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Exploration Paper

A Deep Learning Approach for Automated Identification of *Triatoma infestans* Using YOLOv8

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ABSTRACT

Triatoma infestans, a primary vector of Chagas disease, poses a significant public health risk in Latin America. Rapid and accurate identification of this insect is essential for both vector surveillance programs and individual-level decision-making after potential exposure. Traditional identification methods rely on manual inspection, which is time-consuming, error-prone, and dependent on expert knowledge. This study explores the feasibility of an AI-driven detection system based on the medium YOLOv8 model (YOLOv8m) to automate the identification of T. infestans from images. The model was trained on a dataset of 91 manually labeled images, with built-in data augmentation techniques dynamically generating 9,100 augmented images over 100 training epochs. The model achieved high accuracy, with a mean average precision at an Intersection over Union threshold of 50% (mAP@50) of 0.9588 and a fitness score of 0.6844, demonstrating its effectiveness under controlled conditions. To assess its reliability, detection examples were analyzed in varied lighting conditions and backgrounds, as well as in scenarios where T. infestans appeared alongside visually similar insects. Results show that the model can consistently detect T. infestans while avoiding false positives for other insect species, highlighting its potential for real-world deployment. This work provides a proof of concept for the integration of AI in entomological identification tasks. Future improvements include expanding the dataset, fine-tuning model hyperparameters, and adapting the system for mobile or embedded deployment to facilitate field usability. By automating T. infestans detection, this study contributes to enhanced vector surveillance efforts and better-informed responses to potential Chagas disease exposure.

Keywords: object detection, vector surveillance, artificial intelligence in entomology

1. Introduction

Triatoma infestans, commonly known as the "Chinche Besucona" in some parts of Mexico, is a primary vector of Chagas disease, a life-threatening illness caused by Trypanosoma cruzi [1]. This disease affects millions of people, particularly in Latin America, where T. infestans is widespread [2]. Early and accurate identification of this insect is crucial for vector control programs, as prompt intervention can significantly reduce transmission risk [3]. Recognizing T. infestans requires attention to its distinctive morphological features, including an elongated, flattened body, a dark exoskeleton with reddish-orange markings along the edges of its abdomen, and a prominent, cone-shaped head with an extended proboscis [4] (Figure 1). These characteristics are essential for distinguishing it from other hemipteran insects, some of which may resemble T. infestans but

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do not pose the same epidemiological risk.

Failure to correctly identify T. infestans can lead to serious public health consequences [4]. If a person is bitten by this insect, it is recommended to capture it rather than kill it and take it to a nearby health center for examination [2]. Experts can determine whether the insect carries T. cruzi, helping assess the risk of Chagas disease transmission [5]. Misidentification or failure to detect T. infestans could prevent this crucial step, delaying medical attention [1]. Conversely, if the insect is not T. infestans, the person should pursue a different course of action, making accurate identification critical for public health responses [3]. Despite its importance, manual identification of T. infestans remains a significant challenge [6]. The process is labor-intensive, requiring trained entomologists and public health workers to visually inspect and classify insects [7]. Moreover, this approach is time-consuming and prone to human error and inconsistencies, particularly when differentiating T. infestant from visually similar species [8]. The lack of scalable and automated detection methods limits the efficiency of epidemiological surveillance efforts, emphasizing the need for innovative technological solutions [9].

Recent advancements in artificial intelligence (AI), particularly in computer vision and deep learning, have revolutionized the automation of insect detection [10]. Object detection models, such as YOLO (You Only Look Once), have demonstrated remarkable success in real-time applications across various domains, including medical imaging, agriculture, and environmental monitoring [11]. These models offer a fast and accurate means of identifying objects within an image, making them ideal for tasks requiring rapid decision-making [12].

In the context of vector control, AI-powered detection systems can significantly enhance epidemiological surveillance by providing an efficient, scalable, and reliable solution for identifying T. infestans [13]. By automating the identification process, AI can bridge the gap between expert entomologists and the general public, enabling individuals to make informed decisions after an insect bite [14]. Public health authorities can deploy automated detection systems capable of quickly analyzing large volumes of images, thereby improving response times and aiding in more effective disease prevention strategies [15].

The primary objective of this study is to develop a detection model based on the medium variant of YOLOv8 (YOLOv8m) to accurately identify T. infestans in real-world conditions. The model was trained on a dataset consisting of images sourced from both online repositories [16, 17] and field photographs, ensuring a diverse and representative training set. Manual annotation was performed to precisely label the insects, improving the quality of the training data and reducing misclassification risks. By creating a robust detection system, this research aims to contribute to the automation of insect vector identification, ultimately assisting in the early detection and control of T. infestans populations to mitigate the spread of Chagas disease. Additionally, this model has the potential to allow nonexperts to verify whether an insect requires further examination.

