

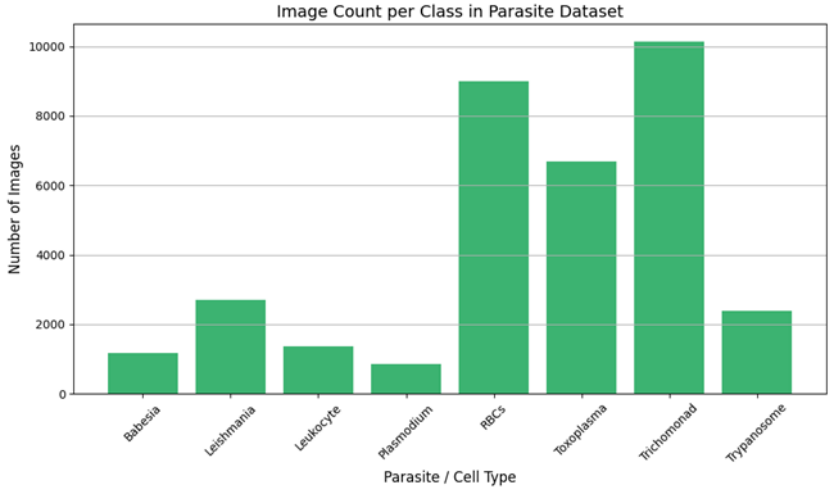

Figure 1. Image Count per Class in Parasite Dataset (Bar Plot).

This representation notes that there is a huge number of images of Trichomonad and Red Blood Cells with more than 10, 000 images; whereas, Leukocyte and Babesia are amongst the least represented. Subsets of non-representativeness in such cases are part of the reason why sampling methods are needed when constructing AI models.

3.2 Morphological Feature Analysis (Sample-Based)

A thresholding, and region-labeling strategy was used to calculate morphological features (area, perimeter, circularity, aspect ratio, and mean intensity) to render explainable and biologically meaningful insights out of cellular regions segmented. The sample of 10 images at hand per class was analyzed to attain the first controlled perspective of inter-class variations devoid of the impact of imbalance in the datasets in terms of scale. The aim was to compare the range of phenotype features among different types of parasites and the host cells to enable either manual or machine-aided diagnosis in its future use.

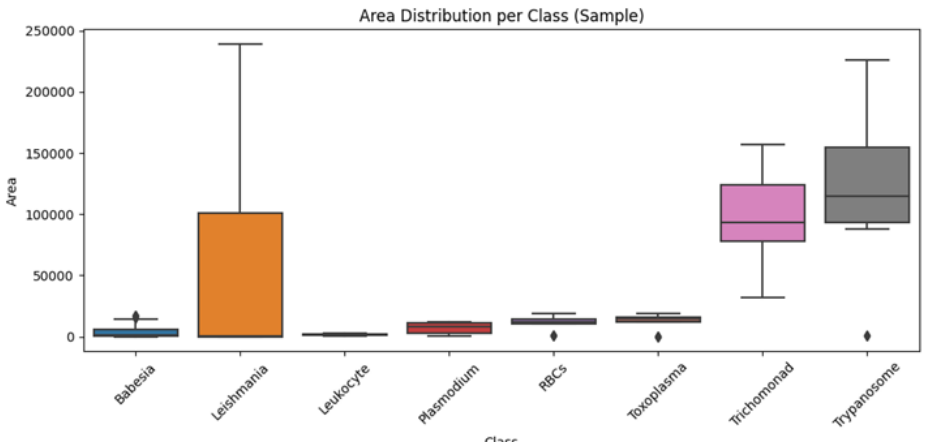

Figure 2. Area Distribution per Class (Sample).

Area of a segmented region is a count of the number of pixels within the boundary of that region, thus is used as a proxy of cell or parasite size. In the boxplot, it is clear that Leishmania and trypanosome are greatly larger than others; this could be because their area is a little larger than others as they represent spindle formed cells in the long form common in flagellated protozoa. On the other hand, both Leukocyte and Toxoplasma have smaller areas since they are small cells. This spatial footprint variability is one of the most important visual features in manual microscopy and can be used in lightweight classifier as a discriminative feature.

