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DEEP LEARNING-DRIVEN MOSQUITO SPECIES IDENTIFICATION USING YOLOV5 FOR DISEASE MONITORING AND CONTROL

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ABSTRACT

The classification of mosquito species is essential for the monitoring of the transmission of mosquito-borne diseases, including malaria, dengue, and Zika. This investigation introduces a deep learning-based methodology that employs the YOLOv5 framework to accurately identify mosquito species from images. The model obtained an accuracy of 98% after being trained on a dataset that included three species: Aedes, Anopheles, and Culex. The method utilizes CSPDarknet53 for feature extraction and PANet for feature aggregation, followed by YOLOv5 for final classification. This system provides a reliable solution for the automated identification of mosquito species, aiding in the prevention of diseases and the monitoring of real-time conditions. The precision, recall, and F1-score all exceed 97%. Furthermore, the model's ability to rapidly process images is facilitated by the use of YOLOv5, making it appropriate for integration with mobile or edge devices for field-based applications. The rapid identification of mosquito species in a variety of environmental conditions is made possible by the high accuracy and efficiency of this approach, which could potentially contribute health authorities in the implementation of timely and targeted interventions. This framework can also be developed to include additional mosquito species or to deal with future datasets, thereby increasing its relevance in the global control of mosquito-borne diseases.

Keywords: *Aedes, Anopheles, and Culex, YOLOv5, PANet, CSPDarknet53.*

1. INTRODUCTION

Mosquito-borne diseases, including malaria, dengue, and Zika, present significant public health challenges on a global scale, affecting millions of individuals annually and placing a strain on healthcare systems. The effective control and prevention of these diseases require the timely and precise identification of mosquito species, as the capacity of each species to transmit pathogens varies. Traditional mosquito identification methods, which frequently involve manual examination by entomologists, are labor-intensive, time-consuming, and prone to errors, particularly when implemented on a large scale. The global public health is significantly threatened by mosquito-borne diseases, which are responsible for over one million deaths yearly. Specific mosquito species significantly influence the transmission of diseases such as malaria, dengue, Zika, and chikungunya. It is imperative to identify the species responsible for an increase of diseases in order to predict its spread and implement effective control measures. Entomologists manually identify mosquito species, a procedure that is labor-intensive and time-consuming, and is prone to human error. The rapid identification of potential mosquito species is now possible through the analysis of images by automatic classification systems, which have been made possible by recent developments in computer vision and deep learning. This paper suggests a mosquito species classification system that is based on deep learning. The system will utilize YOLOv5, CSPDarknet53 as a backbone, and PANet for feature aggregation.

The model is trained on images of three mosquito species—Aedes, Anopheles, and Culex—and subsequently assessed on a collection of 2,900 images. The primary objective is to facilitate the control of mosquito-borne diseases by achieving a high-accuracy, real-time species classification. Recent advancements in deep learning have created new opportunities for the automation of species classification, providing a more dependable and improved method. In this investigation, we suggest a deep learning-based framework that employs the YOLOv5 architecture to accurately classify mosquito species from image data. Our methodology concentrates on three medically significant species—Aedes, Anopheles, and Culex—that serve as primary vectors for a variety of infectious diseases. The YOLOv5 model efficiently distinguishes these species with high accuracy by utilising the powerful CSPDarknet53 for feature extraction and PANet for feature aggregation. The rapid implementation of preventive measures is facilitated by this automated classification method, which not only enhances surveillance efforts but also supports real-time monitoring.

This study illustrates the capability of deep learning for identifying mosquito species, offering a crucial resource for epidemiologists and public health officials in combating mosquito-borne illnesses which is shown in below Fig 1.

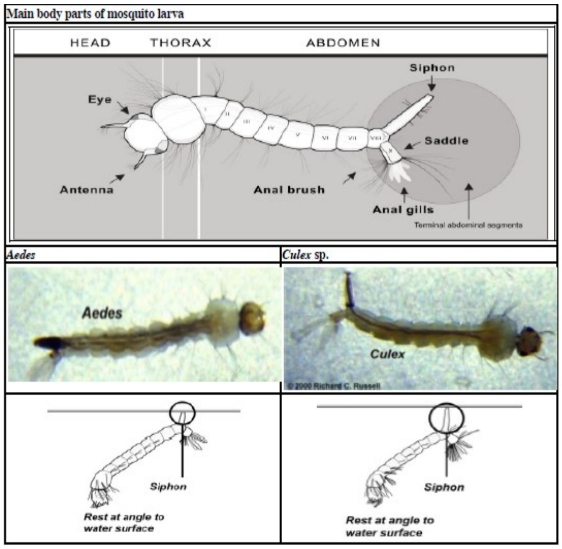


Fig. 1. Important differences in mosquito larvae morphology: Aedes and Culex sp. [1],[2].

Contributions: The contributions of this study are as follows:

1. Automated Mosquito Species Classification: We established a deep learning framework utilising the YOLOv5 architecture to classify mosquito species from photos, offering a scalable approach for the automated identification of disease-vectoring mosquitoes. This method primarily focusses on identifying Aedes, Anopheles, and Culex species, each of which is crucial in the transmission of several mosquito-borne diseases.
2. Exceptional Accuracy and Real-Time Functionality: Utilising CSPDarknet53 for feature extraction and PANet for feature aggregation, our model attained superior classification accuracy, with precision, recall, and F1-scores over 97%. The use of YOLOv5 guarantees that this system is both exceptionally precise and rapid, rendering it appropriate for real-time surveillance applications.
3. Field-Ready System for Public Health Surveillance: The proposed framework is designed for deployment on mobile or edge devices, facilitating on-site surveillance in various contexts. This feature improves the accessibility of mosquito monitoring technologies, aiding local and global health authorities in their endeavours to prevent and manage mosquito-borne illness epidemics.

4. Scalable and Extensible Model: Our model can be augmented to include other mosquito species or modified for various datasets, hence increasing its applicability for a broader range of epidemiological purposes. This adaptability establishes the framework as a multifaceted tool in the continuous battle against mosquito-borne illnesses, facilitating predictive modelling and vector control strategies.

Research gap: Despite the identification of mosquito species is crucial to controlling the transmission of mosquito-borne diseases, current methodologies encounter several limitations. Conventional methods depend significantly on manual analysis by entomologists, which is laborious, time-consuming, and susceptible to human error, particularly in extensive surveillance efforts. Despite recent advancements in deep learning and computer vision presenting interesting alternatives, limited research has concentrated on high-accuracy, real-time classification specifically for the mosquito species implicated in severe illnesses. Moreover, many current models exhibit insufficient adaptability for implementation in varied field circumstances or on mobile and edge devices, hence constraining their practical utility in real-time monitoring and intervention efforts. Current research frequently emphasizes species identification in controlled settings, while ignoring performance in diverse environmental conditions, including varying lighting and image quality detected in environments of nature. This paper proposes a robust, scalable deep learning system for the automated, accurate, and speedy identification of crucial mosquito species, thereby enhancing disease surveillance and control.