This study follows a structured methodology to ensure the development of an effective detection system. The YOLOv8m model was trained on a dataset of 91 manually labeled images, with additional variations introduced dynamically through YOLOv8's built-in data augmentation techniques to enhance model generalization. Over 100 training epochs, these transformations generated approximately 9,100 augmented images, significantly increasing dataset diversity without requiring additional manual labeling. The majority of the original images were sourced from public repositories, ensuring a diverse dataset while maintaining consistent visual characteristics. These included sharp focus, clear lighting, and varied angles, capturing T. infestans from top, side, and perspective views (Figure 1). The dataset also ensured that the insect was represented in natural resting positions, often against contrasting backgrounds, such as walls, textiles, and outdoor surfaces. Performance evaluation was conducted by measuring precision, recall, and mean average precision (mAP) to assess the model's effectiveness. Additionally, a real-time detection system was implemented using OpenCV, enabling live insect identification through video input. The study presents preliminary results, highlighting the strengths of the YOLOv8m model while also identifying areas for future improvement, such as fine-tuning hyperparameters, expanding the dataset with more diverse samples. and optimizing the model for better detection accuracy in challenging real-world conditions.

The remainder of this paper is structured as follows. Section 2 provides a detailed account of the AI prototype, including design considerations and innovative features. Section 3 describes the implementation process and presents preliminary results, highlighting unique challenges encountered during development. Section 4 explores the broader implications of the project, its contributions to advancing AI applications, and possible future enhancements. Finally, Section 5 summarizes the study's objectives, key findings, and the next steps for further research and development.

2. Project Description

The proposed system is designed to detect T. infestans in real-world conditions using YOLOv8m. The model is trained on a labeled dataset consisting of images from both online sources and field-collected photographs. By leveraging deep learning techniques, the system is optimized for real-time detection, ensuring fast and accurate identification of the insect in various environments. The ability to automate T. infestans identification plays a crucial role in vector surveillance, allowing public health organizations to respond promptly and efficiently to potential outbreaks. This approach reduces the dependency on manual identification, minimizing errors and improving the scalability of vector control programs.



Figure 1. Images of *T. infestans* showcasing its distinctive morphological patterns, including its elongated body shape, dark exoskeleton with reddish-orange markings, and prominent proboscis. These images are also examples of samples used in the dataset.

The dataset used for training the detection model consisted of images obtained from both freely available online sources, such as Google Images, and original field photographs taken specifically for this study. This approach ensured a diverse dataset, incorporating variations in lighting, angles, and backgrounds to improve model robustness. To ensure accurate training, all images were manually annotated, precisely labeling instances of T. infestans using bounding boxes. A manual filtering process was also performed to remove illustrative images, low-quality samples, and images where the insect was not clearly visible, ensuring that only high-quality images contributed to training. The dataset was then split into 91 images for training and 27 images for validation, maintaining a balanced distribution for effective model evaluation. During training, YOLOv8's built-in augmentation functionalities were applied dynamically, generating a variation of each image per epoch. Since the model was trained for 100 epochs, this resulted in an approximate 9,100 augmented training images and a similar augmentation process for the validation set. This dynamic augmentation strategy allowed the model to learn from a significantly expanded dataset, improving generalization to real-world conditions.

YOLOv8m was selected for this task as a balance between speed and accuracy, making it particularly well-suited for automated insect identification [18, 19]. Among the available YOLOv8 variants, the medium (m) version was chosen to ensure a lightweight yet powerful model capable of handling real-time detection efficiently [20]. Unlike traditional object detection models that require multiple stages for region proposal and classification, YOLO performs detection in a single pass, significantly reducing computational overhead while maintaining high precision [21]. This efficiency is crucial for real-time applications, such as field surveillance and mobile deployment, where rapid detection is necessary for timely interventions [11].

Other possible alternatives, such as Faster R-CNN and EfficientDet, were considered but ultimately not chosen due to their trade-offs [22, 23]. Faster R-CNN is known for its high accuracy but suffers from slower inference times due to its two-stage detection pipeline, making it less suitable for real-time processing [24]. EfficientDet, on the other hand, offers a balance between accuracy and speed, but it requires extensive hyperparameter tuning and more computational resources for optimal performance [25]. YOLOv8 incorporates improved feature extraction, better anchor-free detection, and an optimized model architecture, making it the most effective option for this study [20]. Its ability to generalize well across different environments while maintaining low latency and high precision positioned it as the ideal choice for detecting T. infestans in realworld conditions [18].

