

Real time microscopic level virus detection using YOLO

Abstract:

In several areas, including medicine, epidemiology, and research, it is crucial to identify viruses accurately. Numerous diseases can be brought on by viruses, and early discovery is essential for efficient treatment and outbreak management. Under a microscope, conventional methods for viral detection are time-consuming and subject to human error. This is where machine learning (ML) and artificial intelligence (AI) come into play, especially when applying variations of the YOLO (You Only Look Once) algorithms.

Real-time object identification is possible using YOLO algorithms like YOLOv5 and YOLOv8. These models can be modified to quickly and effectively detect viruses in microscopic images while processing massive amounts of data. We can discriminate between several viruses thanks to YOLO's multi-class classification feature, which broadens the scope of our investigation.

The ability of AI-powered virus identification to accommodate differences in virus shape, staining methods, and image quality is a key advantage. The model becomes robust and flexible to numerous scenarios by being trained on a variety of datasets, ensuring reliable results under various circumstances.

The creation of a virus detection system using YOLO-based algorithms for precise and effective virus identification under a microscope is presented in this study. Real-time virus detection, multi-class classification, adaptation to changes in virus morphology and image quality, generalisation to unknown data and virus strains, and scalability to handle expanding datasets are some of the system's goals. Our method accomplishes these goals and offers a reliable and adaptable virus detection tool with applications in epidemiology, research, and healthcare.

Introduction:

Viruses, mysterious organisms that exist on the cusp of life and death, have had a significant influence on society, health, and human history. These little genetic packages, made of either DNA or RNA, are renowned for their extraordinary capacity to invade host cells, take over cellular functions, and proliferate—often with disastrous results. The human immunodeficiency virus (HIV), which causes AIDS, and the influenza virus, which has released pandemics that have altered global demographics, have demonstrated their potency to the globe. Last year we experienced a deadly outbreak of Covid-19 virus which resulted in an emergency. These instances highlight how dangerous viruses may be and how they can cause extensive havoc.

Advancements in a variety of scientific disciplines have been sparked by efforts to comprehend and combat viral dangers. Researchers have created thorough approaches to categorise viruses in the field of virology based on their genetic makeup, structural characteristics, and ways of infection. Although extremely useful, these current methods frequently necessitate a lot of physical labour and subject-matter knowledge. There is an urgent need for automatic and precise classification methods as the variety of viruses continues to grow as new strains and variants are discovered.

This study sets out on a quest to employ cutting-edge technologies to categorise various viruses. We focus on the You Only Look Once (YOLO) object recognition technique, which is well known for its speed and precision in real-time image analysis. We want to develop a reliable classification model that can recognise various virus types from microscopic images by utilising the strength of YOLO. This paper will give a comparative analysis of YOLO and various other image classification and object detection methods. This cutting-edge method has enormous potential for not only speeding up the classification procedure but also improving the accuracy of virus identification, aiding in the early detection and efficient management of viral epidemics.

As we go through this virology and machine learning fusion, we picture a time when classification of viruses will go beyond what is currently possible. Our efforts are in line with the necessity to anticipate viral evolution, giving us the means to counter new dangers and protect the public's health. Through this project, we connect the macroscopic world of technology with the microscopic world of viruses, creating a synergy that could transform our understanding of and ability to counteract these powerful agents of change. Our key objectives are as follows:

- 1) Develop a virus detection system that can accurately detect and identify viruses under a microscope.
- 2) Implementing YOLO for real-time virus detection, enabling swift and efficient analysis of large volumes of image.
- 3) To train the YOLO model for multi-class classification and to distinguish between two viruses thus enabling comprehensive analysis.
- 4) Ensure that the model is able to handle variations in virus morphology, staining techniques, and image quality, leading to robust performance across different scenarios.
- 5) To design a model such that it can generalise well on unseen data and virus strains, thus ensuring its usability in various research and diagnostic applications.
- 6) Construct a system that can handle growing datasets as there will be more viruses and more images of a particular virus in near future.