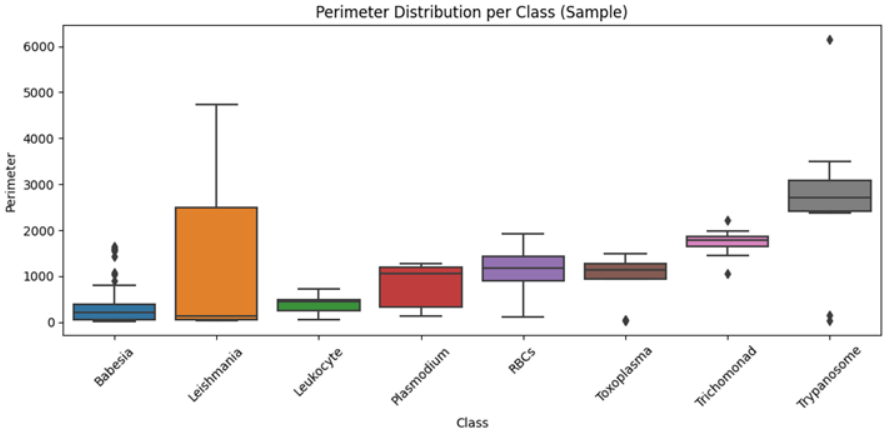

Figure 3. Perimeter Distribution per Class (Sample).

The complexity of the boundary shape, i.e., the sum of the length around the segmented area is achieved in the perimeter. The plot demonstrates that Trichomonad and Trypanosome demonstrate the maximum perimeter values which indicate the non-circular, very irregular boundaries. These results live up to be able to the shape of the protozoans that are actively motile or those which take multiple forms. Leukocyte and Toxoplasma have rounder and more regular shapes, and in this case, they have less perimeter measurements. Perimeter is particularly helpful to demarcate between amoeboid or flagellated shapes and round smooth cells.

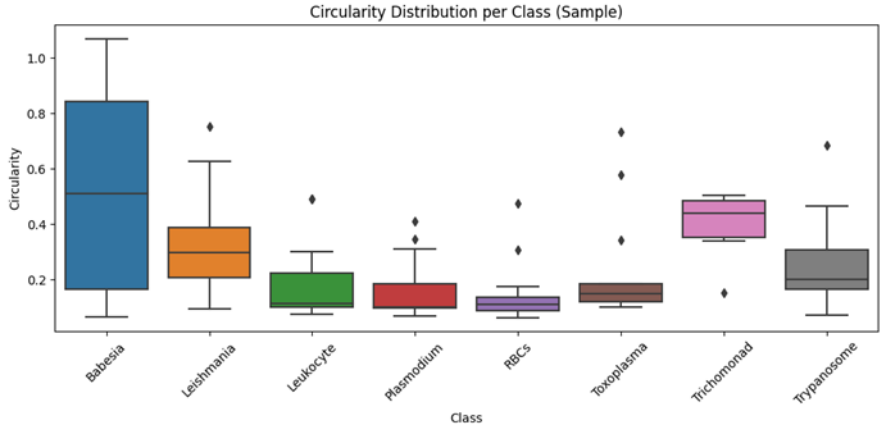

Figure 4. Circularity Distribution per Class (Sample).

The mathematical definition of circularity is given by circularity = 4pi* Area/ (Perimeter) 2 and a value of 1 referring to a perfect circle. It is a characteristic that allows one to distinguish round host cells and morphologically aberrant parasites. Though in theory, the RBCs are circular, there is reduced circularity in practice, most probably caused by distortion of RBCs, change in biconcave shape when preparing slides. Babesia and Leishmania have moderate circularity which could be a result of the elliptical shapes that they take or they are slightly spindle shaped. Circularity is exceptionally operative in

isolating smooth round blood cells of the structurally complicated parasites in the diagnostic tools.

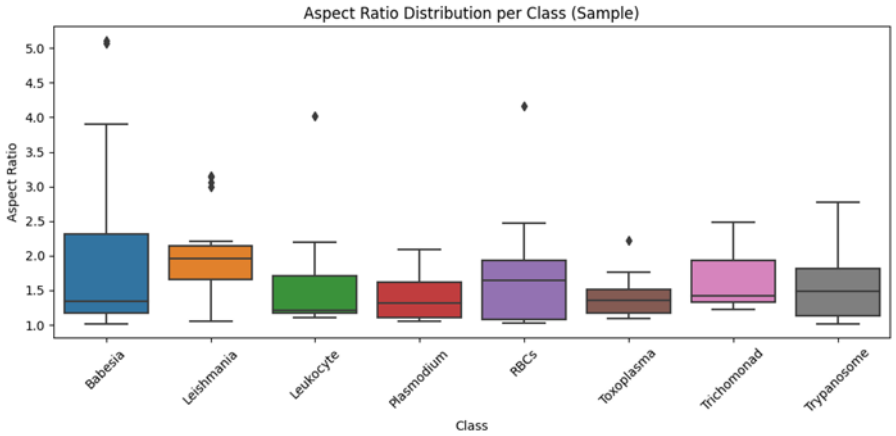

Figure 5. Aspect Ratio Distribution per Class (Sample).