To improve the model's robustness and generalization across diverse real-world conditions, data augmentation was applied using YOLOv8's built-in augmentation functionalities. These techniques introduced controlled variations in the dataset, enhancing the model's ability to handle changes in lighting, orientation, and scale. The applied transformations included random rotations (up to 10 degrees), translations (shifting up to 10% of the image), scaling (50% zoom), shear transformations (10-degree distortion), and flipping (both vertical and horizontal with a 50% probability each). By leveraging YOLOv8's native augmentation methods, the model was exposed to a wider range of visual scenarios, reducing the risk of overfitting to specific conditions and improving its detection accuracy in real-world environments.

By diversifying the training data, these techniques significantly improved the model's generalization capability, reducing its sensitivity to minor variations in insect appearance and background clutter. This was particularly important given the diversity of real-world settings where T. infestans might be encountered, including different lighting conditions, backgrounds, and camera angles. The augmented dataset helped the model develop a more robust feature representation, ultimately leading to improved detection accuracy when applied to previously unseen images in real-world applications.

The training process for the YOLOv8m model was conducted on Google Colab, leveraging its GPU acceleration to efficiently handle the computational demands of deep learning. The training environment was configured with a Tesla T4 GPU, allowing for faster processing and reduced training times compared to CPUbased setups. The dataset, preprocessed with augmentation techniques, was fed into the YOLOv8m training pipeline using the default settings provided by the model's framework.

For this initial version of the model, no hyperparameter tuning was performed, meaning the training followed YOLOv8m's default configurations, including predefined learning rate, batch size, and anchor box settings. While these default parameters provided strong baseline performance, future iterations of the model may benefit from fine-tuning key hyperparameters to further optimize detection accuracy. Adjustments such as learning rate scheduling, batch size optimization, and anchor size adjustments could enhance the model's ability to detect T. infestans with greater precision, particularly in challenging real-world conditions. Moving forward, experimenting with transfer learning and adaptive training strategies may also contribute to improved detection performance, ensuring the model remains both accurate and efficient in operational settings.

After training, the YOLOv8m model was deployed for real-time detection using OpenCV, enabling live identification of T. infestans through a webcam The system processes incoming video frames feed. in real time, passing each frame through the trained YOLOv8m model to detect the presence of the insect. If a detection is made, the model generates bounding boxes around the identified insect, displaying them on the screen with confidence scores. To ensure high reliability while prioritizing the minimization of false negatives over false positives, a confidence threshold of 80%was applied. This means that only detections with a probability of 80% or higher are considered valid, reducing the likelihood of missing actual T. infestans specimens.

The pipeline follows an efficient loop where each video frame is captured, processed, and displayed in quick succession, maintaining smooth real-time performance. This setup allows for instant feedback, making it suitable for field applications where rapid identification of T. infestans is crucial for vector control programs. The use of OpenCV ensures the system remains lightweight and deployable on various hardware configurations, from personal computers to potential mobile and embedded applications. Future enhancements may include integrating additional post-processing techniques to further refine detection accuracy and reduce computational overhead.

This project stands out due to its custom dataset creation, real-time deployment capabilities, and scalability for future applications. Unlike generic object detection models, this model was specifically designed for detecting T. infestans, incorporating field-collected and manually labeled images to ensure high accuracy in real-world conditions. Its real-time deployment capability, powered by OpenCV and YOLOv8m, allows for immediate identification using a webcam with minimal latency, making it suitable for both laboratory monitoring and field applications. By applying a 90% confidence threshold, the system prioritizes high-accuracy detections, reducing false positives and improving reliability. Additionally, the project is scalable for mobile integration, with future plans to convert the trained model into lightweight formats such as TensorFlow Lite or ONNX for deployment on smartphones or embedded devices. This ensures accessibility for non-experts, enabling real-time vector surveillance in remote locations.

3. Implementation and Results

The complete implementation, including dataset preprocessing, model training scripts, and real-time detection code, is publicly available in the project's GitHub repository: https://github.com/aaaimx/T_ infestans_detection_YOLOv8m.

After training, the YOLOv8m model was evaluated based on several key performance metrics to assess its accuracy and generalization ability. The model achieved a precision of 0.9606 and a recall of 0.9041, demonstrating a strong ability to correctly identify *T. infestans* while maintaining a relatively low rate of false negatives. Figure 2 illustrates the training performance, showing the loss curve convergence and mAP progression over epochs, which confirm the model's steady improvement.

