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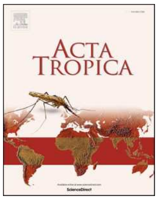

Mosquito species identification accuracy of early deployed algorithms in IDX, A vector identification tool

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A R T I C L E I N F O

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A B S T R A C T

Mosquito-borne diseases continue to pose a great threat to global public health systems due to increased insecticide resistance and climate change. Accurate vector identification is crucial for effective control, yet it presents significant challenges. IDX - an automated computer vision-based device capable of capturing mosquito images and outputting mosquito species ID has been deployed globally resulting in algorithms currently capable of identifying 53 mosquito species. In this study, we evaluate deployed performance of the IDX mosquito species identification algorithms using data from partners in the Southeastern United States (SE US) and Papua New Guinea (PNG) in 2023 and 2024. This preliminary assessment indicates continued improvement of the IDX mosquito species identification algorithms over the study period for individual species as well as average regional accuracy with macro average recall improving from 55.3 % [Confidence Interval (CI) 48.9, 61.7] to 80.2 % [CI 77.3, 84.9] for SE US, and 84.1 % [CI 75.1, 93.1] to 93.6 % [CI 91.6, 95.6] for PNG using a CI of 90 %. This study underscores the importance of algorithm refinement and dataset expansion covering more species and regions to enhance identification systems thereby reducing the workload for human experts, addressing taxonomic expertise gaps, and improving vector control efforts.

1. Introduction

Mosquitoes are the world's most competent vector, but only a limited number of species are responsible for spreading diseases such as malaria, dengue, and West Nile virus, among others (Wilkerson et al., 2021). Routine monitoring to understand the dynamics of local vector populations followed by targeted vector control are among the most effective strategies for reducing downstream disease transmission. Identification of species after collection is a crucial step of mosquito surveillance in order to distinguish vectors from non-vectors and pool vector species for pathogen testing (Briolant et al., 2020; Rodríguez-González et al., 2024). Due to the global taxonomic impediment, there are few experts capable of recognizing the wide range of morphological characters of most species represented in various regions (Engel et al., 2021; Koch, 2023). This challenge is further compounded by shifting species populations (Carlson et al., n.d.; Ryan et al., 2024), migration (Atieli et al., 2023; Huestis et al., 2019) and arrival of invasive species (Giunti et al., 2023; Juliano and Philip Lounibos, 2005; Lühken et al., 2023; Medlock et al., 2012), limited staffing, and high turnover of seasonal personnel who are tasked to identify vectors with limited experience (Gridley-Smith, 2017; Moise et al., 2020; Peper et al., 2022). While morphological and taxonomic identification can be learned, it is arduous and has a high training burden to acquire regional expertise (Harrington and Mader, 2023). Advancements in molecular and genetic analysis complement traditional morphological identification, but remain less accessible in many regions due to the equipment, training burden, costs required, and limited coverage in certain species (Chaiphongpachara et al., 2022; Chan et al., 2014). New tools to support rapid and accessible mosquito identification with a lower training burden are needed to address these challenges.

Originally introduced as MosID (Mosquito ID), IDX (Identification-X) is a high-resolution optical system integrated with computer vision algorithms to provide accurate adult mosquito and tick species identification. The system features a batch process imaging workflow that

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Abbreviations: CI, Confidence Interval; CMU-Net, Conv-Mixer Network; CNN, Convolutional Neural Network; GAN, Generative Adversarial Network; ORSAC, Ordered Sample Consensus algorithm; PNG, Papua New Guinea; RANSAC, Random Sample Consensus; SE USA, Southeastern USA.