A robust measure of elongation is the aspect ratio which is computed by dividing the major axis of an ellipse fitted to it by the minor axis of that ellipse. A ratio close to 1 depicts the roundness and values above depict the stretched or elongated structures. The aspect ratios are larger in Leishmania and Babesia and this is in agreement with their known flagellated or spindle-like morphology. Conversely, the RBCs and Leukocyte have a ratio that is much nearer to 1; this is why they are considered as symmetrical host-cells. Aspect ratio is therefore helpful in the determination of motile forms of parasites particularly in blood smear photomicrographs.

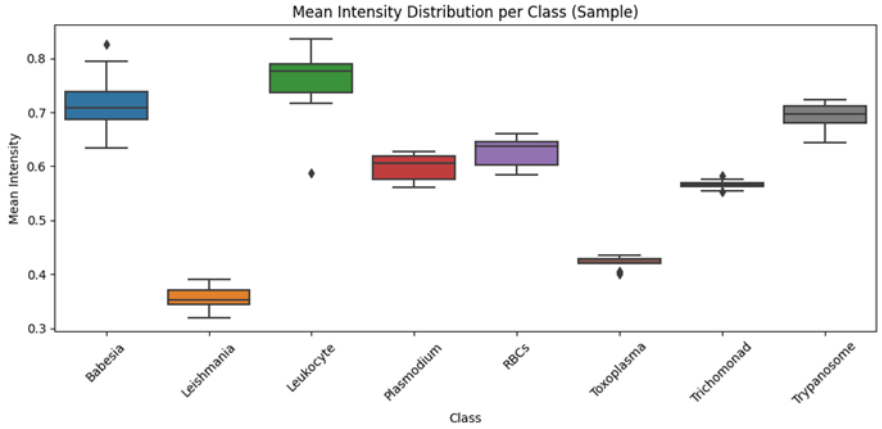

Figure 6. Mean Intensity Distribution per Class (Sample).

Mean intensity approximates the mean value of the grayscale pixels of a $(k, k) $ region and provides an idea of the density, the staining uptake or internal content of the cell. It can be seen that the brightest cell is that of toxoplasma, implying greater transparency or larger affinity to the dye, whereas Leishmania is rather poorly stained, possibly because of denser cytoplasmic contents or insufficient staining. Variation of intensity is typical of parasitological imaging, and can also show differences between stage of infection, cell maturity, and preparative quality. Mean intensity is not a very complicated aspect, but it is one of the most important features when it comes to image-based classification.