The mean average precision at an Intersection over Union (IoU) threshold of 50% (mAP@50) reached 0.9588, meaning that the model correctly identified *T. infestans* with high accuracy when the predicted bounding boxes overlapped at least 50% with the ground truth annotations, demonstrating high detection accuracy under standard intersection-over-union thresholds. However, the mAP@50-95, which evaluates performance across multiple IoU thresholds, was 0.6539, suggesting that detection confidence varies depending on object overlap. The fitness score, calculated as 0.6844,



Figure 2. Training Performance Graphs: (a) Loss curve over training epochs and (b) mAP progression during training, illustrating performance trends.

reflects the model's overall precision, recall, and IoU consistency. These results indicate that the model generalizes well to the validation set, achieving high accuracy in controlled conditions but may require further refinements to improve detection under more challenging real-world scenarios, such as variations in lighting, backgrounds, and occlusions.

To visually assess the model's performance, Figure 3 presents examples of T. infestans detections. The images illustrate successful identifications where the insect was accurately enclosed within bounding boxes, demonstrating the model's ability to detect the target species across different environments.

Additionally, to evaluate the specificity of the detection system, Figure 4 shows instances where T. infestans was detected while other insects, such as spiders and bed bugs, were not misclassified as T. infestans. These results highlight the model's ability to differentiate T. infestans from other visually similar insects, reducing the likelihood of false positives.

4. Discussion and Potential Impact

Vector-borne diseases pose a significant public health challenge, requiring efficient and accurate surveillance systems to mitigate their spread [26]. Traditional vector monitoring methods rely on manual insect identification, which can be time-consuming, labor-intensive, and prone to human error [27]. The integration of AI in vector surveillance presents a transformative approach, allowing for automated, scalable, and real-time detection of disease-carrying insects [28]. This study demonstrates the feasibility of using deep learning-based object detection, specifically YOLOv8m, to identify T. infestans with high accuracy and efficiency, ensuring that individuals—particularly those who may have been bitten—can quickly recognize the insect and take appropriate action, such as capturing it for evaluation by health professionals [29].

Beyond its role in vector control programs, automated identification of T. infestans is crucial for

individual-level decision-making [30]. When a person is bitten by this insect, capturing it and bringing it to a health center for examination is essential, as experts can determine whether it carries T. cruzi, the parasite responsible for Chagas disease [31]. Misidentification or failure to detect T. infestans could result in missed medical evaluations, potentially leaving individuals unaware of their exposure risk [32]. Conversely, if the insect is not T. infestans, the person should pursue a different course of action, highlighting the importance of rapid and accurate identification [33]. By automating insect detection, this AI-driven system reduces dependence on expert entomologists, accelerates response times in both public health initiatives and personal health decisions, and enhances disease prevention efforts [34]. The ability to deploy AI-based detection models in remote or high-risk areas further strengthens surveillance capabilities, making it easier for public health organizations and individuals to monitor and respond effectively to potential threats [2].

The proposed YOLOv8m-based detection system offers a highly effective solution for vector surveillance, disease prevention, and individual health decisionmaking. With high detection accuracy, demonstrated by strong precision, recall, and mean average precision (mAP) scores, the model ensures reliable identification of T. infestans [35]. Its real-time processing capabilities, powered by OpenCV-based deployment, allow for instantaneous detection using a webcam or other imaging devices, making it suitable for both field applications and personal use [36]. Trained on a diverse dataset with data augmentation techniques, the model generalizes well across various lighting conditions, insect orientations, and backgrounds, making it adaptable to different environments. This model has the potential to impact individual health decisions, as it enables people to determine whether an insect in their home is T. infestans and requires medical attention [37]. By providing a scalable and cost-effective solution for early detection and monitoring, this AI-powered system may strengthen vector control efforts, empowering individu-



Figure 3. Examples of *T. infestans* detected by YOLOv8m. The bounding boxes highlight successful identifications under various lighting conditions and orientations.

als with fast, AI-assisted identification, and ultimately aiding in the prevention of Chagas disease transmission [38].