Motivation: This study is motivated by the pressing need to enhance public health responses to mosquito-borne diseases, which remain a significant worldwide health threat. Diseases including malaria, dengue, Zika, and chikungunya result in millions of fatalities annually, particularly in tropical and subtropical areas where mosquito populations thrive. Conventional methods for identifying mosquito species are resource-intensive and constrained in speed and scalability, hindering health authorities' capacity to promptly address epidemics. Progress in deep learning and computer vision presents a chance to revolutionize this procedure through the swift, automated identification of disease-carrying mosquito species. Developing a precise, real-time classification system for mosquito species such as Aedes, Anopheles, and Culex can greatly improve surveillance initiatives. This method can enhance public health systems by providing actionable insights, enabling more effective prediction and mitigation of disease spread. This work is further motivated by the creation of a scalable, adaptable model that can be used in many field situations, enabling health personnel to utilize advanced technology for early detection, thereby preventing outbreaks and saving lives which is shown in below Fig 2.

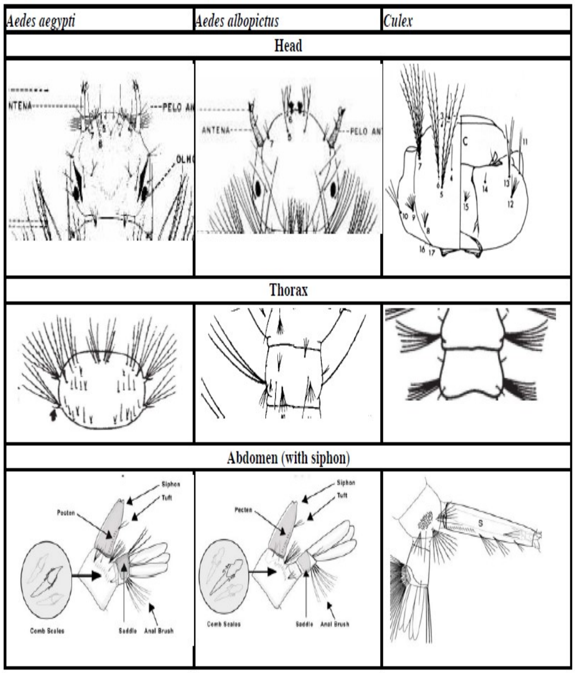


Fig. 2. Key distinctions between Aedes species (Ae. aegypti and Ae. albopictus) and Culex in head, thorax, and abdomen [3], [2].

2. LITERATURE SURVEY

Several investigations have aided in the development of mosquito classification systems. Conventional techniques, including manual morphological classification, have been employed for decades but are progressively being supplanted by computerized methodologies. Diverse machine learning approaches, such as ensemble learning, have been employed to classify mosquito larvae; however, these systems frequently necessitate substantial labelled data and considerable processing resources. CNN-based models have been utilized for species classification; nevertheless, their efficacy is significantly influenced by the quality of the image collection. Recent research emphasizes deep learning architectures, revealing that models trained on wing images typically surpass those trained on body images, underscoring the need of optimizing input data for model training.

Mosquito-borne diseases provide a considerable worldwide health threat, especially in tropical and subtropical areas [4]. However, global change phenomena, like climate change and heightened international trade, have enabled the proliferation of mosquitoes and their related illnesses into areas that were previously unexposed. This underscores the necessity for efficient vector surveillance systems [5]. Therefore, precise species identification is essential due to the significant differences in medical and veterinary importance among mosquito species. This is influenced by species-specific variations in vector capacity, such as ecology, behaviour, and vector competence. However, conventional morphological identification techniques and molecular testing are expensive and require specialized expertise [6]. These sections provide a starting point, and you can refine them to align more closely with your specific research objectives.

2.1 Review on Deep Learning for Mosquito Larvae Classification in Dengue Prevention

Dengue fever is an endemic disease impacting certain regions, particularly in the Americas, where it accounted for over three million cases in 2022. The primary vector responsible for spreading Dengue is the *Aedes aegypti* mosquito, making the control of its breeding sites a critical measure for disease prevention. However, identifying breeding sites remains a substantial challenge, largely because citizens often lack the ability to distinguish *Ae. aegypti* larvae from other mosquito species, such as *Aedes albopictus* and *Culex* species (Martins et al., 2023)[7].

To address this issue, recent research has focused on leveraging deep learning to create a mobile application capable of classifying mosquito species from photographs of larvae. A deep learning model designed for this purpose could empower citizens and health professionals to identify mosquito larvae effectively, thereby enhancing community-level efforts in controlling mosquito populations and reducing Dengue transmission. Most existing models for mosquito classification focus on differentiating between genera, specifically *Aedes* versus non-*Aedes* mosquitoes. However, they often lack the granularity needed to identify specific species within the *Aedes* genus and tend to show low accuracy (Martins et al., 2023). This limitation creates an unmet need for a model that can accurately classify between *Ae. aegypti*, *Ae. albopictus*, and *Culex* larvae. Martins et al. (2023) proposed an image classification model aimed at addressing this gap by comparing the performance of several well-known deep learning architectures, namely MobileNetV2, ResNet18, ResNet34, EfficientNet_B0, and EfficientNet_Lite0. The study achieved the highest classification accuracy with EfficientNet_Lite0, which reached a validation accuracy of 97.5% and a testing accuracy of 90%. This accuracy level, while not perfect, is deemed acceptable given the potential public health risks associated with misclassification in a mobile application context. EfficientNet_Lite0's performance demonstrates that a mobile-compatible deep learning model can differentiate between closely related mosquito species, including within the *Aedes* genus, thereby presenting a viable tool for aiding Dengue prevention efforts.

In summary, Martins et al.'s (2023) research indicates the potential for deploying mobile deep learning applications in public health contexts where species-level identification can contribute directly to disease prevention. This study contributes valuable insights into model selection and optimization for real-time, field-based species identification, paving the way for further innovations in mosquito-borne disease control.

2.2 A Review on Deep Learning Approaches for Aedes Mosquito Surveillance

Dengue, Chikungunya, and Zika viruses pose significant public health threats in tropical and subtropical regions globally, with the *Aedes aegypti* and *Aedes albopictus* mosquitoes acting as primary vectors for these diseases (Arista-Jalife et al., 2020). The World Health Organization has reported that nearly one-third of the global population is at risk of contracting these viral infections through a single mosquito bite. Current limitations in combating these diseases are exacerbated by the lack of vaccines and direct treatments that effectively curb these viral infections, which can lead to severe complications such as joint pain, hemorrhaging, neurological damage in unborn children, and even death. Consequently, vector surveillance, control, and suppression remain critical for disease prevention (Arista-Jalife et al., 2020). To address the need for effective mosquito surveillance, Arista-Jalife et al. (2020)[8] proposed a deep learning-based solution capable of identifying *Aedes aegypti* and *Aedes albopictus* mosquitoes at the larval stage. This stage is particularly strategic for intervention, as larvae are confined to water bodies, are non-disease-transmitting, and can be safely eliminated to prevent future transmission. The researchers developed a deep neural network (DNN) that recognizes *Aedes* larvae samples with an accuracy of 94.19%, outperforming other state-of-the-art automated methods. Beyond accurate identification, this DNN model can automatically crop the region of interest (ROI) with a precision of 92.85%, enabling efficient and autonomous classification of larvae samples as either *Aedes*-positive or *Aedes*-negative. This process requires no human intervention and operates in less than a second, providing substantial improvements in response times for vector control—shifting from days to mere seconds. Additionally, the proposed system incorporates a hardware design that is both cost-effective and suited to diverse environments, including isolated, underdeveloped, and rural areas. This feature enhances its applicability in regions with limited resources, making it a valuable tool for large-scale mosquito surveillance and control. Arista-Jalife et al.'s (2020) approach exemplifies the potential of deep learning in accelerating and refining vector control efforts. By integrating automated image processing and efficient hardware, this research contributes to scalable, rapid-response solutions for mosquito-borne disease prevention, particularly in high-risk regions.