Related Work:

A deep learning model called YOLO, or You Only Look Once, is used to identify objects in photos and videos in real-time. It's useful because it's so quick and precise. YOLO is appropriate for applications like autonomous driving, surveillance, and object tracking where real-time processing is crucial since it can detect many objects in a single trip across the network.

X. Yu, et.al in their paper [1] developed a system for the Self-Driving Sweeping Bot (SDSB); effective data collecting is essential. For training and validation, three target categories—speed bumps, manhole covers, and leaves—were used. Evaluations of the Yolo v5 versions (v5s, v5m, v5l, and v5x) revealed that v5s performed best for real-time object detection. Across epochs, metrics like loss, accuracy, recall, and mAP were examined.

W. Yang, D. BO and L. S. Tong, in their paper [2] introduced TS-YOLO, an improved version of YOLOv4 that uses three Spatial Pyramid Pooling (SPP) modules to address problems with multi-scale object detection. In complicated scenarios, these modules can capture greater semantic information. By adjusting core pooling sizes and adding two SPP modules, TS-YOLO outperforms YOLOv4 on the Pascal VOC dataset with 2.21% greater accuracy, showcasing its superior multi-scale object detection skills.

D. Padilla Carrasco, et.al in their paper [3] used YOLO for use in smart city applications like parking occupancy monitoring, this study offers a modified YOLO-v5-based deep object detection model. The model effectively detects large, small, and minute objects thanks to a multi-scale system. In comparison to YOLO-v5, it decreases trainable parameters while maintaining high precision. It also improves detection speed, especially for little cars, which witnessed a 33% performance boost.

H. Wang and J. Han, in their paper [4] used YOLO in order to overcome the problems of small target loss and sluggish detection, this study introduces YOLO-G2S, a target recognition method for military applications. The YOLO v5 model is perfect for military target recognition deployment since it achieves a 95% average accuracy while decreasing parameters by 7.3% and computation by 17.8% by replacing particular modules and changing the activation mechanism.

Ma, P., Li, C., Rahaman, M.M. et.al in their paper [5] used deep learning for large orders and unusual bacteria, traditional manual microbe detection techniques are slow and unreliable. Deep learning and visual transformers in computer image analysis provide very accurate and effective detection. This study summarises 142 works from 1985 to the present and covers the development of microbe detection technologies, assesses current and

possible approaches, and addresses future difficulties. It helps scholars comprehend the history, current state, and potential directions of the field.

Chi Zhang, et.al in their research [6] stated infectious and parasitic diseases pose significant public health threats, contributing to high morbidity and mortality rates. The intricate life cycles of parasites create challenges for their microscopic diagnosis. Deep learning has exhibited remarkable effectiveness in biomedical image analysis, particularly in diagnosing protozoan parasites. This review highlights recent progress in utilising deep learning for examining protozoan parasites through publicly accessible microscopic image datasets. Furthermore, we address the emerging challenges and future directions in the application of deep learning to protozoan parasite diagnosis.

Sun, L.; Xu, Y.; Rao in their paper [7] used YOLO. This study improves antibiotic susceptibility testing by using a microfluidic device and the YOLOv5 algorithm to precisely identify multi-layer bacteria at different focal depths. High identification rates for both bacteria and microspheres enable the tracking and localization of microorganisms throughout time. By providing improved accuracy and the ability to record microorganisms at various focal depths for 3D reconstruction within 3–10 hours, the technology surpasses enhanced depth of field (EDF) techniques. By using microfluidic channels, this method enables quick, high-throughput, and long-term analyses of bacterial alterations caused by antibiotic exposure.

Hafeez, Umair, et al. in their study [8] stated early in 2020, COVID-19's effects on the world caused existential anxiety. Radiography is essential for diagnosis, however there are difficulties because infections can vary. With accuracy rates of 97%, 89%, and 84% for two, three, and four-class classifications, respectively, this study shows how CODISC-CNN, a chest X-ray-based COVID-19 prediction system, outperforms existing models. Similarly Shankar, VirenViraj, et al. in their paper [9] used CNN for heart disease prediction.

