**Using Machine Learning to Measure Changes in Immunity due to Climate Change in the Fall Armyworm, *Spodoptera frugiperda***

**Abstract:**

The fall armyworm (*Spodoptera frugiperda*) is a major agricultural pest causing millions in damage to farmlands across the globe. With the recent spread into Africa and Asia, the need for understanding the best form of biocontrol is at an all-time high. While viruses are a major biocontrol agentfor controlling insect pests, we still lack knowledge about how fall armyworms react with specialist pathogens and how that reaction may vary with changes in climate. Furthermore, current methods of measuring immune response use manual counting of hemocytes, requiring large amounts of time on the researcher’s part. Here we use machine learning and compare several object detection algorithms on their ability to automatically count hemocytes. To perform counts, we trained YOLOv8 on 398 photos and validated training on 114 photos. We also reared fall armyworms generationally at two temperatures, 26° C and 31° C, and infected each generation with virus, allowing the survivors to reproduce. Hemocytes were extracted by cutting the fourth proleg and mixed with anticoagulant for use in photographing on a hemocytometer. Of the algorithms compared, YOLOv8 was the most accurate and the quickest to train. Counts tended to be fairly accurate and predicted that 26 populations had a higher immune response in infected control populations and in the uninfected coevolved population. The infected coevolved populations showed no significant difference in immune response when comparing temperatures. This new development will drastically speed up the process of measuring insect immune response and open the door for further research on biocontrol methods in insects.

**Introduction:**

Object detection is a computer vision technique that allows for the localization and classification of objects contained within photos. Machine learning is crucial for object detection, allowing users to develop models to automatically detect objects within images. Many object detection approaches use convolutional neural networks (CNNs) to enable direct learning from photo data (Ren & Wang, 2022). Researchers categorize object detection algorithms based on the complexity of the model and the steps involved for detection. Single-stage detectors directly feed image data into a convolutional network to detect the location and classification of the objects. Examples of commonly used single-stage detectors include You Only Look Once (YOLO) and Single Shot Detector (SSD) (Redmon et al., 2016; Liu et al., 2016). In contrast, two-stage detectors incorporate an additional region proposal step during detection before classifying and drawing bounding boxes on the object of concern. Fast R-CNN, Faster R-CNN, and Mask-RCNN are all common examples of two-stage detectors (Girshick, 2015; S. Ren et al., 2016). Two-stage detectors tend to be more accurate at the cost of additional time and computational resources due to the complexity of the network, while single-stage are faster to train, but less accurate overall and struggle more on small objects. For instance, a previous study found Faster-RCNN to be the most accurate model compared to other single-stage detectors (Wang et al., 2022). However, other studies differentiating fish morphology and detecting cars from aerial images found single shot-detectors to be more accurate overall. Additionally, more recent developments in YOLO models (YOLOv8) suggest the potential to overcome their accuracy limitations. (Jocher et al., 2023).

Previous research has used deep learning methods to aid in the detection of cells other than hemocytes. For example, many studies have performed analysis of blood smears to detect infected white blood cells (Poostchi et al., 2018). However, these studies often aim to detect large objects occupying the majority of pixels in the photos. One current obstacle faced in object detection is the difficulty in predicting small objects. This is in part due to the limited data for use in training and to the low resolution that often occurs due to the objects' small size (Nguyen et al., 2020). Additionally, many CNN-based architectures rely on hierarchy feature mapping in predicting objects. While this may work for large and medium sized objects, small objects can easily be lost in the latter layers of these models due to the down sampling required (Liu et al., 2021).

An insect’s primary immune response against small viral particles is initiated through hemocytes. The primary function of hemocytes is to phagocytize or degrade invading small foreign objects through enzyme release. In lepidopteran species, like the fall armyworm, multiple uniquely shaped hemocytes aid in the immune response against foreign invasions (Lavine and Strand, 2002). Hence, hemocyte counting is a vital step in understanding how the immune system of the fall armyworm and other arthropod species responds to pathogens. Hosts infected with high viral concentrations tend to display increased hemocyte counts when compared to healthy individuals and to those exposed to a low dose (Eslin & Prévost, 1998). Conversely, other studies have shown that hemocyte counts are lower in infected caterpillars compared to their healthy counterparts and may depend on time since infection (Smilanich et al., 2018; Li et al., 2019). Additionally, temperature influences the immune response insects have in the presence of a pathogen. As temperature increases, hemocyte counts tend to increase, until approaching the species thermal maximum where they decline (Catalán et al., 2012; Laughton et al., 2017; Silva & Elliot, 2016). Due to the variability in immune response, it is important to understand how each organism reacts to its corresponding viruses.