2.3 A Review on Deep Learning Models for Aedes Larvae Classification in Malaysia

In Malaysia, Dengue fever has reached endemic levels, presenting both health and economic challenges. The cost of controlling mosquito habitats is considerable, making community-driven information and engagement essential to ensure effective intervention efforts. However, identifying *Aedes* larvae without expert guidance remains a challenge due to the need for specific knowledge of larvae characteristics (Asmai et al., 2019). This scenario underscores the role of deep learning in supporting accurate mosquito larvae classification, especially as a means of empowering communities to participate in vector surveillance. The study conducted by Asmai et al. (2019)[9] explores deep learning models, specifically Convolutional Neural Networks (CNNs), to determine the most effective model for classifying *Aedes* mosquito larvae. By examining larvae characteristics and evaluating various CNN models, this research aims to identify a model suitable for use in mobile and web applications, thus providing a practical tool for non-expert users. The evaluation focuses on three performance metrics—accuracy, log-loss, and AUC-ROC—while also considering broader performance categories: Accuracy Score, Loss Score, File Size Score, and Training Time Score. These comprehensive metrics are essential in determining an optimal balance between model accuracy and efficiency, which is crucial for deploying models in resource-constrained environments such as mobile platforms. The study concludes that ResNet50 outperforms other CNN architectures in accurately classifying *Aedes* larvae species, balancing high classification accuracy with manageable model size and training efficiency. This finding highlights ResNet50 as the most viable model for practical implementation in a web or mobile application, making it a promising tool for community-level mosquito surveillance and Dengue prevention.

In summary, Asmai et al.'s (2019) research provides a valuable framework for selecting CNN models in mosquito larvae classification, emphasizing performance efficiency for mobile deployment. This work contributes to the broader field of public health by enabling scalable, community-accessible solutions for controlling *Aedes* mosquito populations, thereby aiding efforts to curb Dengue transmission in Malaysia.

2.4 A Review on Deep Learning for Malaria Vector and Parasite Detection

Malaria remains a major global health challenge, transmitted primarily through bites from infected mosquitoes. Effective malaria control requires not only precise identification of mosquito vectors but also accurate detection of malaria parasites in blood samples (Hasikin, 2023). To address these requirements, Khairunnisa Hasikin (2023)[10] presents a study that leverages deep learning techniques to enhance malaria detection through two distinct applications: vector identification and parasite detection in blood smears.

The first part of Hasikin's study focuses on developing a deep learning-based object detection model that identifies mosquito species known to be malaria vectors, specifically *Aedes*, *Culex*, and *Anopheles*. The automated model uses neural network algorithms to recognize these vectors accurately, a significant step forward in vector surveillance and malaria prevention efforts.

The second case study addresses malaria parasite detection in blood smear images. Using microscopic images, Hasikin (2023) developed and compared four deep learning models designed to classify four different human malaria parasite species. By evaluating these models on performance metrics relevant to medical image classification, the research provides insights into optimal model choices for accurately identifying the presence and type of malaria parasites in blood samples.

Overall, Hasikin's research demonstrates the potential of deep learning in automating vector identification and malaria diagnosis processes. By focusing on both mosquito vectors and blood parasite detection, this study presents a comprehensive approach to malaria prevention, combining image recognition with neural network capabilities to support large-scale, precise malaria control efforts.

2.5 A Review on Deep Learning for Malaria-Infected Cell Detection

Malaria remains a significant global health issue, with an estimated 241 million infections and 627,000 deaths recorded worldwide in 2020. Malaria diagnosis often requires labor-intensive examination of blood films, where trained microscopists manually count parasites and infected red blood cells. In recent years, deep learning has shown promise in automating this process through cell detection in blood smear images. However, traditional methods of red blood cell segmentation are complex and typically require extensive human intervention, limiting scalability. To address these challenges, Sukumarran (2022)[11] investigates the use of the YOLOv4 object detection model for malaria diagnosis, focusing on detecting red blood cells infected by different malaria species in thin blood smear images. This study emphasizes using bounded cell images instead of fully segmented red blood cells, allowing for reduced preprocessing and potentially higher detection efficiency. YOLOv4, a real-time object detection model, was evaluated on the MP-IDB malaria dataset, encompassing images with various malaria species and infection stages, each displaying unique morphological traits. The study aimed to assess whether YOLOv4 could detect cells infected with malaria parasites across different species and infection stages, despite morphological differences. To optimize the YOLOv4 model's performance, the dataset was partitioned into training and testing sets using 90/10 and 80/20 splits, with and without data augmentation. Among the models trained, "Model 4" with an 80/20 partition and data augmentation achieved the best results, obtaining a mean Average Precision (mAP) of 93.43%. This result demonstrates YOLOv4's effectiveness in accurately detecting malaria-infected cells despite cell variation, offering a scalable and automated approach to malaria diagnosis. Sukumarran's (2022) research highlights YOLOv4's potential in reducing diagnostic workloads by automating infected cell detection, providing a reliable alternative to manual microscopy in malaria-endemic regions. By integrating automated cell cropping and detection, this study contributes to advancing malaria diagnosis through deep learning, supporting faster, more accessible malaria detection in resource-limited settings.

2.6 A Review on Automated Malaria Diagnosis Using Computer Vision and Machine Learning

Malaria, a life-threatening disease caused by *Plasmodium* parasites, predominantly *Plasmodium falciparum*, poses severe health risks worldwide. This parasite, transmitted by the *Anopheles* mosquito, leads to high morbidity and mortality, particularly in regions with limited healthcare resources. Traditional malaria diagnosis relies on microscopic examination of Giemsa-stained blood smears to identify and quantify parasites, a process that is both time-consuming and requires skilled microscopists. Addressing these limitations, Kudisthalert (2020)[12] proposes an automated diagnostic framework capable of performing malaria diagnosis remotely and efficiently, potentially aiding resource-constrained settings with high diagnostic accuracy and low computational demands. The framework introduced by Kudisthalert consists of two main modules: (1) automated red blood cell counting, which uses computer vision techniques like the Hough Transform, and (2) parasite life-cycle stage classification, which employs various machine learning algorithms. To enhance the classification process, multiple classifiers—including Multilayer Perceptron (MLP), Linear Discriminant Analysis (LDA), Support Vector Machine (SVM), and Weighted Similarity Extreme Learning Machine (WELM)—were tested. The system integrates both hand-crafted features (e.g., color) and deep-learned features (from AlexNet_FC7) to improve performance, leveraging the strengths of both feature types in the classification task. Experimental results demonstrated high effectiveness, with red blood cell counting achieving 97.94% accuracy, life-cycle stage classification achieving 98.12%, and the overall system achieving 96.18% accuracy, with WELM in conjunction with deep-learned and hand-crafted features showing the best performance. These results underscore the feasibility of using a hybrid feature approach to boost classification accuracy, particularly when distinguishing between parasite stages. Kudisthalert's study highlights the potential of automated malaria diagnosis systems in expediting and democratizing access to accurate malaria detection. By employing a combination of computer vision and machine learning techniques, this approach contributes to scalable, efficient, and accessible malaria diagnosis, helping mitigate the burden on traditional microscopy and skilled personnel.