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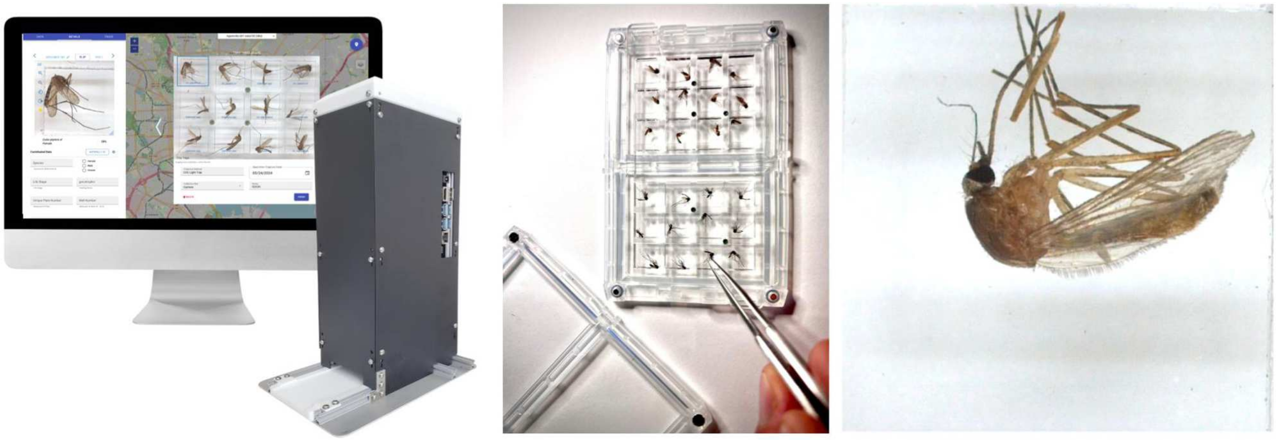

Fig. 1. Vectech's IDX, a digital microscope for imaging and automated identification of mosquitoes and ticks. Left. The IDX device, and the website dashboard used to operate it. Center. The IDX specimen tray being loaded with mosquitoes. Right. A sample image of a Cx. pipiens s.l. specimen taken in IDX.

acquires two distinctly oriented images of each specimen and provides immediate digital aggregation of data in template report formats (Brey et al., 2022, Fig. 1). As accuracy improves, IDX offers vector control districts the opportunity to task-shift mosquito identification to an individual with little-to-no experience identifying mosquitoes, such as a seasonal technician, in less than a day of training.

In order to expand species coverage, increase accuracy, and track deployed accuracy, IDX allows users to contribute identification data for a given mosquito image. After a controlled data verification process, contributed data is used to retrain the algorithm, improving performance for future versions.

Recent advancements include both greater species diversity due to the expansion of global partners contributing data through IDX and methodological improvements to algorithm development. In this paper we aim to compare the performance of IDX species identification for the most recent three deployed versions of the algorithm in two regions: the Southeastern United States, a region with robust data collection and more species represented in the algorithm; and Papua New Guinea, a geographic region new to the algorithm whose contributed data is not yet included in algorithm development, thus representing the initial translation of the IDX algorithms to new regions.

2. Materials and methods

2.1. IDX

IDX (Vectech Inc. Baltimore, MD) images mosquitoes and ticks, and then applies deep learning-based computer vision models to output specimen species and sex. All specimen image data included in this analysis was obtained using an IDX device.

2.2. Study population

In this paper, we present a comparative analysis of regional algorithm performance over the last three IDX releases, spanning September 2023 through July 2024. Regions were included if there was more than one known species represented in all three algorithm versions in the region, and there were at least 100 specimens with species information contributed; thus, the analysis includes Southeastern (SE) US (two organizations, grouped due to similar mosquito species diversity) and Papua New Guinea (PNG, one organization) (Fig. 1). Additionally, for our species-specific analysis we selected species that had at least one specimen with species information that contributed to all algorithm releases, so as to allow for comparisons.

2.3. Data validation

Initial species identifications were provided by collaborators with regional expertise in mosquito taxonomy at the collection site. Once received, data was further validated to reduce inaccuracies in the taxonomic identification provided by users (also referred to as label noise) using the Ordered Sample Consensus (ORSAC) method (Jenkins et al., 2023). ORSAC is an in-house developed human-in-the-loop Convolutional Neural Network (CNN)-based approach to data cleaning (also referred to as label verification) similar to the commonly used Random Sample Consensus (RANSAC) algorithm (Fischler and Bolles, 1981) for outlier detection. ORSAC iteratively trains and tests CNN models on different dataset splits, flags species labels that may be inaccurate, and involves expert review by Vectech entomologists of flagged specimens.