The current method for detecting and counting hemocytes requires manually tallying their presence by hand. This approach can be tedious and time-consuming since each image may take up to 60 seconds to process accurately. These manual counting methods may not always be reliable due to the potential for user error when counting out-of-focus hemocytes and other cells. To mitigate this problem, programs like ImageJ have the ability to count objects in images (Schneider et al., 2012). However, ImageJ often struggles to provide accurate counts due to the unique and diverse shape of hemocytes, the presence of other miscellaneous cells in samples, and the placement of cells on the hemocytometer grids. Additionally, hemocytes will cluster together after a period of time which can further compound these challenges (Theopold et al., 2002). Moreover, camera quality and contrast can introduce additional inaccuracies in counts and skew the results. In particular, images taken in low light conditions result in reduced visibility of hemocytes and skew the analysis. Additionally, it is important we consider how to account for the small size of hemocyte cells since many algorithms struggle with smaller objects. This raises the need for detection methods other than manual counting or the use of ImageJ that can account for the small size of hemocytes.

To our knowledge, no studies have investigated the automation of hemocyte counts in insects driving the need for new methods. Using machine learning should lead to accurate hemocyte counts that take significantly less time when compared to manual counting. We expect single-stage detectors to be faster and more efficient during training, but we also expect two-stage detectors to be more accurate. For trial data on temperature comparisons and hemocytes, we expect hemocyte counts to be stronger at the higher temperature. Finally, larvae exposed to virus should show a stronger hemocyte response than those that were not exposed.

**Materials and Methods:**

* **Study System**

The fall armyworm (*Spodoptera frugiperda*) is a major agricultural pest thought to originate from the tropical environments of Central and South America. The larvae feed primarily on corn, rice, and grasses, but have also been known to destroy crops like tobacco and cotton (Wang et al., 2022). In the last 10 years, fall armyworms have spread into Western and Central Africa causing massive agricultural damage to maize plots within the area (Goergan et al, 2016; Wan et al., 2021). While pesticides have traditionally been used to help cull outbreaks, the emergence of resistance to commonly used pesticides such as carbamates and organophosphates has made it increasingly challenging to control the populations (Tay et al, 2023). Biocontrol practices like the use of predators, parasitoids, and pathogens can reduce the number of pest species present in agricultural fields (Eberle et al., 2012). Compared to pesticides, biocontrol methods have the unique ability to adapt and overcome host resistance, thereby leading to more long-term control options. Despite the potential aforementioned benefits, only a limited number of studies have investigated the use of biocontrol agents to control populations of the fall armyworm, with those available focusing primarily on parasitoids and pheromone traps (Allen et al., 2021; Varshney et al., 2021).

*Spodoptera frugiperda* multicapsid nucleopolyhedrovirus (SfMNPV) is a specialist virus that has been shown to reduce fall army worm populations(Behle & Popham, 2012; Fuxa, 1991). SfMPNV resides in the soil and on infected plants. When occlusion bodies are consumed by S. frugiperda, growth of the larva ceases, and the virus reproduces within the host until it lyses. When lysing occurs, the larva die and release the occlusion bodies into the environment, often releasing on plants other *S. frugiperda* are consuming (Elderd, 2013). SfMNPV and other baculoviruses often cause behavioral changes within hosts to maximize transmission. SfMNPV infected fall armyworms will often climb to high leaves on plants before dying to increase the spread of the virus. These factors make this virus an important candidate for further study