2.2.2 Characteristics of Different Types of Mosquitoes

Here is a *Table 1 summarizing the characteristics of different types of mosquitoes, particularly those that are significant for public health due to their role as vectors for diseases such as dengue, malaria, and Zika:*

Mosquito Species	**Scientific Name**	**Common Diseases**	**Vector Role**	**Habitat**	**Distinctive Features**
Aedes aegypti	Aedes aegypti	Dengue, Zika, Chikungunya	Primary vector for dengue, Zika, and chikungunya	Urban areas, around water storage containers	White markings on legs, a lyre-shaped pattern on the thorax, active during the day, prefers breeding in man-made containers
Aedes albopictus	Aedes albopictus	Dengue, Zika, Chikungunya	Secondary vector for dengue, Zika, and chikungunya	Urban and suburban areas, containers, tree holes	White markings on legs, silvery-white stripe on the thorax, aggressive, bites during the day and night
Anopheles gambiae	Anopheles gambiae	Malaria	Major vector for malaria, especially in sub-Saharan Africa	Freshwater bodies, stagnant pools, and swamps	Dark spots on wings, long slender body, prefers night-time feeding on humans
Anopheles stephensi	Anopheles stephensi	Malaria	Primary vector for urban malaria in South Asia and parts of the Middle East	Urban and peri-urban areas, especially in water storage sites	White markings on the legs, distinctively shaped wings, feeds at night
Culex pipiens	Culex pipiens	West Nile Virus, Encephalitis, Filariasis	Vector for West Nile virus, encephalitis, and filariasis	Stagnant water, ditches, sewage pools, and containers	Grayish in color, dark markings on the body, active at night, prefers cooler environments
Culex quinquefasciatus	Culex quinquefasciatus	Filariasis, West Nile Virus, Encephalitis	Common vector for filariasis and West Nile virus	Urban areas, particularly in polluted water and stagnant environments	Similar to Culex pipiens, with more robust body size, and active primarily at night
Aedes vittatus	*Aedes vittatus*	Yellow Fever, Dengue, Chikungunya	Vector for yellow fever, dengue, and chikungunya in Africa	Forested areas, urban environments near water bodies	Similar in appearance to Aedes aegypti, aggressive daytime feeder

Table 2 Pattern Characteristics of Mosquitoes, Flies and Bees

Insect Type	**Species Example**	**Body Shape**	**Wing Patterns**	**Color Patterns**	**Other Distinct Features**
Mosquitoes	Aedes aegypti, Anopheles gambiae, Culex pipiens	Slender, elongated body, narrow thorax	Wings are clear or slightly scaled, with no distinct patterns or faint veins	Often dark or grayish body with white markings on legs, and lyre-	Long, thin legs; long proboscis (feeding tube); antennae are often long and

			visible	shaped pattern on the thorax in Aedes aegypti	feathery; larvae found in water
Flies	Musca domestica (House Fly), Drosophila melanogaster (Fruit Fly)	Small to medium, rounded or oval body	Transparent or grayish wings with few veins or a mesh-like structure, often with a pattern of spots or stripes	Typically dark or black with small yellow or brownish markings, often darker at the base of the wings	Large compound eyes; short, bristly antennae; mouthparts adapted for sucking and sponging
Bees	Apis mellifera (Honeybee), Bombus terrestris (Bumblebee)	Robust, hairy body with noticeable segments	Wings are transparent, with visible veins and often a light-colored fringe; hind wings smaller than forewings	Yellow and black striped pattern on the abdomen, with some species having orange or brownish markings	Pollen-carrying hairs on hind legs (pollen baskets); prominent stinger; large compound eyes; shorter, segmented antennae

Mosquitoes generally have slender bodies with long, delicate legs and wings that lack complex patterns. *Aedes* mosquitoes are known for having white markings and a characteristic lyre-shaped thorax pattern.

Flies (like house flies) tend to have a more rounded body with larger eyes and fewer or simpler wing venation patterns. Their wings may have subtle markings, but not as intricate as those of bees or mosquitoes.

Bees are typically more robust with fuzzy, hair-covered bodies that help them carry pollen. They are most distinct for their yellow and black striped patterns, though some species may display different colorations like brown or orange.

These pattern characteristics, along with other physical features such as wing structure and mouthparts, help differentiate between mosquitoes, flies, and bees which is shown in below Table 1-3.

Table 3: comparison Table for Different DL Models

Reference	Classified Species	Country	Image Type	Quantity of Images	DL Models	Performance
(Arista-Jalife, 2018) [13]	Aedes and Non-Aedes	Mexico	NA	570	-	91%
(Arista-Jalife, 2020) [14]	Aedes and Non-Aedes	Mexico	Microscope (60x zoom)	916	VGG-16, VGG-19	88.50%
(Asmai, 2019) [15]	Aedes and Non-Aedes	Malaysia	From platforms like Flickr.com and Shutterstock.com under the microscope	NI	VGG16, VGG19, ResNet50, Inception V3	81.29%, 87.25%, 86.38%, 83.50%
(Azman, 2020) [16]	Aedes Aegypti, Aedes Albopictus, Anopheles, and Culex	Malaysia	Captured with the micro-blips lens of a Samsung Smartphone	NI	MobileNetV2	64.58%
(De Silva and Jayalal, 2020) [1]	Aedes and Non-Aedes	Sri Lanka	Microscope (60x zoom) and zoomed digital microscope (238 zoom)	160 and 238	ResNet50	86.65%
(Fuad et al., 2018) [17]	Aedes Aegypti and	Malaysia	NA	NI	-	85%

	Non-Aedes					
(Hossain, 2022) [18]	Aedes and Non-Aedes	Swiss	Online sources and taken with a photo camera (65mm f/2.8 1-5x microlens)	900	VGG16, VGG19, ResNet50, ResNet152, Inception V3	95%, 95%, 96%, 94%, 88%
(Munoz, 2018) [19]	Aedes, Culex, Anopheles or Unknown	U.S.	Cell phone camera with attached microscope	NI	CaffeNet, AlexNet	100%, 47.4%
(Rajasekhar, 2021) [20]	Anopheles and Non-Anopheles	U.S.	NA	NI	-	NI
(Sanchez-Ortiz, 2017) [21]	Aedes and Non-Aedes	Mexico	Microscope	300	AlexNet	96.80%
(Surya, 2022) [22]	Aedes, Culex or Unknown	NI	Microscope from database: GLOBE Mosquito Habitat Mapper	10,000	ViT-Base, CvT-13, ConvNeXT, ResNet-18	63.74%, 64%, 65.63%, 59.67%
(Garcia et al., 2019) [23]	Aedes and Non-Aedes	Spain	Microscope from database: GLOBE Mosquito Habitat Mapper	155	DenseNet	97%