Similarly Suo, Qiuling, et al in their paper [10] stated in healthcare, predicting disease risk is essential. Utilising patient-specific data, personalised predictive modelling had advantages over general models. In order to learn patient representations, assess similarity, and improve disease predictions, that study introduces a time fusion CNN framework. The efficiency of various vector formats and similarity criteria were evaluated. Moreover G. Priyadarshini and D. R. Judie Dolly in their paper [12] used CNN and described how to recognise and categorise tomato leaf diseases using a variety of techniques, such as Convolutional Neural Network (CNN) and Faster R-CNN. Early disease detection is crucial in agriculture. The study's use of deep learning and image processing techniques resulted in an amazing 98% accuracy.

V. N. Gridin, I. A. Novikov et.al in their paper [15] used YOLOv5. The prompt identification of pathogenic microorganisms and microbial communities in the patient's tissues in order to quickly prescribe and correctly employ medications from mutually exclusive approaches is a pertinent and highly demanded problem in many fields of modern medicine. The use of lanthanide staining in combination with scanning electron microscopy to retrieve a series of high-resolution images with subsequent automatic labelling and classification of microbiological objects allows for a step change in the speed of visualisation of the contents of the samples taken and the accuracy of diagnostics. This research describes the findings of detecting 15 different most prevalent opportunistic groups of bacteria in 380 photos using the YOLOv5 neural network model. Consequently, using the YOLOv5 base model without freezing layers, a 71.5% average accuracy and a 69.8% recall were attained.

P. Juyal and A. Kundaliya, in their paper [14] stated that the effective automatic labelling is necessary due to the increase of image data. In order to solve the problems associated with multi-label picture categorization, this study uses a dual-channel convolutional neural network (DC-CNN). It outperformed traditional approaches by using two CNN channels for low-frequency and total data training, achieving an average maximum accuracy of over 95% on the Pascal VOC 2012.

S. Kido, Y. Hirano and N. Hashimoto,in their paper [11] used CNN. Convolutional neural networks (CNNs) are used by image-based computer-aided diagnosis (CADx) and detection (CADe) algorithms to diagnose lung abnormalities such as nodules and diffuse lung illnesses. CNN-based image-based CADx is more effective than feature-based CADx, which uses an image-feature extractor. With regard to a variety of lung abnormality kinds, such as nodules and diffuse lung illnesses, we evaluated the efficacy of image-based CADx with CNN and image-based CADe with R-CNN.

M. -Y. Lee, J. -H. Lee et.al in their paper [13] used CNN. In this study, we demonstrate the effect of CNN compression on increasing sparsity on six typical CNN networks, including the well-known localization CNN network VGG16-SSD-300. We will also demonstrate the results of an activation analysis using a CNN HW accelerator model and compressed CNN networks. The CNN HW accelerator model's processing time estimation results, which take into account the faster transmission of sparse weights, will serve as the conclusion to this study.

Dhiraj Dahiwade et.al in their paper [16] used KNN and CNN. In this study, by examining large symptom datasets, data mining techniques like K-Nearest Neighbour (KNN) and Convolutional Neural Network (CNN) algorithms are utilised to increase the accuracy of disease prediction. The CNN-based technique outperforms KNN while using less time and memory, achieving an astonishing 84.5% accuracy.

Dutta, Aniruddha, et al. [17] concludes that in order to identify clinical data that is unbalanced, this work offers a two-layer CNN that uses NHANES data to forecast the occurrence of coronary heart disease (CHD). Our CNN exhibits balanced performance across classes, in contrast to previous models that are susceptible to class imbalance. We use a two-step process that includes feature selection using a majority vote and LASSO feature weight evaluation, followed by homogenization using a fully linked layer. We use a unique training procedure that boosts classification accuracy via simulated annealing-like operations. Despite the class imbalance in NHANES, our CNN correctly identifies 77% of CHD cases and 81.8% of CHD absence cases on a testing dataset, proving generalizability to other healthcare research. Our approach outperforms SVM and random forest at predicting negative (Non-CHD) cases, opening the door to better diagnoses and lower healthcare costs. The model is symmetric.