* **Rearing and Hemocyte Extraction**

The first generation of fall armyworms were collected from cornfields in West Lafayette, Indiana. Caterpillars were reared on a mix of corn-based diet until reaching fourth instars. For the first generation, caterpillars were split into two treatments: 26° C and 31° C. The 26° C treatment was kept at 26° C for 12 hours during the day and 16° C at night, while the 31° C treatment was kept at 31° C for 12 hours during the day and 21° C at night. Temperature regimes were based on unpublished thermal performance experiments and correspond to a low temperature *S. frugiperda* survive and an optimal temperature were survival was maximized (Elderd, 2023). For each treatment, a dose response was initially performed to calculate the lethal viral dose for 50% of the population (LD50). We isolated and starved 180 caterpillars for 24 hours to ensure consumption of SfMNPV. Caterpillars were then transferred to individual cups containing small cubes of diet laced with 3 **μl of** virus solutions. The dosage of virus ranged from 100 cells/μL of virus to 106 cells/μL of virus, increasing by a factor of 10 for each virus treatment. The control group’s diet cubes were dosed with DI water containing no virus. We left caterpillars in cups with the virus (or water) laced cubes for another 24 hours to ensure full consumption of diet. Once the 24 hours had passed, caterpillars were transferred back into individual containers half full of the corn-based diet. The date of mortality or pupation was recorded for each individual for use in calculating the LD50 for the subsequent generation. Once all caterpillars had pupated or died, individuals infected with SfMNPV were processed to collect remaining viral particles. This processed virus was then used to infect the next generation of caterpillars. For individuals that survived infection and pupated, caterpillars were transferred to cages containing forty to sixty individuals to ensure reproduction. Eggs were collected every 24 hours and labeled as the next subsequent generation. Neonates that emerged from the new generation were isolated into 1 oz cups filled with ½ ounces of diet. Once the neonates grew into fourth instars, they were then starved, and another dose response was performed to calculate the LD50 for that generation. This was repeated every generation infecting each subsequent generation with virus collected from the previous generation. This accounts for the coevolution of virus and host under different temperature regimes.

Within each temperature treatment, 27 caterpillars were set aside as controls while an additional 27 caterpillars were dosed with enough virus to kill 95 percent of the population of virus. Nine caterpillars from the control and nine caterpillars from the infected treatment were taken for collection every 24 hours, until 72 hours had passed and all caterpillars were used. As per USDA protocol for extracting hemocytes, larvae were initially placed at 4°C for 30 minutes. Once the insects were mostly immobile, they were transferred on ice for extraction. The fourth abdominal prolegs were sterilized with ethanol and then amputated using surgical scissors. Hemolymph from the incision was allowed to pool for collection. Three caterpillars per treatment were bled, and the total hemolymph of these caterpillars were collected. This was repeated two more times for both controls and infected, leading to three sets of photos. Once hemolymph was extracted, the solution was mixed with a chilled anti-coagulant saline solution in a ratio to ensure at least 10 µl of solution were present. Generally, a ratio of 1 hemolymph: 2 anticoagulants was used for 48 hour and 72 hour treatments, while a ratio of 1:3 hemolymph to anticoagulant was used for 24 hour treatments. The solution was then placed on a hemocytometer (Hausser Scientific, Horsham, PA) for counting under a 40x magnification lens. A Canon Powershot G10 14.7MP digital camera was used to photograph 5 of the 25 squares for estimating the total number of hemocytes.

* **Machine Learning**

To gather data used in training the model, the same approach was used for collecting and gathering hemolymph. Nine photos were taken on the hemocytometer grid (Figure 1). Additional photos were taken off of the grid if hemocytes exhibited a unique shape or was in a large cluster. Light intake and camera zoom were varied for each set of photos to account for differences when capturing photos. 571 photos were collected for use as training, validation, and test sets. Each photo was manually annotated using the program LabelImg (<https://github.com/qaprosoft/labelImg>) to ensure annotation accuracy. Halos of light present around hemocytes were included in boxes to increase the size of detection and give more context to the objects when training. Hemocytes out of focus or lacking definition were not included during annotation.

Photos underwent random separation into training, validation, and testing with 70% of photos entered as training data, 20% as validation, and 10% as test. Training data was used to train the models, the validation set was used during training to estimate the current model accuracy and help prevent overfitting, and the test set was used once training finished to measure the accuracy of each algorithm in counting hemocytes. After data was sorted, the photos labeled training were augmented to increase the size of the dataset (Shorten & Khoshgoftaar, 2019). Data in training was then augmented by flipping the photo 180 degrees to account for any unusual orientation of hemocytes and to better account for changes in light. The contrast of photos was further exaggerated to ensure hemocyte detection could occur even with different levels of exposure. This tripled the size of our training data. Models were then trained twice, once with and once without the additional training data to determine if the additional computational time required to train more photos was beneficial to overall accuracy.