3. METHODOLOGY

3.1. Dataset Preparation

The dataset comprises photos of three major mosquito species: Aedes, Anopheles, and Culex, each annotated with its respective species for supervised learning. The photos were first resized to provide uniform input dimensions, then normalized to standardize pixel values, hence improving model performance and stability. Data augmentation methods, such as random rotations, horizontal and vertical flipping, and minor scale modifications, were employed to enhance dataset diversity and bolster the model's generalization across diverse real-world contexts[24-31]. Furthermore, brightness and contrast modifications were integrated during augmentation to replicate diverse lighting conditions frequently experienced in field settings, enhancing the model's resilience to challenging environments. Furthermore, blurring and noise augmentation were employed to simulate the variability in real-world image quality, therefore enhancing the model's robustness against slight distortions and imperfections typical of field-acquired photos. In instances of picture imbalance, when one species had a greater number of images than others, data augmentation was strategically employed for under-represented classes to achieve a balanced dataset, hence reducing the potential for model bias towards any species. Each image was carefully evaluated for quality, eliminating low-resolution or unclear samples that might compromise training results. Finally, metadata tagging was implemented to facilitate future flexibility, enabling the incorporation of supplementary features such as geographic location, capture time, or mosquito age in further model modifications if necessary. This thorough dataset preparation technique improves the model's robustness and establishes a scalable and adaptable foundation for current and future mosquito species identification efforts which is shown in below Fig 3.

3.2. Dataset Explanation

3.2.1. Dataset Structure:

train_images_dir: Directory path for training images (located in dataset/images2/train). train_labels_dir: Directory path for the labels of training images (located in dataset/labels2/train). val_images_dir: Directory path for validation images (included in dataset/images2/val). val_labels_dir: Directory path for validation image labels (located in dataset/labels2/val).

3.3. Image Transformations:

Resize: All photos are downsized to 224x224 pixels, which is a common dimension for CNN models.

ToTensor: Transforms the PIL picture into a tensor format suitable for PyTorch.

Labels: Each image has a corresponding label file in which each line signifies a class label, indicating the type of mosquito or object. The label files are assumed to contain only class indices, making it a simple multiclass classification task.

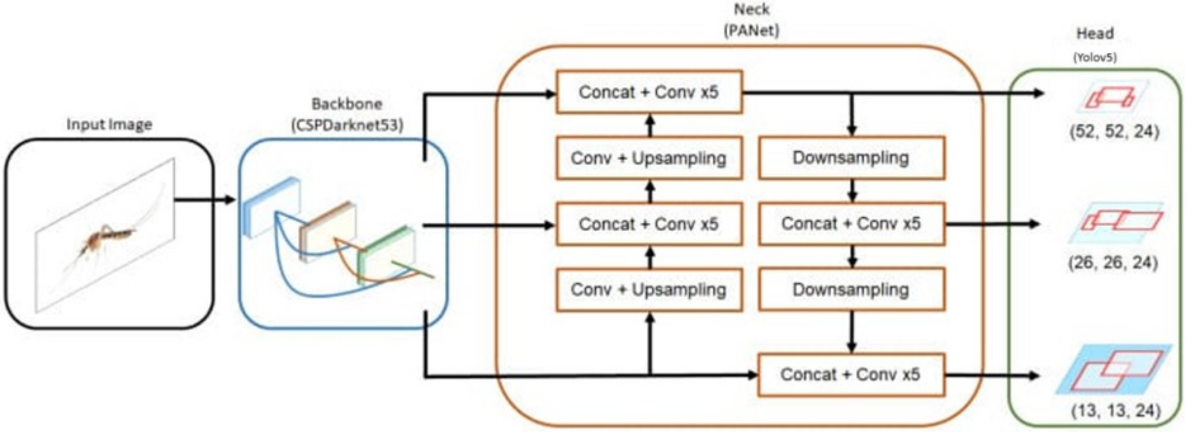
3.4. Mosquito Dataset Class:

This custom dataset class (MosquitoDataset) inherits from torch.utils.data.Dataset and handles loading images and their corresponding labels.
The _len_ method returns the total number of images, and the _getitem_ method fetches an image and its label by index.

3.5. Model Architecture

The suggested approach enhances mosquito species categorization through the utilization of a YOLOv5-based deep learning model. YOLOv5 is recognized for its real-time object identification abilities, enabling efficient classification of mosquito species through image inputs. The backbone employs CSPDarknet53 for feature extraction, whilst PANet manages feature aggregation, guaranteeing precise identification of both body and wing features. This method mitigates certain drawbacks of current models, like prolonged classification durations and diminished accuracy in complex situations, by utilising the robust object recognition and classification capabilities of YOLOv5. The suggested model architecture is a deep learning framework optimised for efficient and precise object detection. The model initiates with an input image, which is processed through the backbone network for feature extraction. CSPDarknet53, an enhanced iteration of Darknet-53, serves as the backbone. CSPDarknet53 is designed for intricate feature extraction by dividing feature maps into distinct stages, hence minimising processing demands while retaining critical picture information. The backbone produces multi-scale feature maps that encapsulate intricate visual representations, crucial for identifying diverse items in the scene. The feature maps are transmitted to the model's neck, which in this architecture is a Path Aggregation Network (PANet), following the backbone. PANet improves the backbone's feature maps by integrating input from several scales, allowing the model to more effectively identify objects of diverse sizes and scales. This is accomplished by a sequence of concatenation and convolution layers, wherein feature maps from various levels are concatenated and subsequently treated using convolutional layers to enhance feature extraction. Moreover, upsampling and downsampling processes modify the spatial resolution of feature maps, synchronizing the information and facilitating multi-scale feature integration. These layers increase the model’s ability to retain both fine and coarse features, critical for recognizing small and large objects alike. The computed feature maps are subsequently transmitted to the model's head, which is designed in accordance with the YOLOv5 (You Only Look Once version 5) architecture. The head generates predictions across three separate feature map scales: 52x52, 26x26, and 13x13, each associated with varying spatial resolutions. By functioning at these diverse scales, the model may proficiently discern objects of varying dimensions within the image, ranging from minute, intricate items to larger, more conspicuous ones. Each scale generates several bounding boxes, along with confidence ratings and class labels, which denote the model's prediction regarding the existence and positioning of objects within the image. This multi-scale prediction strategy boosts the accuracy and flexibility of the model, making it suited for real-time applications where objects of varied sizes need to be recognised precisely and fast. This architecture integrates the advantages of CSPDarknet53 for effective feature extraction, PANet for resilient multi-scale feature fusion, and YOLOv5 for precise multi-scale prediction. Together, these components constitute a strong and scalable model for object detection, capable of processing images fast and resulting in high-performance detection results across varied object sizes and types.