2.4. Training data

Mosquito specimen image data is provided by users, partners and collaborators. To date, over 30 organizations across 11 countries have contributed data. Cumulatively, as of July 2024, the IDX dataset comprised 177,052 images across 164 mosquito species, 76 tick species and various non-target species, with various associated attribute labels and data origin information.

Species contributions by organization depend on native diversity and seasonality. In general, a species reaches candidate status for inclusion in training data if there are >100 specimens verified through ORSAC and 20 samples verified by Vectech entomologists. Based on collaborator contributions over the period under review, our algorithm identification capability has expanded from 43 to 53 species. A comprehensive summary table of the training data and species used in training the algorithm versions in this study is included in Supplementary Information Table 1.

2.5. Analysis

This study focuses on the identification accuracy of species known to the CNN. Species outside the known species set for that release were considered unknown and were excluded from this analysis. For each region and each software release, performance is primarily measured as *recall* (synonymous with sensitivity, defined as the true positives divided by the sum of true positives and false negatives) for individual species. *Precision* (defined as true positives divided by the sum of true positives and false positives) is not measured due to imbalance of deployed test samples, many species being without any data. Distribution of error between species is presented in normalized confusion matrices comparing algorithm identification to the verified identification

Table 1
Algorithm version release details.

Version	Deployment date range[1]	Number of species in version[2]	Macro Avg. Recall in cross regional development test set	Major Methodological changes
V2.1.1	9/30/2023 - 5/20/2024	43	97.5 %	Xception (Chollet, 2017) closed set identification, Ranger21 Optimizer (Wright and Demeure, 2021), Focal Loss (Lin et al., 2017), CMU-Net masking (Tang et al., 2023), custom white balancing methods, image reconstruction as data augmentation using generative adversarial networks (GANs) (Chlap et al., 2021; Waheed et al., 2020), region-based species exclusion used as an unknown species detection method.
V3.0.0	3/5/2024 - 6/4/2024	53	97.1 %	Distillation loss added to the loss schema to preserve quality learnings from prior releases and targeted models (Zhang et al., 2019), Monte Carlo simulation-based unknown species detection added to the schema (Gal and Ghahramani, 2016; Ianni et al., 2020), additional label verification applied to training data.
V4.0.0	5/20/2024 - present	53	96.7 %	Fusion of both specimen images through late score fusion (Seeland and Mäder, 2021) to ensure a single species prediction for each specimen. Modification of Monte Carlo confidence thresholds. Center loss is used in final model finetuning (Wen et al., 2016).

[1] Overlap in algorithm release version deployment date ranges is observed due to IDX devices only checking for updates upon restarting. If a customer leaves the device running for an extended period without restarting, data may continue to be captured using a prior algorithm version, even if a new release has been deployed. This overlap persists until the device is restarted and the updated algorithm is applied.

[2] The specific species in each algorithm release, and the number of unique specimens used in the training set for each version, may be reviewed in the Supplementary Information Table 1.

Table 2
Species recall for all species included in (a) the Papua New Guinea and (b) the Southeastern USA region over versions 2.1.1, 3.0 and 4.0 of the IDX algorithm. Recall is given as Recall (Specimen Count) [lower confidence limit, upper confidence limit]. For each region, a micro average for the recall, computed over all contributed specimens, and a macro average, computed over species that were represented in all versions of the algorithm, along with associated confidence intervals are reported.

a)

PNG Species	Version 2.1.1	Version 3.0	Version 4.0
Ae. aegypti	55.3 (38) [40.8,69.2]	46.1 (280) [41.1,51.2]	88.8 (197) [84.4,92.9]
Ae. albopictus	100.0 (2) [22.4,100.0]	98.1 (157) [95.2,99.5]	100.0 (74) [96.0,100.0]
Cx. pipiens s.l.	91.8 (400) [89.2, 93.9]	76.7 (722) [74.0,79.3]	94.3 (332) [91.7,96.2]
Micro average (over all specimens)	88.7 (440) [85.9,91.1]	72.2 (1159) [70.0, 74.4]	93.2 (603) [91.3,94.8]
Macro average (over 3 species)	82.4 (440) [56.0,100.0]	73.6 (1159) [71.5, 75.8]	94.4 (603) [92.2, 96.5]

b)