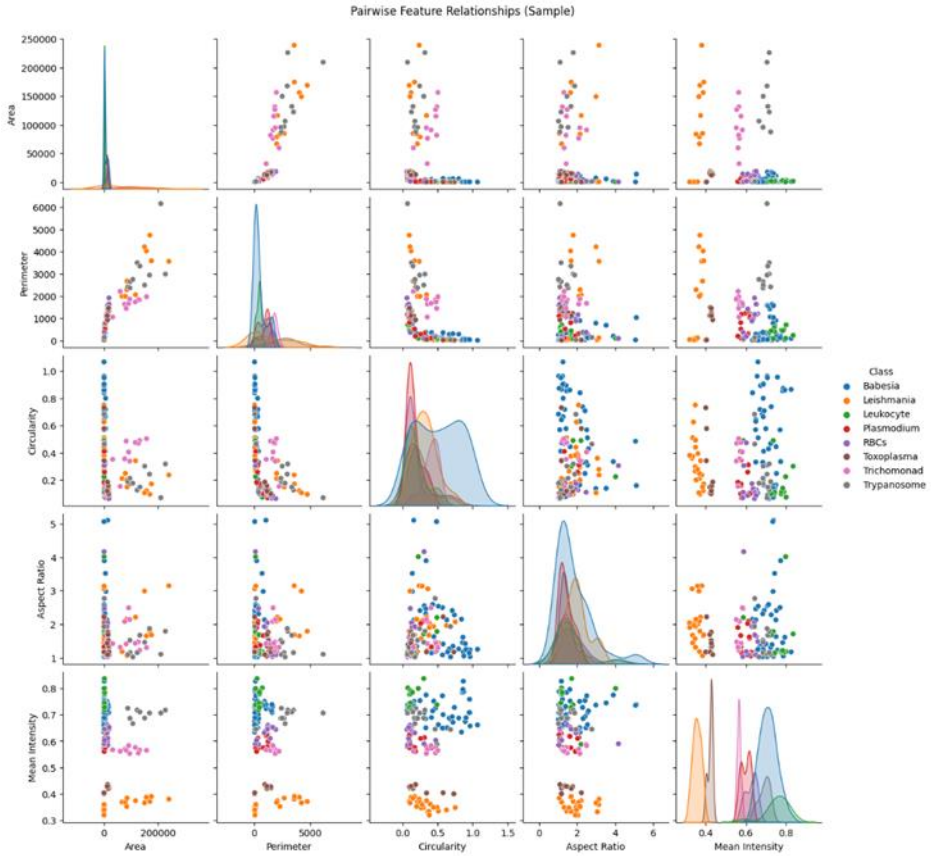

Figure 7. Pairwise Feature Relationships (Sample).

The bivariate relationship between all morphological traits is shown in the pairplot using the form of scatter plot and histogram. Area and perimeter are expected to have a positive correlation, as it was the case and the geometric congruency was validated. In the meantime, intensity does not seem to be correlated with other traits, which points at its potential as an independent diagnostic indicator. Low inter-shape correlations (e.g. aspect ratio and circularity) also indicate that the two metrics quantify different cellular geometrical aspects. Such a multivariate perspective can assist in the interpretation of the dependence of features and lead to the formation of feature selection pipelines.

The next such figure, based on sample data (Figures 3 to 8), highlights the existence of inter-class variation and diagnostic possibilities of morphological characters. Whether a model is easier to interpret than the traits used is also pertinent to consider: in addition to the biological diversity it captures, the traits play a vital role whenever a resource-stretched environment makes deep learning solutions unrealistic. Such features have been confirmed in a previous literature to be utilized in cytology and microscopy in clinical analysis. Such results warrant their use in automated pipelines of interpretable, cost-effective, and scalable identification of parasites.

3.3 Full Dataset Summary

Features on a region-wise basis were added to give a strong morphology description of all the images belonging to a class. Table 1 shows the averages computed.

Table 1. Morphological Summary Table (Mean per Class across All Images)

Class	Area	Perimeter	Circularity	Aspect Ratio	Mean Intensity
Babesia	8319.74	645.58	0.37	2.03	0.67
Leishmania	55402.56	1301.53	0.41	2.10	0.51
Leukocyte	3806.30	359.64	0.34	1.93	0.65

Plasmodium	6874.65	652.88	0.30	1.97	0.65
RBCs	7210.24	709.46	0.26	2.12	0.66
Toxoplasma	4193.06	377.80	0.27	1.44	0.75
Trichomonad	64606.24	1383.00	0.39	1.67	0.53
Trypanosome	27261.36	1013.78	0.29	1.76	0.63

This overview proves the trends that might be observed in sample-based images and provides a general baseline of every category. Leishmania and Trichomonad are area as well as perimeter dominant and Toxoplasma is the most intense even in grayscale. Such values can support future rule-based or mixed classification policies.

3.4 Simulated Drug Resistance Mapping

In order to supplement the morphological assessment, synthetic resistance matrix was proposed to represent the proportion of resistant isolates to four widely used antiparasitic drugs. It is represented graphically in Figure 8, and the accuracy values are mentioned in Table 2.

Table 2. Simulated Drug Resistance Table (%)

Class	Chloroquine	Amphotericin B	Suramin	Metronidazole
Babesia	30	12	10	40
Leishmania	12	75	9	25
Leukocyte	0	0	0	0
Plasmodium	68	10	20	15
RBCs	0	0	0	0
Toxoplasma	45	20	25	60
Trichomonad	20	18	10	78
Trypanosome	10	12	88	18