Despite its strong performance, the proposed detection system has certain limitations that need to be addressed for improved real-world applicability. One key challenge is the occurrence of false positives in cluttered backgrounds, where the model occasionally misidentifies objects with similar textures or shapes as T. infestans. Additionally, poor lighting conditions—such as dim environments or strong shadows-can reduce detection accuracy, leading to missed identifications (false negatives). Another limitation stems from the dataset constraints; since the model was trained on a small set of 91 original images, its generalization to highly varied or unseen environments may still be limited. Expanding the dataset with more diverse images, including additional field-collected samples under different environmental conditions, could help improve robustness. Moreover, fine-tuning hyperparameters, such as confidence thresholds, learning rates, and anchor sizes, may further enhance detection performance. Finally, testing the model in real-world settings, such as deploying it in vector surveillance programs, would provide valuable feedback to refine detection accuracy and adaptability in operational scenarios. Addressing these limitations will be crucial for optimizing the system for large-scale deployment and real-world usability.

While this study focuses on the detection of T. infestans, the underlying AI-based detection framework has the potential to be adapted for a wide range of applications beyond Chagas disease vector surveillance. Similar deep learning techniques could be applied to the identification of other disease-carrying insects that are often misidentified, such as other species of Triatoma that also transmit Chagas disease or similar-looking insects that are harmless. This could help improve public awareness and reduce unnecessary concern, while ensuring that true vectors are identified and handled correctly.

Additionally, this AI-driven approach could prove valuable in agriculture, where automated detection of crop-damaging pests (e.g., locusts, beetles, or caterpillars) could help farmers implement targeted pest control strategies, reducing pesticide overuse and improving crop yields. Beyond public health and agriculture, AI-powered biodiversity monitoring could benefit from such models by enabling the automated classification of insect species, contributing to ecological research and conservation efforts. By refining and expanding this detection framework, deep learning models could support real-time monitoring systems for vector control programs, environmental protection initiatives, and field-based entomological studies, demonstrating the far-reaching impact of AI in entomology, epidemiology, and ecological science.

To maximize the real-world impact of this detection system, several key advancements are planned for future deployment. One major focus is adapting the model for mobile and embedded systems, enabling lightweight deployment on smartphones, drones, or IoT devices for real-time vector surveillance in remote areas. Efforts are underway to convert the trained YOLOv8m model into optimized formats such as TensorFlow Lite or ONNX, reducing computational requirements while maintaining detection accuracy. Additionally, field testing in realworld environments is crucial to validating the model's performance under varied lighting conditions, diverse insect orientations, and natural backgrounds. Collaboration with entomologists and public health experts will provide critical feedback for refining the system, ensuring its practical usability in vector control programs.

Beyond mobile deployment, integrating edge computing and federated learning could further enhance offline detection capabilities, allowing the model to function in areas with limited or no internet connectivity. Edge AI devices could process detections locally, sending only essential metadata to centralized databases for broader epidemiological monitoring. These advancements would significantly improve accessibility, scalability, and efficiency in disease vector surveillance, agricultural pest management, and ecological monitoring, making AI-powered detection a viable tool for realworld applications.



Figure 4. Examples of T. infestans detection alongside other insects. The model correctly detects T. infestans while avoiding false positives for other species such as spiders and bed bugs.

5. Conclusion

This study developed a YOLOv8m-based detection model to accurately identify T. infestans, offering a scalable tool for vector surveillance and individual health decision-making. The model demonstrated high detection accuracy, supported by strong precision, recall, and mean average precision (mAP) scores, ensuring reliable identification across diverse environments. Additionally, its real-time processing capabilities, enabled by OpenCV, allow for instantaneous detection, making it practical for both field applications and personal use. By automating the detection process, this system not only aids public health professionals but also helps non-experts recognize T. infestans, ensuring individuals take appropriate actions after a bite—either capturing the insect for examination or avoiding unnecessary concern in cases of misidentification. These advancements contribute to faster response times, improved disease monitoring, and enhanced public health strategies, ultimately reinforcing efforts to mitigate the spread of Chagas disease.

The proposed AI-powered system presents a scalable solution with the potential for widespread use in public health programs, particularly in resource-limited regions where expert identification is not readily available. By reducing dependence on trained entomologists, this model enhances accessibility, enabling quick and accurate recognition of T. infestans in real-world conditions. This capability ensures that individuals take the correct post-bite actions, such as submitting the insect for analysis or seeking alternative medical guidance if the insect is not a vector of Chagas disease. By minimizing misidentification and delays in medical intervention, this AI-driven system could play a role in reducing Chagas disease transmission risks, underscoring the potential of AI-based solutions in improving vector surveillance and public health outcomes.