SE US Species	Version 2.1.1	Version 3.0	Version 4.0
Ae. albopictus	98.1 (104) [94.1, 99.7]	97.0 (202) [94.2, 98.7]	100.0 (120) [97.5, 100.0]
Ae. atlanticus			83.3 (84) [75.1, 89.6]
Ae. canadensis			88.5 (104) [82.0, 93.2]
Ae. japonicus			100.0 (2) [22.4, 100.0]
Ae. sollicitans		88.5 (52) [78.5, 94.9]	69.2 (26) [51.3, 83.6]
Ae. taeniorhynchus	20.4 (274) [16.5, 24.8]	84.4 (372) [81.0, 87.4]	74.1 (278) [69.4, 78.4]
Ae. triseriatus s.l.		87.2 (94) [80.1, 92.4]	66.7 (24) [47.9, 82.2]
Ae. vexans s.l.	50.0 (2) [2.5, 97.5]	93.2 (118) [88.1, 96.6]	89.9 (258) [86.3, 92.8]
An. crucians s.l.	5.0 (80) [1.7, 11.1]	92.5 (534) [90.4, 94.3]	98.9 (182) [96.6, 99.8]
An. quadrimaculatus			90.3 (62) [81.8, 95.7]
Cq. perturbans	97.0 (198) [94.1, 98.7]	97.0 (100) [92.4, 99.2]	96.2 (104) [91.5, 98.7]
Cx. erraticus		92.6 (54) [83.9, 97.4]	94.7 (38) [84.3, 99.0]
Cx. nigripalpus	25.0 (76) [17.0, 34.5]	55.3 (264) [50.1, 60.5]	
Cx. pipiens s.l.	93.8 (258) [90.7, 96.1]	70.8 (144) [63.9, 77.0]	61.5 (26) [43.5, 77.4]
Cx. restuans	0.0 (16) [0.0, 17.1]	17.3 (104) [11.5, 24.6]	25.6 (78) [17.7, 35.0]
Cx. salinarius		30.6 (180) [24.9, 36.7]	38.6 (202) [32.9, 44.6]
Ps. columbiae	62.5 (8) [28.9, 88.9]		100.0 (56) [94.8, 100.0]
Ps. ferox	78.0 (364) [74.1, 81.5]	83.3 (6) [41.8, 99.1]	95.7 (46) [87.0, 99.2]
Ur. sapphirina			76.0 (100) [67.9, 82.9]
Micro Average (over all specimens)	65.5 (1380) [63.4, 67.7]	77.1 (2224) [75.6, 78.6]	79.2 (1790) [77.6, 80.8]
Macro Average (over 8 species)	55.3 (1296) [48.9, 61.7]	79.4 (1580) [74.0, 84.9]	80.2 (1092) [77.3, 83.2]

(Supplementary Information, Figs. 1–6). For each species, confidence intervals are calculated at the 90 % level using the Clopper-Pearson interval (Clopper and Pearson, 1934) to account for sparse data and small sample sizes; significance for comparisons was confirmed using a two-proportion z-test. Additionally, we report the *micro average recall* for all species from the specific region, which shows an average with specimens equally weighted and pooled regardless of species, and the *macro average* of species recall, which was calculated as the average of recall for species under consideration; confidence intervals were calculated based on a weighted sum of the standard errors of the included species. Only species with data in all three versions were considered in macro average recall comparisons. Analyses were conducted using Tableau, Python and R.