Rustum, Furqan, et al. in their paper [18] used CNN features in an ensemble classifier to improve cardiovascular disease prediction is covered in this article. The study deals with the difficulties in detecting CVDs because of the wide range of symptoms and the sparse feature sets in electronic health records (EHRs). The suggested approach exhibits excellent performance with an accuracy of 0.93 and high precision, recall, and F1 score, demonstrating its usefulness and generalizability across various datasets by utilising an ensemble model and CNN-based feature extraction.

Jain, Arushi, et al. in their paper [19] found that identification of cardiac illness is essential, but conventional techniques that rely on medical history have drawbacks. We suggest the Levy Flight - Convolutional Neural Network (LV-CNN) for image-based cardiac disease evaluation in order to overcome this. The Sunflower Optimization Algorithm (SFO) is used in the LV method to decrease loss functions in CNN and avoid local minima problems. The experimental results in MATLAB demonstrate the superiority of the suggested model with accuracy of 95.74%, specificity of 0.96%, error rate of 0.35, and time consumption of 9.71 s.

Proposed Work:

Convolutional Neural Network (CNN)

Deep learning models known as convolutional neural networks (CNNs) are designed for grid-like data such as photos and videos. By automating feature extraction, CNNs have revolutionised computer vision and made

manual feature engineering unnecessary. They can learn increasingly abstract elements thanks to their hierarchical structure, which mimics how humans interpret visual information.

Thanks to convolutional filters, CNNs are excellent at translation-invariant recognition, recognising patterns independent of their location. They are adaptable and capable of managing enormous datasets and high-dimensional data. CNNs regularly perform at the cutting edge in applications including object detection, segmentation, and picture classification.

CNNs do have certain limits, though. For training, they need a sizable amount of labelled data, which may be hard to come by in specialised applications. They are computationally demanding, relying on GPUs or TPUs, and overfitting might be a problem that calls for regularisation. CNNs are frequently thought of as "black-box" models, making interpretation difficult.

Recent developments include enhanced object identification (Faster R-CNN, YOLO, SSD), deeper architectures like ResNet and EfficientNet, efficient transfer learning using trained models, and improvements to semantic segmentation (U-Net, Mask R-CNN). While addressing their shortcomings, researchers are actively working on interpretability and model efficiency to ensure CNNs stay at the forefront of computer vision applications.

YOLOv8

Modern object identification technology, known as YOLOv8, was created by Alexey Bochkovskiy and his team at Ultralytics. It is the most recent model of the object detectors from the YOLO (You Only Look Once) series, which are renowned for their quickness and precision.

In order for YOLOv8 to function, an image must be divided into a grid of cells, with each cell's bounding box and class probability predicted. The final detection results are then provided by the network after combining these predictions. YOLOv8 can recognize a wide range of items, including viruses, because it was trained on a huge dataset of photos and labels.

YoloV8 can be used in a number of ways to find viruses. For instance, it can be used to find viruses in images from histopathology or electron microscopy. Additionally, it can be used to find viruses in environmental samples like food or water samples. YoloV8 is highly quick, which is one of its benefits for virus identification. This is crucial for applications requiring real-time detection, like environmental monitoring and medical diagnostics. The high accuracy of YoloV8 is another benefit. This is crucial in applications like medical diagnostics and food safety where false positives and false negatives can have detrimental effects.

There are a number of critical phases involved in training a YOLO or CNN model for virus identification. First and foremost, data collecting is crucial. You must compile a broad and thorough dataset of photos that include the viruses you want to find. The positions and classes of the viruses inside the photos are defined by the accurate annotations, which are crucial.