All models were trained using the programming language Python. Two versions of YOLO models (YOLOv5x and YOLOv8x) were used to represent single-shot detectors. Both YOLOv5 and YOLOv8 use CSPDarknet53 as a backbone and use an Adam optimizer during training. However, YOLOv8 does not use anchor boxes and uses different convolutions during training. YOLO models were allowed to run until no improvement had been made in the past 50 runs, up to a maximum of 200 epochs. Code for training YOLO models was sourced from Ultralytics for use in training on our own models (Jocher, 2020; Jocher et al., 2023). All models other than YOLO models were trained using MMDetection and code available on Github due to their extensive model library and easy to configure models (Chen et al., 2019). The faster-RCNN model with a backbone of R-101-FPN was run until 200 steps were performed and no significant changes in loss rates were observed. Single-Shot Detector (SSD) was run until 100 steps occurred and no significant change in loss rates occurred. The results from YOLO models were compared to all other models to determine the fastest and the most accurate algorithm.

Training on sample data used two NVIDIA V100S GPUs, each with 32 GB of memory. We randomly cropped all photos to a size of 1280 x 1280 pixels to reduce the overall training time. Batch sizes were kept constant at 8 across all models to better measure training times. Validation of models occured during and after training to calculate precision and recall. Once training and validation of models finished, detection was performed on a subset of the data. This test data was then compared to the counts performed by hand to estimate the accuracy of our counting models.

Models were characterized using the recall, precision, and the mean average precision (mAP). Precision is the total correct positive detections compared to both detections (Equation 1) Recall is defined as the total correct positive detections for that class compared to all the samples in that class (Equation 2). Average Precision (AP) takes into account both precision and recall so that when AP is high, both precision and recall are also high. mAP is the mean AP across all classes where k is the number of classes (Equation 3). Since we only have one class, here mAP is equal to AP. mAP50, or when predicted boxes overlap actual boxes more than 50% (mAP50), was used to determine the best model for use. mAP50-95, or the average precision across multiple overlap thresholds ranging from .5 to .95, was used to further classify the best model. Training time and detection time were also recorded to determine the most accessible model for hardware with lower power.

Once all models were trained, the model with the highest mAP50 was used for counting and further comparisons. Counting was compared by taking the best model’s outputs on detections and comparing them to manual annotations on the test data. Counts were multiplied by 2 or 3 depending on the ratio of anticoagulant to hemolymph that was used. Temperature treatments were initially compared using all photos regardless of infection status and a T-test was performed to test for significance. Once all photos were cropped down to the hemocytometer square, counts were retaken, and another T-test was performed to compare hemocyte counts. Once comparing temperature treatments, we divided cropped photos based on their temperature and infection status. A ANOVA test was performed on generation twelve, the last generation with all treatments completed to determine statistical significance between treatments. A one-way ANOVA test was performed on the uninfected populations to compare temperature treatments. A two-way ANOVA was performed on the infected populations to determine the the effects of temperature and how coevolving *S. frugiperda* with SfMNPV affects hemocyte counts.

**Results:**

Initial comparison of models showed YOLOv8 has the highest mAP50 at 98.5% on unaugmented with a precision of 95.4% and a recall of 94.2% (Figure 2). This model showed a small increase of 0.04% higher mAP50 than the most complex YOLOv5 model, the SSD model, and faster R-CNN models. Additionally, compared to the faster-RCNN model, both YOLOv5 and YOLOv8 had overall shorter training times (Table 1). YOLOv8 also showed a higher mAP50-95 than both models. Augmenting photos to increase training data had surprisingly little effect on accuracy and precision. YOLOv8 trained on augmented photos had a slightly higher mAP50 of 0.01, but a lower mAP50-95 compared to YOLOv8 models trained on unaugmented data. Other models followed similar trends where augmentation had little to no effect on the accuracy of the model. Due to having the highest accuracy, we performed counting hemocytes and further analysis using the YOLOv8 model. Compared to actual counts, counts generated from the model were mostly accurate, only missing one or two hemocytes for the most part. The accuracy of counts also tended to decrease as more hemocytes were present within the photo (Figure 3). False positives tended to be small objects on the edge of photos, or cells with a similar size and shape to hemocytes. False negatives tended to occur when a hemocyte was out of focus or clustered together with many other hemocytes. Counting by hand took on average 339 seconds for a set of 15 photos while detection using the YOLOv8 model on the same images took a total of .78 seconds, saving significant amounts of time.