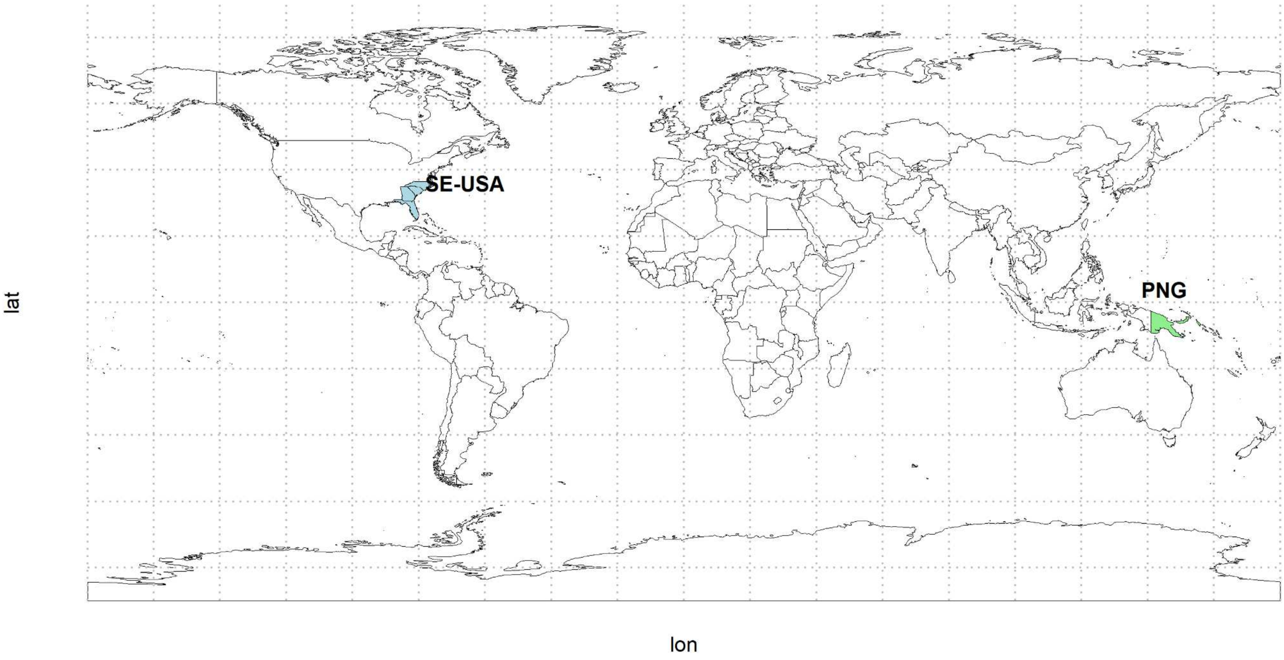

Fig. 2. Specimen image data used for this analysis was collected from the Southeastern US and Papua New Guinea.

2.6. Algorithm methodology

IDX species identification models are based on modified versions of the core closed-set species identification methods developed by Goodwin et al. (Goodwin et al., 2021). Algorithm development is an iterative process to enhance performance; as a result, three recent versions of the algorithm were introduced in the time period under consideration in this study. These versions differed both in methodology and in the dataset used to train them. Improvements to the algorithm methodologies between releases are described in Table 1. This illustrates the evolving nature of the deployed algorithms as new data becomes available and methods mature, highlighting the significant differences between releases. Additional details of model development can be found in the Supplementary information - Methods Section.

3. Results

We present deployed recall results from Papua New Guinea (PNG) and the Southeastern United States (SE US). For PNG, these include *Aedes aegypti, Ae. albopictus* and *Culex pipiens* s.l. (Table 2(a)). For SE US, these range across five genera and 19 distinct species (Table 2(b)); out of those we selected, eight species (*Ae. albopictus, Ae. taeniorhynchus, Ae. vexans* s.l.*, Anopheles crucians, Coquillettidia perturbans, Cx. pipiens* s.l., *Cx. restuans* and *Psorophora ferox*) which had species labels as contributed data available for all three algorithm versions were used for group comparisons and visualization purposes.

Overall algorithm performance improved from version 2.1.1 to 4.0, increasing from 55.3 % (48.9, 61.7) to 80.2 % (77.3, 83.2) in the Southeastern US region and 82.3 % to 94.3 % in PNG. There was a notable decrease in performance of version 3.0 in the PNG region, dropping from 82.4 % to 73.6 % on the macro average level. This was driven by a notable drop in the recall of *Cx. pipiens* s.l. (Note: *Cx. pipiens* is not found in Papua New Guinea (PNG). During the time period discussed, *Cx. quinquefasciatus* was being classified as *Cx. pipiens* (s.l.)).