Data preparation is essential when you get your dataset. This entails employing data augmentation methods like rotation and flipping as well as standardising image sizes and pixel values. These stages guarantee that your model is reliable and flexible enough to accommodate changes in input data.

Data pretreatment is followed by model selection. Depending on the difficulty of your assignment and the amount of computational power at your disposal, pick a suitable YOLO or CNN architecture.

Transfer learning is a crucial stage when pre-trained weights are used to initialise your model. This enables your model to utilise data from a huge dataset like ImageNet. To make the model more useful for your purpose, fine-tune it using the virus detection dataset that you have.

Divide your dataset into training and validation sets during the training and validation process. Metrics like accuracy and loss should be used to track the training progress. By enabling you to fine-tune model parameters and modify hyperparameters like learning rate and batch size, validation data helps minimise overfitting.

The performance of your model can be improved through iterative hyperparameter adjustment. Investigate various hyperparameter settings and architectural alterations to find the optimal balance between accuracy, recall, and computing efficiency.

It's critical to test your trained model. To make sure it applies well to new data, assess its performance on a different test dataset. You can evaluate the accuracy of the detection using metrics like precision, recall, and F1-score.

Implement post-processing strategies after testing to fine-tune and filter detection data, lowering false positives and boosting overall accuracy.

The last step is to deploy your trained model in the environment you want, whether it be a local application, a cloud-based service, or a broader system integrated for real-time virus detection. These actions taken together guarantee the successful creation and application of YOLO and CNN-based virus detection models.