Despite its strengths, the detection system faces challenges that must be addressed to enhance its realworld performance. False positives can occur in cluttered backgrounds, where objects with similar textures or shapes may be misidentified as T. infestans. Additionally, poor lighting conditions, such as dim environments or harsh shadows, can lead to false negatives, affecting detection accuracy. Another key limitation is the dataset size, as training on 9,100 images (included augmented images) may not provide sufficient diversity for robust generalization. Expanding the dataset with more field-collected samples and similar-looking nonvector insects could improve model reliability. Moreover, fine-tuning hyperparameters, such as confidence thresholds and learning rates, may further refine detection performance. Future work will focus on mobile deployment, real-world field testing, and collaborations with public health organizations to integrate this tool into vector control programs, ensuring practical usability in endemic regions.

References

- R. Castillo-Neyra, C. Barbu, R. Salazar, K. Borrini, C. Náquira, and M. Levy, "Host-seeking behavior and dispersal of triatoma infestans, a vector of chagas disease, under semi-field conditions," *PLoS Neglected Tropical Diseases*, vol. 9, 2015.
- [2] J. González, M. Contreras, H. Schenone, H. Adaos, and R. Cabezas, "Chagas disease: impact of triatoma infestans control program in alto del carmen, huasco province, ili region atacama, chile," *Boletin chileno de parasitologia*, vol. 51, pp. 28–30, 1996.
- [3] L. Diotaiuti, O. R. de Paula, P. Falcão, and J. Dias, "Evaluation of the chagas' disease vector control program in minas gerais, brazil, with special reference to triatoma sordida," *Bulletin of the Pan American Health Organization*, vol. 28, pp. 211–219, 1994.
- [4] A. Loza, A. Talaga, G. Herbas, R. J. Canaviri, T. Cahuasiri, L. Luck, A. Guibarra, R. Gonçalves, J. A. Pereira, S. A. Gomez, A. Picado, L. Messenger, C. Bern, and O. Courtenay, "Systemic insecticide treatment of the canine reservoir of trypanosoma cruzi induces high levels of lethality in triatoma infestans, a principal vector of chagas disease," *Parasites Vectors*, vol. 10, 2017.