In PNG (Fig. 3(a)), there was a significant decrease in recall of *Cx. pipiens* s.l. ($p<.001$) between versions 2.1.1 and 3.0 but a significant increase in the recall of *Ae. aegypti* ($p<.001$)) and *Cx. pipiens* s.l. ($p<.001$)) between version 3.0 and 4.0. Examination of the confusion matrices shows the distribution of *Ae. aegypti* error is almost entirely in *Ae. albopictus* (Supplementary Information, Figs. 4 and 5).

Similar trends were observed in the SE USA. Between v2.1.1 and v.3, *Ae. taeniorhynchus* ($p<.001$))*, An. crucians* ($p<.001$)) and *Ae. vexans* ($p=.02$) recall increased significantly and*, Cx. restuans* and *Ps. ferox* showed a non-significant increasing trend, while *Cx. pipiens* s.l. recall decreased significantly ($p<.001$)). Between v3.0 and v4.0, *An. crucians* ($p=.002$) increased significantly while *Ae. taeniorhynchus* ($p=.001$) decreased significantly. Changes in *Ae. albopictus, Ps. ferox* and *Cx. restuans,* were positive, whereas changes in *Cx. pipiens* s.l., *Ae. vexans*, and *Cq. perturbans* were negative, but none reached the level of significance. While there is variability in species recall between algorithm versions, the macro average recall over the eight species represented in all three algorithms was significant from v2.1.1 to v4.0 increasing from 55.3 [48.9, 61.7] to 80.2 [77.3, 83.2]. *Cx. pipiens* s.l. had the largest decrease in recall falling from 93.8 [90.7, 96.1] to 61.5 [43.5, 77.4]. In the corresponding confusion matrices found in the Supplementary Information, one can see that in v2.1.1 much of the *Culex* genus error was biased to *Cx pipiens* s.l., whereas in v3.0 and v4.0 the classification error became more localized to other species under the same genus and resulted in recall that was at least nominally improved for every other *Culex* species except *Cx. pipiens* s.l., indicating increased precision within the genus. (Supplementary Information, Figs. 1–3).

4. Discussion

This study presents, to the best of our knowledge, the first published assessment of iterative deployments of deep learning based image classification algorithms for mosquito species identification. We show the continued improvement and expansion of these algorithms over time in two distinct regions: Papua New Guinea (PNG) and the Southeastern United States (SE US). Despite the absence of specimen images from PNG in training datasets, the performance in this region was notably high and improved with the latest algorithm release, suggesting that some generalizability of the algorithms to new regions is possible without extensive region-specific data supplementation for species already incorporated in the algorithm.

However, the analysis also underscores challenges. In general, we find that species which are harder for humans to identify also prove more challenging to the IDX algorithm to identify accurately. In