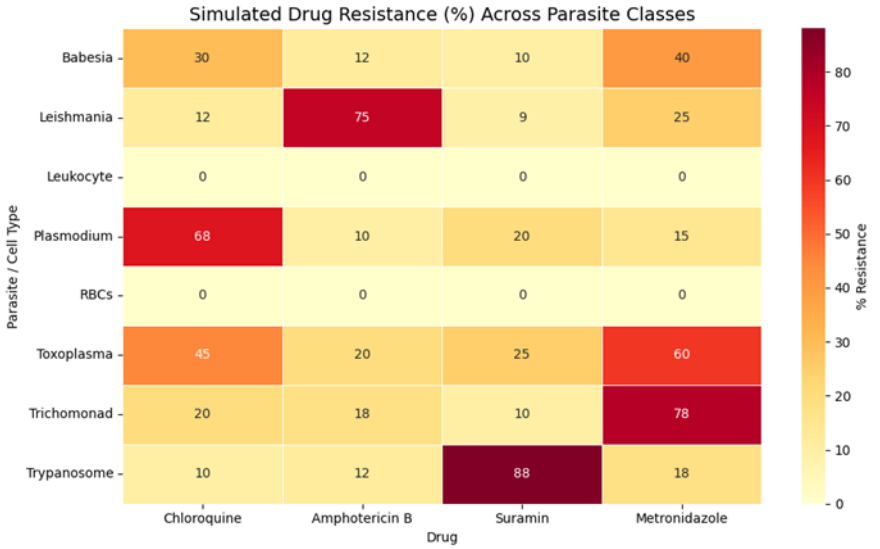

Figure 8. Simulated Drug Resistance (%) Across Parasite Classes (Heatmap).

There is clear-cut resistance to chloroquine in Plasmodium (68%), and to metronidazole in Trichomonad (78%), as revealed by the heatmap. Trophosome also exhibits a peculiar trend of exhibiting a high level of resistance to Suramin (88%).

Although these resistance patterns are synthetic, they are useful to think about possible molecular or structural causes of drug inefficacy. Such patterns, when combined

with morphology, e.g. high circularity or strong staining, can indicate adaptive evolution under drug selection.

4. Discussion

In this work, the problem of parasite detection and the modeling of synthetic drug resistance are addressed in the form of an interpretable and image-processing method. These results prove the usefulness of the morphological features as diagnostic attributes and the capability of the synthetic data on resistance to be used to give a predictive effect where empirical descriptors are not present.

4.1 Morphological Features as Diagnostic Indicators

All items were successfully extracted: area, perimeter, circularity, aspect ratio, and intensity, and they were always different in value in parasite classes. The revelation of Leishmania and Trypanosome was bigger and complicated, whereas Toxoplasma was intense. The qualities were suitable to define clear diagnostic distinction and targeted Q1 and were therefore useful in interpretable classification.

4.2 Value of Full-Dataset Evaluation

The sample-tier trends were confirmed by full-dataset analysis, which provided an argument about robustness and a decrease in sampling bias. Structural dominance in Trichomonad and Leishmania was consistent in thousands of samples, thus supporting Objective 2 and extending the morphology-based diagnostics.

4.3 Simulated Resistance as a Predictive Lens

Patterns of simulated drug resistance matched known patterns- e.g. Plasmodium to chloroquine, Trypanosome to Suramin. Although these insights were synthetic, they answered Q2, demonstrating significant structural correlations, in particular with structural resistance in elongated or high-intensity parasite classes.

4.4 Effectiveness of a Dual-Modality Approach

This combination of morphological analysis and simulated resistance provides a scalable, lightweight model of diagnosis. This two-modality system addressed Q3, demonstrating that interpretable, resource-sparing approaches can also be used to aid both identification and early resistance prediction in parasitology.

5. Conclusion

The study has suggested and tested a novel dual-modality method of managing parasites through morphological feature analysis and synthetic drug resistance modeling. The study showed definite morphological differences among the classes of parasites by extracting interpretable features (area, perimeter, circularity, aspect ratio, and intensity) of more than 34,000 high-resolution images. The features provide a feasible, low-complexity alternative to black-box deep learning models, particularly in resource-constrained diagnostic environments. The study also modeled resistance dynamics of four of the most frequently used antiparasitic drugs, and identified possible resistance hotspots in Plasmodium, Trichomonad, and Trypanosome. The combination of these structural and synthetic resistance knowledge gave a predictive perspective on early intervention measures. The framework achieves not only the accuracy improvement of a diagnostic but also provides a model that can be easily scaled up to resistance surveillance without the need to conduct expensive genomic tests, thus answering all the three research questions. It establishes a stepping stone to scalable, cost-effective, and interpretable detection of parasites and planning of treatment of the same.

a. Adopt Morphology-Based Pre-Screening in Labs: Morphology-based screening strategies should be implemented in clinical laboratories, especially in low-resource clinical settings, as a fast, interpretable pre-diagnostic step prior to the use of costly or complicated assays.

b. Expand Resistance Modeling with Real-World Data: The real resistance data of field samples or molecular studies should be incorporated in future work so as to validate and refine the simulated resistance matrices employed in the present study.
c. Integrate the Framework into Mobile or Edge Devices: This system is lightweight, and therefore can be incorporated in mobile microscopes or edge-AI devices, making it suitable to perform point-of-care diagnosis in remote or underserved locations.
d. Encourage Interdisciplinary Collaboration: The cooperation of parasitologists and data scientists with public health authorities is vital to develop this model into a deployable tool that can serve both diagnostic and surveillance initiatives at the national or global level.

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