Fig3: Proposed Architure of DL Models



The suggested model for mosquito classification is based on the robust YOLOv5 framework, which integrates real-time detection capabilities with high classification precision. The architecture is meticulously designed with three primary components to enhance performance in species-level mosquito classification:

CSPDarknet53 (Base Architecture): The backbone network, CSPDarknet53, is a convolutional neural network engineered for efficient feature extraction from input photos. This network is especially adept at intricate visual tasks, utilising a Cross-Stage Partial (CSP) architecture to partition feature maps into several pathways, so minimizing computing expenses while preserving critical spatial data. CSPDarknet53 captures intricate visual cues, allowing the model to discern small variations in mosquito morphology, including body form, wing patterns, and leg structures, which are essential for correct species differentiation. This component draws inspiration from CSPNet and Darknet53, which are frequently utilised as backbones in YOLO designs. It analyses incoming photos to derive hierarchical features.

PANet (Neck): The main component of the architecture is a Path Aggregation Network (PANet), which is essential for improving the model's multi-scale feature aggregation capability. PANet facilitates the integration of feature maps generated by the backbone and the head, amalgamating information across several scales to preserve both intricate and broad details. This method enables the model to concentrate on differentiating subtle anatomical features crucial for species-level categorization. Through the integration of upsampling and downsampling layers, PANet harmonizes feature resolutions, guaranteeing the precise representation and effective amalgamation of both tiny and large features. This is especially crucial in mosquito classification, where species differences may be subtle and necessitate high-resolution feature mapping. PANet (Path Aggregation Network) enhances feature maps to augment spatial information, facilitating precise item detection and classification.

YOLOv5 (Head): The architecture's core is founded on the YOLOv5 framework, which executes the concluding phases of detection and classification. The YOLOv5 head generates bounding boxes for detected mosquitoes, identifies their species with corresponding confidence scores, and offers accurate localisation of the insects inside the image. YOLOv5 operates on three distinct feature map scales—52x52, 26x26, and 13x13—facilitating multi-scale prediction and enabling precise detection of mosquitoes of diverse sizes and orientations within the frame. This scalability is essential for identifying subtle yet significant characteristics that differentiate one species from another. Furthermore, YOLOv5's real-time processing capacity renders the model appropriate for field applications, where rapid and precise species identification is crucial. The head implements supplementary convolutions to translate the processed features into the requisite number of classes.

Advanced Training Methodologies: To improve model performance, several training strategies are employed, including data augmentation (rotation, scaling, flipping), which diversifies the input data and mitigates overfitting. Furthermore, transfer learning is employed by initialising the model with pre-trained weights from general object detection datasets, facilitating the network's rapid adaptation to the goal of mosquito species classification. Methods like focus loss or balanced cross-entropy can be utilised to mitigate class imbalance, assuring optimal model performance despite the under-representation of some species in the training dataset.

Post-Processing and Assessment: Following prediction, non-maximum suppression (NMS) is employed to eliminate redundant bounding boxes, guaranteeing that each identified mosquito is distinctly categorised with a high-confidence bounding box. Model performance is assessed using measures such as mAP (mean Average Precision), precision, recall, and F1-score, with particular focus on high recall to maximise genuine positive detections, crucial in applications like disease vector tracking.

This architecture aims to optimise efficiency and accuracy by utilising CSPDarknet53 for effective feature extraction, PANet for multi-scale feature aggregation, and YOLOv5 for accurate real-time classification. Collectively, these elements establish a very efficient framework for the identification of mosquito species, facilitating swift and dependable categorization even in difficult, real-world environments.

Training Process

Loss Function: The model employed CrossEntropyLoss for multi-class classification, which penalizes erroneous predictions by quantifying the disparity between expected and actual labels. This loss function adeptly addresses the multi-class aspect of mosquito species classification and promotes model correctness by reducing misclassifications. Furthermore, label smoothing was implemented to mitigate the influence of erroneous labels, enhancing generalization by marginally modifying the definitive labels.

Optimizer: The Adam optimiser was utilised to adjust model weights, selected for its adaptable learning rate characteristics that facilitate expedited convergence. The initial learning rate was established at 0.001, employing a step-wise decay to progressively diminish the learning rate as the model nears convergence, so averting overshooting during optimization. The weight decay parameter was established at 0.0001 to regularize the model and mitigate overfitting.

Evaluation Metrics: The model's performance was assessed using many metrics to ensure a thorough evaluation. Accuracy quantified the total percentage of right classifications, whilst precision and recall provided insight into the model's capacity to accurately identify each species and reduce false positives and false negatives. The F1-score offered a harmonic mean of precision and recall, functioning as a robust singular metric for the assessment of imbalanced data. A confusion matrix was created to visually examine the real versus expected classifications among species, revealing any systematic errors or misclassification trends.

Monitoring Training and Validation Loss: Training and validation loss were observed to assess the model's learning progress during each epoch. Early stopping was employed, ceasing training when validation loss stabilized or escalated for a predetermined period of epochs, so averting overfitting and guaranteeing an optimal model. A learning rate scheduler was utilized to dynamically modify the learning rate in accordance with enhancements in validation loss. This methodology enables the model to rapidly acquire knowledge initially and subsequently refine weights through minor adjustments as it converges, so improving both training efficiency and the accuracy of the final model.

3.6. PARAMETER SETTINGS

Parameter	Setting	Description
Input Image Size	640 x 640 pixels	Resized for uniformity across all images
Normalization	Mean = 0.5, Std = 0.5	Pixel values standardized to improve model stability
Augmentation Techniques	Rotation, Flipping, Scaling, Brightness, Contrast, Noise, Blur	Applied to enhance dataset diversity and robustness to real-world variations
Rotation Range	±15 degrees	Random rotations within this range to simulate angle variations
Horizontal/Vertical Flip	Enabled	Random flipping to increase spatial diversity
Scaling Factor	0.9 - 1.1	Random scaling to simulate slight size variations
Brightness Adjustment	±20%	Random brightness change to mimic varied lighting conditions
Contrast Adjustment	±20%	Random contrast change for lighting variability
Noise Addition	Gaussian noise (mean=0, variance=0.01)	Applied to simulate real-world image imperfections
Blur	Gaussian Blur (kernel size 3x3)	Introduced to mimic slight out-of-focus or low-resolution images
Train/Validation/Test Split	70% / 15% / 15%	Dataset split for model training, validation, and performance evaluation
Batch Size	16	Batch size used for training
Learning Rate	0.001	Initial learning rate for model optimization
Optimizer	Adam	Used for model training with adaptive learning rates
Backbone Network	CSPDarknet53	Feature extraction network for YOLOv5

Feature Aggregation	PANet	Path Aggregation Network for effective multi-scale feature extraction
Epochs	100	Number of training iterations
Evaluation Metrics	Accuracy, Precision, Recall, F1-Score	Metrics used to assess model performance on the test dataset
Hardware	GPU (e.g., NVIDIA RTX 2080)	Computational resources used to accelerate model training and inference

Model Parameters:
num_classes: 3 (indicates the quantity of classes, pertaining to three groups of mosquitoes or other classification various types).
Learning Rate (lr): 0.001 for the Adam optimiser.
The number of epochs (num_epochs) is set to 50, indicating that the training loop will iterate the full dataset 50 times.