When using uncropped photos and comparing all photos from the 26 °C to the 31 °C treatment, caterpillars at temperature treatment 26 °C showed a higher mean hemocyte count of 70.67 with a standard deviation of 51.80. Caterpillars reared in the 31 °C treatment showed a mean count of 62.16 with a standard deviation of 43.98 (Fig 4). A t-test of the two treatments yielded a p-value of 0.0486, meaning that the lower temperature populations showed an overall stronger response regardless of disease presence. When cropping the photos down to squares on the hemocytometer, the 26 °C treatments had an average of 32.04 hemocytes with a standard deviation of 23.27 and the 31 °C had an average of 29.65 hemocytes with a standard deviation of 23.21 (Fig. 5). However, there was no significant difference between hemocytes when focusing specifically on squares (p = 0.216).

Temperature caused a significant difference in hemocyte counts among the uninfected control population (p = .031). Hemocytes tended to be higher in the lower temperature compared to the 31°C population (Figure 6). Hemocyte counts in infected populations showed significant differences based on both temperature (p <.0001) and if previous exposure to SfMNPV had occured (p<.0001). In the infected populations, temperature showed the opposite effect compared to the uninfected control population where higher temperatures produced lower hemocyte counts. Control populations saw lower hemocyte counts compared to populations that had been coevolved with SfMNPV in both temperatures (Figure 7).

**Discussion:**

Using object detection algorithms to count hemocytes in images was significantly faster than counting manually. Utilizing this method has the potential to reduce the amount of time and effort required for counting and analyzing large volumes of immune response data. Although the detection is not always completely accurate, the predictions consistently follow a trend close to a 1 to 1 line (Figure 2). Additionally, the predicted counts typically only differ by one or two hemocytes, thus making it an effective tool for predicting count trends. All models tested had a lower detection time than manual counts. Based on our results, unless computational power is a limiting factor, YOLOv8 is the most accurate and efficient model to use when detecting hemocytes. When compared to YOLOv5 and Faster-RCNN, YOLOv8 had higher accuracy and very short overall detection times. It is unsurprising that YOLOv8 is the most accurate compared to other single-stage models since it is the newest model in the YOLO family and is predicted to be more accurate on the standard datasets like the Microsoft Common Objects in Context (COCO) compared to the other models (Jocher et al., 2023). It is surprising that YOLO outperformed Faster-RCNN, as Faster-RCNN is a two-stage detector while YOLO is a one-stage model. The performance difference could potentially be attributed to factors like background contrast or the fact that Faster-RCNN is an older model. More surprising, however, was how little augmenting the training data changed the overall accuracy of predictions. . In other studies, augmented photos improved the accuracy of the model (Shorten & Khoshgoftaar, 2019). This may indicates that the level of data augmentation during training was not sufficient or that performance was already optimized to find hemocytes based on the data we provided. It is possible training requires more extensive augmentation techniques beyond changing contrast and flipping photos horizontally before seeing substantial improvements. Additionally, reducing brightness may have led to loss of features in the photos, making it difficult for the machine to accurately predict the location of hemocytes within the photos.

Uncropped photos grouped by temperature treatments showed a low significance indicating that caterpillars in the 26 °C treatment showed higher hemocyte count compared to the 31 °C (Figure 3). While previous studies have shown infected insects tend to prefer hotter temperatures, this could mean that caterpillars raised at the 31°C treatment may be expending more energy on temperature regulation rather than mounting an immune response (Catalán et al., 2012). In contrast, photos cropped to the hemocytometer squares showed no significant differences between temperature treatments (Figure 4). This suggests that cropping to the hemocytometer squares helped eliminate bias from camera zoom meaning that the significance found on uncropped photos could be an error due to the irregular area captured.