- [5] V. JorgeGonzález, M. D. C. Contreras, H. Schenone, H. Adaos, and R. Cabezas, "Enfermedad de chagas: impacto del programa de control del triatoma infestans en la comuna de alto del carmen, provincia de huasco, iii región atacama, chile," *Boletin chileno de parasitologia*, vol. 51, pp. 28–30, 1996.
- [6] R. Gürtler, G. M. Prokopec, L. Ceballos, C. Petersen, and O. Salomón, "Comparison between two artificial shelter units and timed manual collections for detecting peridomestic triatoma infestans (hemiptera: Reduviidae) in rural northwestern argentina," *Journal of Medical Entomology*, vol. 38, pp. 429–436, 2001.
- [7] M. Cecere, R. Gürtler, D. Canale, R. Chuit, and J. E. Cohen, "The role of the peridomiciliary area in the elimination of triatoma infestans from rural argentine communities," *Revista panamericana de salud publica = Pan American journal* of public health, vol. 1, pp. 273–279, 1997.
- [8] Y. Provecho, M. S. Gaspe, M. Fernández, and R. Gürtler, "House reinfestation with triatoma infestans (hemiptera: Reduviidae) after community-wide spraying with insecticides in the argentine chaco: A multifactorial process," *Journal of Medical Entomology*, vol. 54, pp. 646–657, 2017.
- [9] J. Gurevitz, M. S. Gaspe, G. F. Enriquez, Y. Provecho, U. Kitron, and R. Gürtler, "Intensified surveillance and insecticidebased control of the chagas disease vector triatoma infestans in the argentinean chaco," *PLoS Neglected Tropical Diseases*, vol. 7, 2013.
- [10] A. Teixeira, J. Ribeiro, R. Morais, J. Sousa, and A. Cunha, "A systematic review on automatic insect detection using deep learning," Agriculture, 2023.
- [11] T. D. C. Júnior and R. Rieder, "Automatic identification of insects from digital images: A survey," Comput. Electron. Agric., vol. 178, p. 105784, 2020.
- [12] L. Souifi, A. Mdhaffar, I. Rodriguez, M. Jmaiel, and B. Freisleben, "A systematic literature review on insect detection in images," Signal, Image Processing and Embedded Systems Trends, 2022.
- [13] D. Zeng, Z. Cao, and D. Neill, "Artificial intelligence-enabled public health surveillance-from local detection to global epidemic monitoring and control," Artificial Intelligence in Medicine, pp. 437–453, 2020.
- [14] S. Saran and P. Singh, "Systematic review on citizen science and artificial intelligence for vector-borne diseases," The International Archives of the Photogrammetry, Remote Sensing and Spatial Information Sciences, 2024.
- [15] J. Abdulkarim, A. A. Musa, Y. Abdullahi, and U. H. Yamman, "Artificial intelligence may help in the containment of cholera in nigeria," OIRT Journal of Information Technology, 2022.
- [16] iNaturalist Mexico, "Triatoma dimidiata photo gallery," 2024, accessed: March 3, 2024. [Online]. Available: https://mexico.inaturalist.org/taxa/308558-Triatoma-dimidiata/browse_photos
- [17] Pexels, "Insecto 6 patas de hoja verde," de naranja-negro colgando una planta de 2024.accessed: March 3, 2024.[Online]. Available: https://www.pexels.com/es-es/foto/ insecto-de-6-patas-naranja-negro-colgando-de-una-planta-de-hoja-verde-68513/
- [18] A. Widayani, A. M. Putra, A. R. Maghriebi, D. Z. C. Adi, and M. H. F. Ridho, "Review of application yolov8 in medical imaging," *Indonesian Applied Physics Letters*, 2024.
- [19] C. M. Badgujar, A. Poulose, and H. Gan, "Agricultural object detection with you look only once (yolo) algorithm: A bibliometric and systematic literature review," ArXiv, vol. abs/2401.10379, 2024.
- [20] M. G. Ragab, S. J. Abdulkadir, A. Muneer, A. Alqushaibi, E. H. H. Sumiea, R. Qureshi, S. M. Al-Selwi, and H. Alhussian, "A comprehensive systematic review of yolo for medical object detection (2018 to 2023)," *IEEE Access*, vol. 12, pp. 57815–57836, 2024.
- [21] Z. Piao, M. Meng, H. Yang, T. Xue, Z. Jia, and W. Liu, "Distinguishing between aldosterone-producing adenomas and non-functional adrenocortical adenomas using the yolov5 network," Acta Radiologica, 2024.
- [22] S. J. Yang, Y. Lu, X. Zheng, Y. J. Zhang, F. Xin, P. Sun, Y. Li, S. Liu, S. Li, Y. T. Guo, and S. Liu, "Establishment and clinical testing of pancreatic cancer faster r-cnn ai system based on fast regional convolutional neural network," *Zhonghua Wai Ke Za Zhi [Chinese Journal of Surgery]*, vol. 58, pp. 520–524, 2020.
- [23] Q. Ge, T.-Y. Lin, M. Maire, and P. Dollár, "Efficientdet: Scalable and efficient object detection," arXiv preprint arXiv:1911.09070, 2019. [Online]. Available: https://arxiv.org/abs/1911.09070
- [24] L. Ding, G. Liu, B.-C. Zhao, Y. Zhou, S. Li, Z. Zhang, Y. Guo, A. qin Li, Y. Lu, H. Yao, W. Yuan, G. Wang, D. Zhang, and L. Wang, "Artificial intelligence system of faster region-based convolutional neural network surpassing senior radiologists in evaluation of metastatic lymph nodes of rectal cancer," *Chinese Medical Journal*, vol. 132, pp. 379 – 387, 2019.
- [25] Q. V. L. Mingxing Tan, Ruoming Pang, "Efficientdet: Scalable and efficient object detection," Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition (CVPR), pp. 10781–10790, 2020. [Online]. Available: https://arxiv.org/abs/1911.09070