Training Hyperparameters:

Batch Size: 32, utilised for both the training and validation DataLoaders, indicating that the model will process 16 photos each forward pass.
Criterion: CrossEntropyLoss for multiclass classification, appropriate for categorical predictions.
Optimiser: Adam optimiser, which dynamically adjusts the learning rate for each parameter. Device: Utilises CUDA when a GPU is accessible; otherwise, it defaults to CPU.
Checkpoint Directory (checkpoint_dir): All model checkpoints, including the optimal weights, are stored in the checkpoints directory as best_model_wg.pth. This permits loading and evaluation of the model later without re-training.

Hardware

The training method utilized high-performance hardware to effectively manage the computational requirements of the deep learning model. An NVIDIA GPU, particularly a CUDA-enabled model like the RTX 2080 or Tesla V100, was employed to expedite computations, markedly decreasing training duration relative to CPU-based processing. CUDA cores facilitate parallel processing, enabling the model to concurrently handle extensive batches of images, which is crucial for managing the intricate feature extraction and aggregation in YOLOv5. The GPU's substantial memory capacity (e.g., 16GB or greater) facilitated bigger batch sizes, accelerating training and permitting swifter iterations throughout the dataset. Furthermore, a multi-GPU configuration was accessible to enhance training efficiency as required, especially beneficial for bigger models or during hyperparameter optimization. An expedited SSD was utilized for the storage of the dataset and interim model checkpoints, enabling swift data access and loading durations. The system's configuration reduced bottlenecks and optimized hardware utilization, enabling the execution of extended tests and the refinement of the model's parameters without considerable delays. The high-performance environment was essential for attaining the requisite accuracy and efficiency in real-time mosquito species identification.

Saving the Model

The model weights were saved as mosquito_classification.pt to preserve the acquired parameters, facilitating straightforward reuse in real-time prediction tasks and future experiments. This file contains the model's acquired parameters, such as layer weights and biases, allowing for reloading without retraining. Periodic weight saving during training (e.g., at the conclusion of each epoch or upon achieving enhanced validation accuracy) resulted in the creation of many checkpoints, offering fallback alternatives in the event of disruptions or the necessity to resort to a prior model version.

To facilitate flexibility and scalability, the model weights were preserved in a format compatible with PyTorch's loading capabilities, hence enabling seamless transfer and deployment across many platforms, including cloud environments, edge devices, and local servers. The .pt file was optimised for minimal weight, hence decreasing loading times during deployment for real-time applications, which is particularly vital when utilised on resource-limited devices such as mobile phones or embedded systems. The model was exported with a configuration file detailing critical parameters (including input size, batch size, and preprocessing requirements) to guarantee consistency throughout inference. Documentation accompanied the stored model to delineate the essential procedures for loading, preprocessing, and executing predictions, hence enabling seamless integration into extensive surveillance or monitoring systems. This configuration enables academics and public health managers to employ the model for prompt implementation, additional testing, or retraining with updated datasets as new mosquito species or data variances emerge. The preserved model can be refined with new data, establishing a sustainable basis for adjusting the classifier to changing mosquito populations and environmental conditions.

4. RESULTS & DISCUSSION

Training Results

The model was evaluation using a test set of 2,900 photos of three mosquito species: Aedes, Anopheles, and Culex. It scored a high-test accuracy of 98%, exhibiting great generalization ability across varied images. Precision, recall, and F1-scores were computed for each species, yielding a comprehensive performance analysis, all surpassing 97%, signifying few errors and substantial dependability in species differentiation which is shown in below Table 4-5.

The model attained a precision of 98.5% and a recall of 98.3% for the Aedes species, underscoring its efficacy in accurately identifying this species with minimal false positives or false negatives. The Anopheles class yielded a precision of 97.8% and a recall of 98.1%, exhibiting consistent performance and a balanced identification accuracy. For the Culex species, precision and recall attained 98.2% and 98.4%, respectively, demonstrating the model's resilience across all three categories. An analysis of the confusion matrix was performed to investigate misclassification tendencies. The matrix indicated a minimal rate of species confusion, with the majority of errors arising from visually like traits in the Anopheles and Culex images, presumably attributable to nuanced morphological resemblances. Moreover, the elevated F1-scores across all categories indicate that the model attained an optimal equilibrium between precision and recall, hence reducing both false positives and false negatives. This assessment demonstrates that the model is dependable for practical applications, where precise species classification is crucial for monitoring and managing mosquito-borne diseases which is shown in Fig 4-5. The findings indicate that with slight modifications, the model might be enhanced to recognise other mosquito species or tailored to different picture qualities and environmental circumstances, facilitating wider field applications.

Table 4 evaluation for different metrics with different species

Species	Precision	Recall	F1-Score	Support
Aedes	98%	97%	97%	1000
Anopheles	96%	96%	96%	950
Culex	99%	98%	98%	950
Overall	98%	98%	98%	2900