. Uninfected populations showed an increase in hemocytes at 31°C compared to 26°C treatments. Hemocyte counts have been shown to increase with increases in temperature in other insect species and our results match this (Catalán et al., 2012; Silva & Elliot, 2016). Hemocyte counts from populations infected with SfMNPV showed the opposite effect where hemocytes tend to be lower in the populations raised at 31°C compared to the populations raised at 26°C. A past study by Elderd and Reilley (2013) show that the transmission of SfMNPV increases at higher temperatures. Unpublished data shows that the amount of occlusion bodies increases as surrounding temperatures increase (Elderd, 2023). Hemocyte counts may be lowered due to an increased amount of resources required to fend off the additional occlusion bodies. Counts may also be lower if SfMNPV is able to reduce hemocyte counts during infection. Higher temperatures may lead to an increased virulence and as a result, a stronger ability to fight off and destroy immune cells. Populations of *S. frugiperda* coevolved with SfMNPV at both temperatures showed a significant difference with higher hemocyte count than the control populations that had not been previously exposed to virus. Caterpillars who have been previously exposed are selected for a better immune response than their naïve counterparts. As a result, we would expect hemocyte counts to be higher to better prepare for potential future infections.

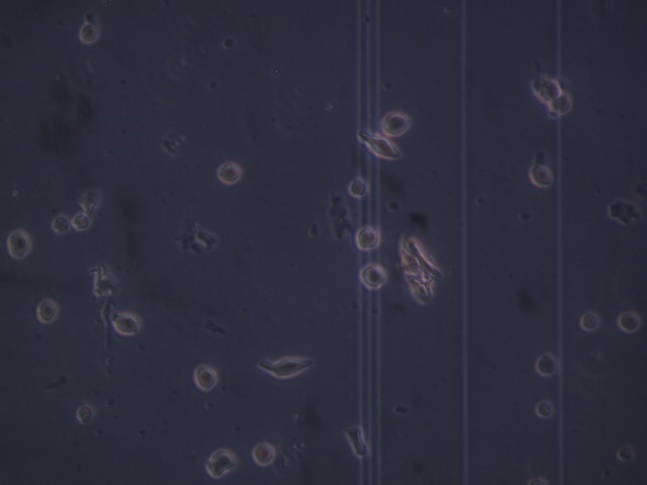
Hemocyte collection may have been skewed by excess cutting during extraction. If the stomach of a larva was ruptured, the hemolymph could have been diluted, decreasing the presence of hemocytes on the hemocytometer. Additionally, foreign cells from the gut may have entered the solution that had similar appearances to hemocytes. While we took photos directly after extraction, cells may coagulate before photos were taken, skewing the amount of hemocytes in each photo. The random assortment of photos may have also affected the training of the model. For example, if underrepresented types of hemocytes were separated into the testing set during class separation, detection may have struggled to correctly detect similarly shaped hemocytes. While incubators were set to consistent temperatures, fluctuations may have occurred due to power outages and when opening the incubator. These changes should have been minor, but may have influenced the growth rate and fecundity if exposed for long periods of time Additionally, while incubators were kept sterile, the presence of other pathogens may have entered causing a higher immune response than we would expect.

Large amounts of training data are required for machine learning to increase accuracy in detection of all objects. Further increasing the number of photos to train on would allow for better predictions and account more for underrepresented hemocyte shapes. The models tested here are primarily used for detection using high powered graphics cards. Training models specialized for low-powered computers and mobile devices would allow for further work to be performed with cheaper computers or even mobile devices. Additionally, using our training data, programs can be made to detect and count hemocytes without the need for taking photos. Additional work should be performed with caterpillars at different temperatures to obtain a better understanding of how changes in climate affect host-pathogen dynamics. Generational experiments could also be run past generation 15 allowing for more coevolution to occur. Collection of hemocytes in every generation would also allow for a better idea of how hemocyte counts change and show more information on changes between temperature treatments. Finally, the use of genetic material would provide further insight into the nature of coevolution between both *S. frugiperda* and SfMNPV.

Overall, here we used machine learning to count hemocytes and estimate immune response in fall armyworms. While the YOLOv8 model was the most successful, all models tested are viable options for detecting hemocytes and should be chosen based on needs and hardware available. Counts made by machine learning algorithms were mostly accurate and followed a 1:1 trend. Understanding how fall armyworms respond to and coevolve with their pathogens will allow us to better predict how biocontrol agents will act, and potentially save farmers from significant crop damage.