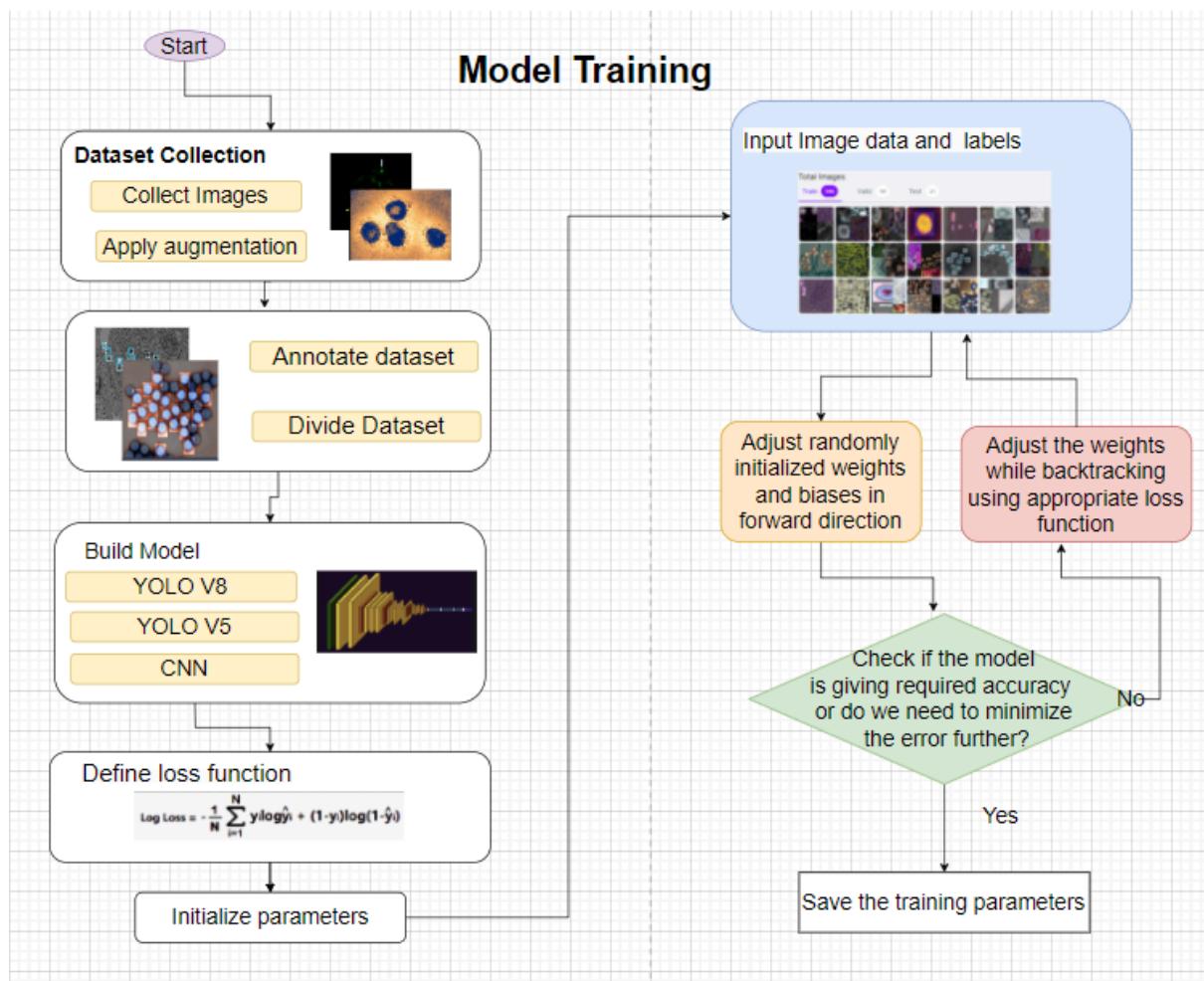


Fig 4.1 Architectural diagram

Dataset:

Our dataset for virus detection under a microscope includes a wide range of microscopic images that were gathered from several web sources and databases. The wide range of viral kinds, stains, and imaging settings are carefully represented in this collection of photos, ensuring the dataset's richness and application. In order to simulate real-world situations, we carefully chose photos that depict various staining methods frequently employed in virology research and diagnostics. This diversity increases the robustness of our model by enabling it to pick up on and adjust to changes in staining intensity, background noise, and image quality.

As we wished to train our model on a larger database, we used the technique of data augmentation. Enhancing the robustness and generalizability of our viral detection approach requires data augmentation. With a wide variety of microscopic pictures from different sources, the dataset can be improved by using methods like rotation, flipping, and colour modifications to address any biases and restrictions. We enable the model to better adapt to various staining methods, lighting conditions, and perspectives by artificially increasing the dataset's size and adding variability. This method of augmentation not only increases the reliability of virus identification in a variety of settings, but also equips the model to handle real-world complications.

We chose annotation for our YOLO implementation and painstakingly drew bounding boxes around the viruses in the photographs. By creating ground truth data through the annotation process, the model is trained to precisely identify viral sites. We enable the YOLO algorithm to understand spatial relationships and improve viral detection in actual microscopic pictures by precisely labelling virus cases. This method serves as the cornerstone of our comprehensive and powerful virus detection system, delivering accurate and dependable outcomes for a range of staining procedures and virus types. The following depicts the annotated images:

The use of numerous transformations, such as brightness modification, rotation, flipping, and mosaicing, is essential to the success of data augmentation, a vital approach in machine learning and computer vision. Because it tackles two major problems with training robust models—limited data and model generalisation—augmentation is crucial.

First off, real-world datasets are frequently small, which can cause overfitting when complicated models are trained on them. By enhancing the dataset artificially, augmentation aids in mitigating this. Examples of how we might generate new instances of the same data include applying brightness tweaks or flipping photographs horizontally. By doing this, we essentially enrich the training set and provide the model a wider variety of examples to draw from.

Second, augmentation improves the generalisability of the model. We enhance the model's capability to handle real-world situations where the input may not exactly match the training data by exposing it to changes in data, such as different orientations (rotation), lighting conditions (brightness), or perspectives (mosaicing).