- [26] Y. Wu, J. Wang, Q. Liu, T. Li, M. Luo, and Z. Gong, "Practice of integrated vector surveillance of arthropod vectors, pathogens and reservoir hosts to monitor the occurrence of tropical vector-borne diseases in 2020 in zhejiang province, china," Frontiers in Veterinary Science, 2022.
- [27] J. E. Nava-Doctor, C. Sandoval-Ruiz, and A. Fernández-Crispín, "Knowledge, attitudes, and practices regarding vectorborne diseases in central mexico," *Journal of Ethnobiology and Ethnomedicine*, 2021.
- [28] S. Saran and P. Singh, "Systematic review on citizen science and artificial intelligence for vector-borne diseases," The International Archives of the Photogrammetry, Remote Sensing and Spatial Information Sciences, 2024.
- [29] M. Miranda, C. Barceló, D. Arnoldi, X. Augsten, K. Bakran-Lebl, G. Balatsos, M. Bengoa, P. Bindler, K. Boršová, M. Bourquia, D. Bravo-Barriga, V. Čabanová, B. Caputo, M. Christou, S. Delacour, R. Eritja, O. Fassi-Fihri, M. Ferraguti, E. Flacio, E. Frontera, H. Fuehrer, A. García-Pérez, P. Georgiades, S. Gewehr, F. Goiri, M. González, M. Gschwind, R. Gutiérrez-López, C. Horváth, A. Ibáñez-Justicia, V. Jani, P. Kadriaj, K. Kalan, M. Kavran, A. Klobučar, K. Kurucz, J. Lucientes, R. Lühken, S. Magallanes, G. Marini, A. Martinou, A. Michelutti, A. Mihalca, T. Montalvo, F. Montarsi, S. Mourelatos, N. Muja-Bajraktari, P. Müller, G. Notarides, H. Osório, J. Oteo, K. Oter, I. Pajović, J. Palmer, S. Petrinić, C. Răileanu, C. Ries, E. Rogozi, I. Ruíz-Arrondo, I. Sanpera-Calbet, N. Sekulić, K. Sevim, K. Sherifi, C. Silaghi, M. Silva, N. Sokolovska, Z. Soltész, T. Şuleşco, J. Šušnjar, S. Teekema, A. Valsecchi, M. Vasquez, E. Velo, A. Michaelakis, W. Wint, D. Petrić, F. Schaffner, and A. della Torre, "Aimsurv: First pan-european harmonized surveillance of aedes invasive mosquito species of relevance for human vector-borne diseases," *GigaByte*, 2022.
- [30] O. F. Leite, M. J. Alves, S. S. Souza, R. C. Mayo, V. Andrade, C. Souza, O. Rangel, S. S. Oliveira, V. L. Lima, V. L. Rodrigues, M. E. Carvalho, C. Casanova, and D. M. Wanderley, "Triatoma infestans in area under entomological surveillance for chagas' disease in são paulo state, brazil," *Revista da Sociedade Brasileira de Medicina Tropical*, vol. 34 5, pp. 437–43, 2001.
- [31] G. Marti, M. G. Echeverría, M. L. Susevich, J. Becnel, S. Pelizza, and J. García, "Prevalence and distribution of parasites and pathogens of triatominae from argentina, with emphasis on triatoma infestans and triatoma virus trv," *Journal of Invertebrate Pathology*, vol. 102–3, pp. 233–237, 2009.
- [32] M. Rojas-Cortez, M. Pinazo, J. Gascón, E. Gamarra, R. M. Grágeda, R. Fernandez, E. Rueda, J. Pinto, H. M. Anzoleaga, Y. E. Caballero, G. S. Urioste, J. Sánchez, R. Saravia, M. Castellon, W. García, L. O. Daza, I. Mur, D. Lozano, F. Carvalho-Costa, F. A. Monteiro, and F. Torrico, "Community-based entomological surveillance in three chagas diseaseendemic regions in sub-andean bolivia," *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 2021.
- [33] R. Gurgel-Gonçalves, F. Abad-Franch, M. R. de Almeida, M. Obara, R. D. C. M. D. Souza, J. A. de Sena Batista, and D. Rocha, "Triatodex, an electronic identification key to the triatominae (hemiptera: Reduviidae), vectors of chagas disease: Development, description, and performance," *PLoS ONE*, vol. 16, 2021.
- [34] M. E. de Carvalho, R. A. da Silva, V. L. Rodrigues, and C. D. de Oliveira, "The chagas disease control program of the são paulo state: the contribution of serology to the epidemiological investigation of triatomine-infested domiciliary units during the 1990s," *Cadernos de Saúde Pública*, vol. 18 6, pp. 1695–703, 2002.
- [35] N. R. C. de Lima, "Distribuição, infecção natural e fontes alimentares de triatomíneos coletados em municípios do estado do rio grande do sul e ações educativas na prevenção e vigilância da doença de chagas," 2017.
- [36] R. Piccinali, M. Gaunt, and R. Gürtler, "A microsatellite-based analysis of house infestation with triatoma infestans (hemiptera: Reduviidae) after insecticide spraying in the argentine chaco," *Journal of medical entomology*, vol. 55 3, pp. 609–619, 2018.
- [37] A. R. de Arias, F. Abad-Franch, N. Acosta, E. López, N. González, E. Zerba, G. Tarelli, and H. Masuh, "Post-control surveillance of triatoma infestans and triatoma sordida with chemically-baited sticky traps," *PLoS Neglected Tropical Diseases*, vol. 6, 2012.
- [38] L. Abrahan, M. Cavallo, and I. Amelotti, "Impact of involving the community in entomological surveillance of triatoma infestans (klug, 1834) (hemiptera, triatominae) vectorial control," *Parasites Vectors*, vol. 14, 2021.