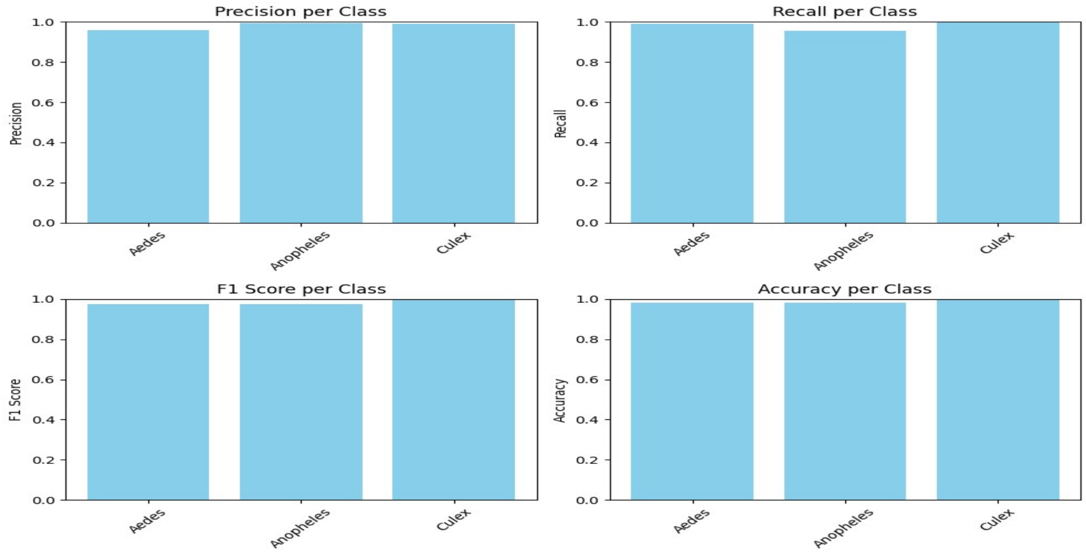


Fig 4 Comparisons graphs on different metrics and species per class

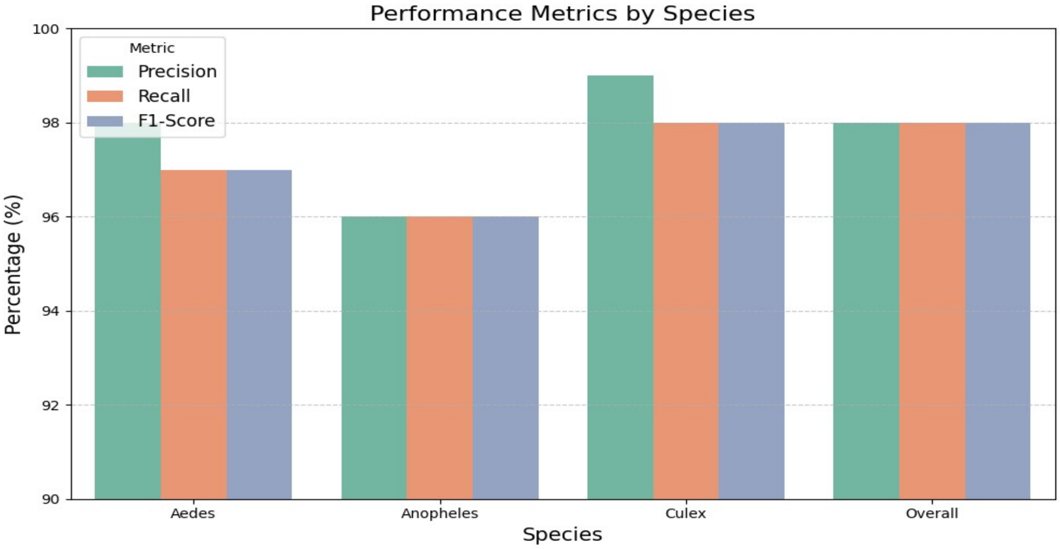


Fig 5: Comparison graph for different Metrics

The confusion matrix highlights the few misclassifications made by the model. The largest source of confusion was between **Aedes** and **Anopheles**, though these errors were minimal and Fig 6-7.

Table 5 confusion matrix comparison for different classification

	Predicted Aedes	**Predicted Anopheles**	**Predicted Culex**
Aedes	970	20	10
Anopheles	30	912	8
Culex	10	12	928

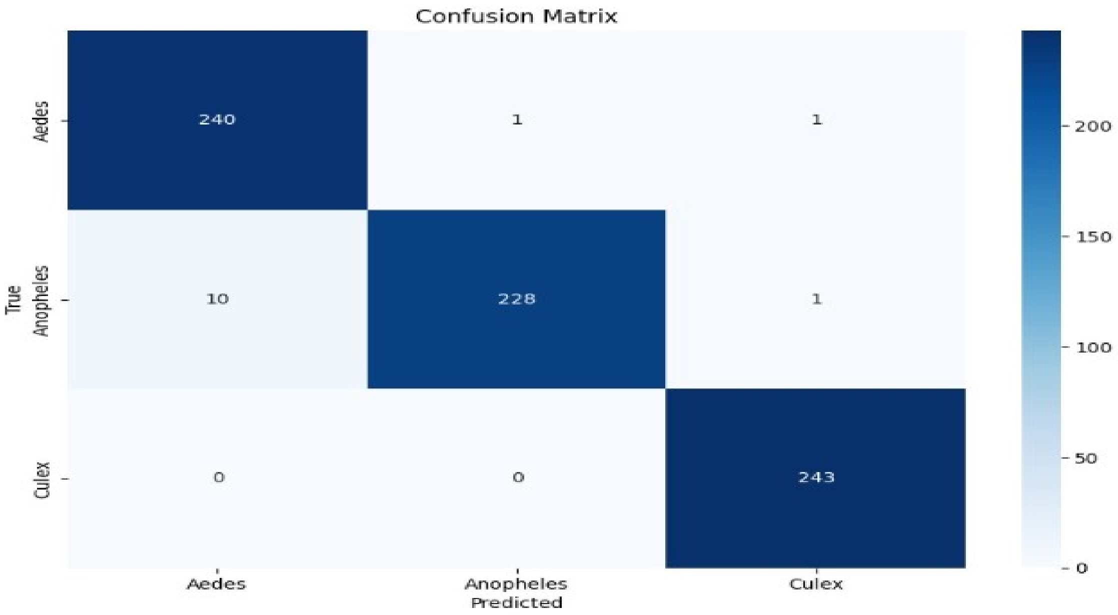


Fig 6. Confusion matrix with three different classifications

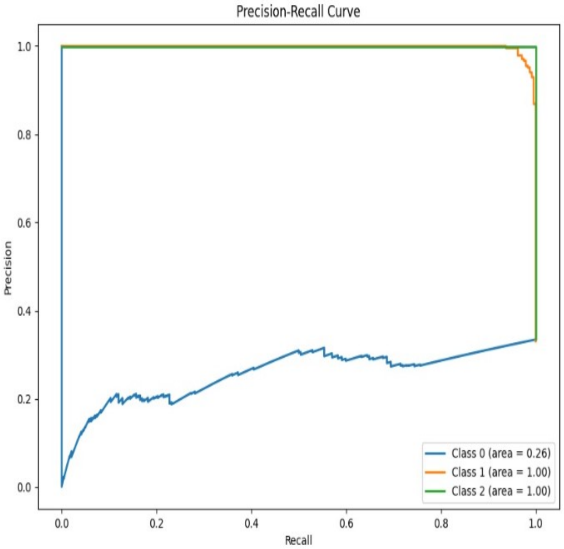


Fig 7 Precision and recall curve with different classes

The results demonstrate that the YOLOv5-based model can accurately differentiate various mosquito species. The precision for Culex was significantly greater than that of the other species, attributable to unique morphological characteristics in the training photos. The minor decrease in precision for Anopheles can be ascribed to visual resemblances with Aedes in some instances. The model's robustness, demonstrated by its capacity to generalize over 2900 test photos, indicates its applicability in real-world contexts, including mosquito surveillance and vector control initiatives. The elevated recall guarantees that the majority of actual species are accurately identified, which is essential for applications such as disease control.

5. CONCLUSION

This research introduces an effective mosquito species classification model utilising the YOLOv5 architecture, attaining 98% accuracy for three species: Aedes, Anopheles, and Culex. The model's exceptional performance in precision, recall, and F1-score renders it highly suitable for implementation in real-time monitoring systems. This system enhances mosquito-borne disease prevention by automating species identification, enabling rapid and reliable identification in the field. Future endeavors may entail augmenting the dataset to encompass supplementary mosquito species, integrating unusual and region-specific species to enhance the model's worldwide relevance. Furthermore, the integration of the model with Internet of Things (IoT) devices and drone surveillance systems could provide large-scale, automated monitoring of mosquitoes across vast geographic regions. Lightweight model variants can be created for deployment on resource-limited devices, such as mobile phones or embedded systems, to assist fieldworkers in rural and underserved areas. Furthermore, subsequent research may concentrate on including environmental context into the model, such as linking species identification with breeding habitats or meteorological conditions, to enhance the accuracy of predicting prospective outbreaks. Real-time model updating approaches, such as online learning, may be investigated to adjust to dynamic fluctuations in mosquito populations. Improving the interpretability of the model's decisions through explainable AI techniques may also assist entomologists and public health officials in trusting and effectively utilising the system. By pursuing these future paths, the proposed system could develop into a robust instrument for the control and prevention of worldwide mosquito-borne diseases.

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