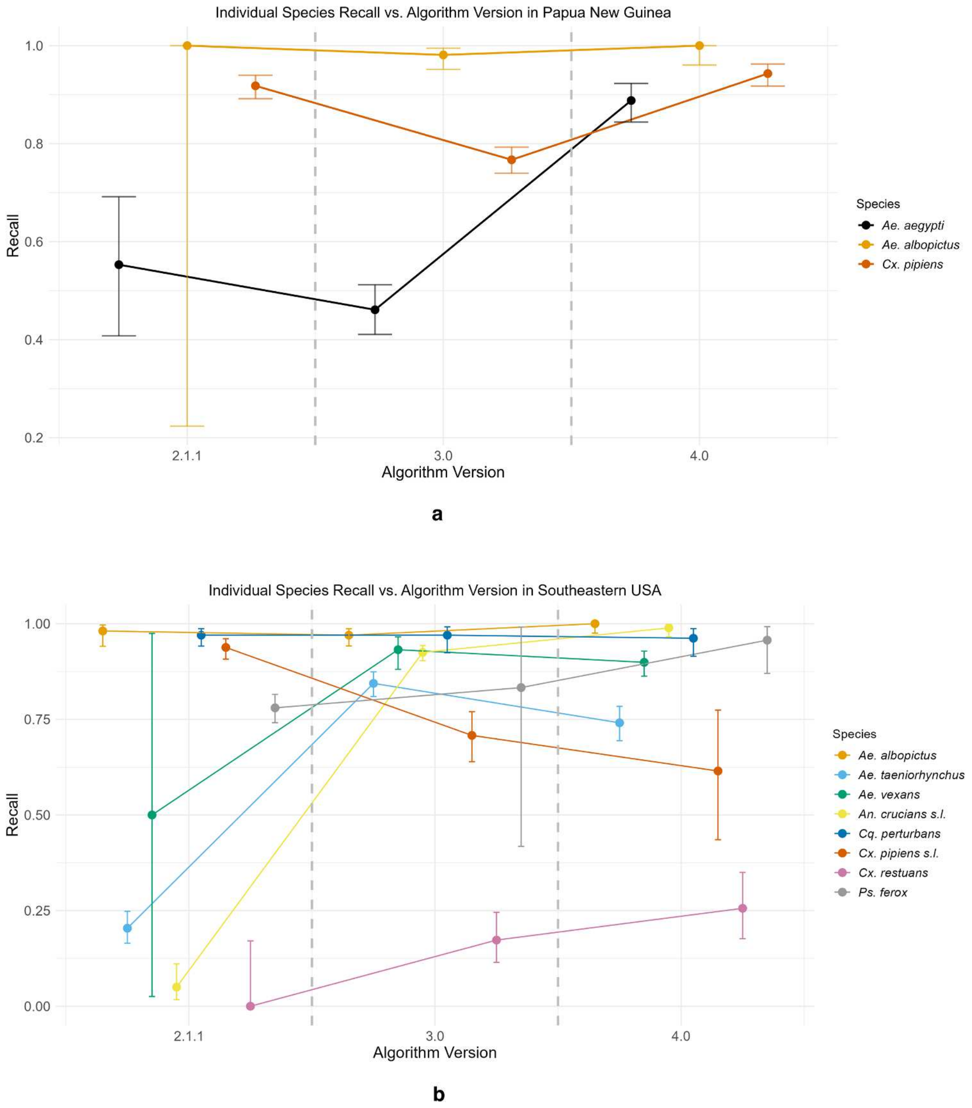

Fig. 3. Individual species recall as a function of algorithm version in (a) Papua New Guinea and (b) Southeastern USA. As discussed, for SE USA only eight species for which we had data for all algorithm versions are presented. For PNG, the three presented species represent all contributed data known to the algorithm releases. Error bars represent 90 % confidence intervals. Individual estimations have been horizontally separated for readability; the dashed gray vertical lines separate the three algorithm versions presented (v.2.1.1, v3.0 and v.4.0).

addition, a training dataset that inadequately represents the natural variability of a species can result in unexpected poor model performance.

This was encountered in differentiating *Ae. aegypti* in PNG, with recall initially recorded at 55 % in v2.1.1 eventually increasing to 89 % in v4.0. While the precision could not be reliably reported due to the lack of data in many of the species known to the CNN, nearly all *Ae. aegypti* samples that were misclassified were predicted as *Ae. albopictus*. Given the extreme morphological similarity between these two species in scenarios with more damaged specimens, this is not surprising. Still, in most cases they remain differentiable by entomologists, underscoring a necessary target for algorithm improvement in future releases. While the reported data shows improvement, continued performance measurement for these important vector species is warranted.

Notably, the greatest decline in recall was observed with *Cx. pipiens* s. l. in the SE US, despite ample data availability. Conversely, recall for all other *Culex* species improved throughout the study period concurrent with a decreasing bias of other *Culex* species being misclassified as *Cx. pipiens* s.l. (Supplementary Information, Figs. 1–3). The algorithm's bias toward *Cx. pipiens* s.l. can be explained from three perspectives. First, many of the traits that differentiate *Culex* species are very subtle and are frequently absent or damaged in field-collected specimens. This makes accurate identification difficult and requires a more detailed examination of specimens. As a result, a CNN-based approach faces greater challenges in achieving reliable performance when these small morphological features are either missing or hard to detect. Secondly, *Cx. pipiens* s.l. is overrepresented in our dataset. While "more data" is often touted as a benefit in fine-grained problems such as this, given imbalanced datasets, it can do more harm than good due to the heightened variability of the overrepresented class. This is likely to introduce bias in the network, as observed here despite trying to address this issue in training. Finally, despite rigorous efforts to maintain data integrity and reduce label noise, the cryptic speciation within the *Cx. pipiens* group can lead to occasional misidentifications. These mislabels are often skewed toward the nominotypical species, complicating accurate taxonomic resolution within the group.