**Figures:**

A picture containing black

Description automatically generated 

**Figure 1.** Two examples of hemocytes placed on hemocytometer grids at different levels of brightness and saturation. A shows hemocytes on one square of the 5 x 5 square hemocytometergrid. B shows uniquely shaped hemocytes with an arrow pointing to it.

Chart, scatter chart

Description automatically generated

**Figure 2.** The comparison between the hemocyte counts obtained by hand and the hemocyte counts as per Yolov8. The solid line is a 1:1 line and represents a perfect count.

**Table 1.** Machine learning algorithms and information on the average precision, speed of training using the training set, and detection times without data augmentation.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Architecture | Precision | Recall | Map50 | Map50-95 | Time to train | Detection time |
| YOLOv5 | 0.964 | 0.958 | 0.981 | 0.773 | 1.9 Hours |  |
| YOLOv8 | 0.954 | 0.963 | 0.985 | 0.785 | 1.14 Hours |  |
| Faster R-CNN | X | X | 0.976 | 0.764 | 2.024 Hours |  |
| SSD | X | X | 0.978 | 0.761 | 0.25 Hours |  |

**Table 2.** Machine learning algorithms and information on the average precision, speed of training using the training set, and detection times with data augmentation. The training size increased to 1,371 after the addition of augmented photos.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Architecture | Precision | Recall | Map50 | Map50-95 | Time to train | Detection time |
| YOLOv5 | 0.968 | 0.95 | 0.982 | 0.768 | 5.75 hours |  |
| YOLOv8 | 0.96 | 0.953 | 0.986 | 0.77 | 1.70 Hours |  |
| Faster R-CNN | X | X | 0.981 |  | Hours |  |
|  |  |  |  |  |  |  |

Chart, box and whisker chart

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Fig 3. Average number of hemocytes in uncropped photos (1 is 26 °C, 2 is 31 °C).

Chart, box and whisker chart

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Figure 4. The average number of hemocytes when focusing on one square of the hemocytometer. (1 is 26 °C, 2 is 31 °C)

Chart, box and whisker chart

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Figure 5. Hemocyte counts at each temperature across treatments.

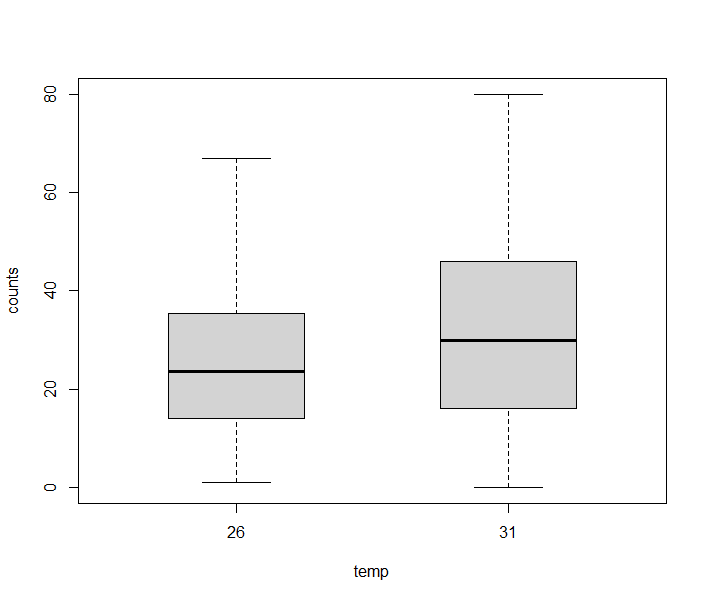


Figure 6. Hemocyte counts for the uninfected control treatments at 26°C and 31°C.

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Figure 7. Hemocyte counts for the infected control and coevolved populations at 26°C and 31°C.

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**Author Contributions:**

Nathaniel Haulk and Bret Elderd designed the ideas and experiments. Nathaniel Haulk collected data and ran analysis. Nathaniel Haulk and Bret Elderd wrote the manuscript.

**Conflict of Interest Statement:**

The authors have no conflicts of interest.

**Data Availability Statement:**

Photos and all code used are made available at <https://github.com/natom24/Machine-Learning>

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