Although these algorithms can produce powerful results, their sensitivity to sampling biases remains a challenge. Training datasets, while growing, may not fully capture the variability found in wild mosquito populations, which can result in accuracy fluctuations during deployment, and misalignment of deployment and development accuracies (see Table 1). Given these often unpredictable fluctuations, regular updates and continuous performance monitoring and adjustment are crucial for maintaining and enhancing accuracy.

A limitation of this study is the restricted number of regions and species analyzed, which may not fully represent typical species distributions. Contributed data are often driven by user needs and specific use cases, potentially skewing the representation. The short timeframe of data collection further constrains the robustness of comparisons. As IDX is more widely adopted and data contributions become more consistent, future analyses are anticipated to provide more comprehensive insights and comparisons, addressing these limitations and enhancing the overall evaluation of algorithm performance. Future analyses will also include assessment of unknown species detection models and sex classification results.

The evolution of the IDX algorithm across versions 2.1.1, 3.0, and 4.0 evaluated here demonstrates significant performance improvements, particularly for species that are challenging to identify. While high recall has been achieved for most species, ongoing efforts are needed to address the remaining variability and ensure consistent performance across all species and regions when deployed. By continuing to improve the algorithm methods and expand training datasets, the IDX algorithm can become a powerful tool for accurate mosquito species identification around the globe, (Fig. 2).

CRediT authorship contribution statement

Khushi Anil Gupta: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Vasiliki N. Ikonomidou:** Writing – review & editing, Writing – original draft, Visualization, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Margaret Glancey:** Writing – review & editing, Writing – original draft, Resources, Project administration, Methodology, Conceptualization. **Roy Faiman:** Writing – review & editing, Writing – original draft, Validation, Methodology, Conceptualization. **Sameerah Talafha:** Writing – review & editing, Visualization, Methodology, Formal analysis. **Tristan Ford:** Writing – review & editing, Resources, Project administration, Methodology, Funding acquisition, Conceptualization. **Thomas Jenkins:** Writing – review & editing, Visualization, Methodology, Formal analysis. **Autumn Goodwin:** Writing – review & editing, Writing – original draft, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

All authors are employed by and partial owners of Vectech, the company developing and distributing the IDX hardware and software

Data availability

Data will be made available on request.

Glossary

1. Label noise- This refers to specimen labeling errors or inconsistencies in the dataset used to train machine learning models.
2. Convolutional Neural Network(CNN)- An artificial model/ network which is primarily used to process image-based data using different filters to extract features and patterns in images, and abstract that information in a condensed form to accomplish a specific task, such as mosquito species identification.
3. Recall- A classification metric used to measure the percentage of specimens of a certain species that have been successfully identified by the model. This is defined by the true positives divided by the sum of the true positives and the false negatives.
4. Precision- A classification metric used to measure the percentage of specimens identified as members of a species that actually belong to it. This is defined by the true positives divided by the sum of the true positives and the false positives.
5. Micro recall- The recall average across all specimens irrespective of species.
6. Macro recall- The average of the recalls for each individual class irrespective of number of specimens per class.
7. Confusion Matrices- These are tables that serve as a visualization tool for the classifier's performance and the distribution of classification error between species.
8. Confidence Interval- Defined as the range of values that contains the true value of a parameter shown with a level of confidence, in this case 90 %.
9. Distillation technique- Method to transfer knowledge from one AI model to another.
10. Focal loss- Loss function used for training CNNs that emphasizes difficult, misclassified examples during model training, by decreasing the relative penalty (loss) for correctly identified cases.
11. Center loss- Loss function used for training CNNs that groups same-class samples closer in the feature space.

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Data statement

Images and associated data may be shared for research use upon request.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.actatropica.2024.107392.

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