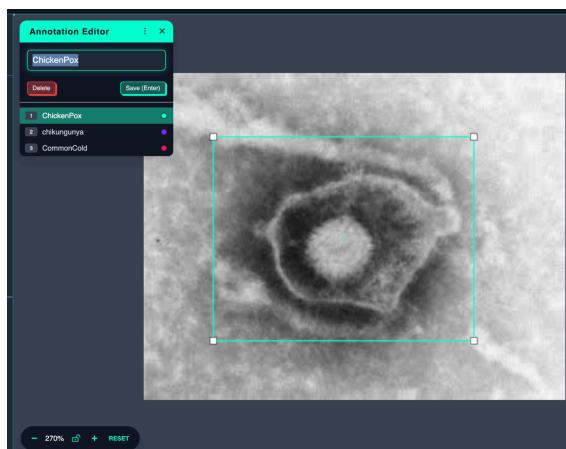


Fig 5.1 Single Class

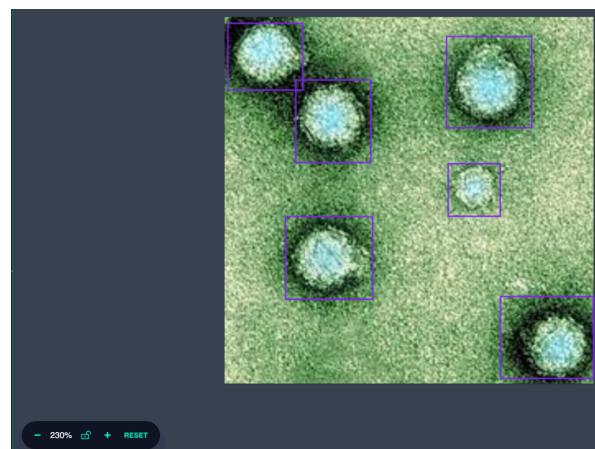


Fig 5.2 Multiple Classes

Fig 5.1 shows a single cell with a painstakingly created bounding box enclosing the whole thing. The boundaries of each individual cell are clearly defined by this precise delineation, which facilitates investigation and identification. Fig 5.2, on the other hand, depicts a more complicated scenario with several cells within a single frame. Each cell has a specific bounding box to identify it. The simultaneous evaluation of many cells using these bounding boxes as visual aids enables researchers, technicians, or AI algorithms to quickly analyse and distinguish between them. The efficiency of tasks like cell counting, classification, or tracking within a larger context is improved by this multi-cell perspective.

Result and Analysis:

MAP (Mean Average Precision)

A popular statistic in information retrieval and information retrieval systems, notably in the fields of computer science and machine learning, is MAP (Mean Average Precision). It is generally used to assess how well ranked list retrieval algorithms, such as those used by search engines, recommendation engines, and object detection models, perform.

By analysing how closely these ranked lists correspond to the real pertinent things, MAP evaluates the relevancy of the lists. The MAP formula is as follows: $(1 / N) * \sum_{i=1}^N (\text{Precision at Rank } i * \text{Relevant at Rank } i)$.

This formula reads:

The number of items that were found in the ranked list overall is N .

The percentage of pertinent items among the first i items in the list is known as precision at rank i .

The binary value "Relevant at Rank i " indicates whether or not the item at that rank is relevant.

Recall

Recall is a metric used to assess the effectiveness of classification and information retrieval systems, notably in machine learning and information retrieval applications. Recall is also known as Sensitivity or True Positive Rate. It gauges a system's capacity to accurately pick out each pertinent item from a dataset.

Recall works like this: $\text{True Positives} / (\text{False Negatives} + \text{True Positives})$.

This formula reads:

True Positives (TP) are instances that the system accurately classifies as positive (relevant).

False Negatives (FN) are situations that the system mistakenly categorised as negative even though they were positive (relevant).

Precision

In especially in machine learning and information retrieval applications, precision is a statistic used to assess the effectiveness of categorization and information retrieval systems. It assesses a system's capacity to appropriately select pertinent items while excluding unimportant ones.

The Precision equation is: $\text{True Positives} / (\text{True Positives} + \text{False Positives})$

This formula reads:

True Positives (TP) are instances that the system accurately classifies as positive (relevant).

False Positives (FP) are situations that the system mistakenly categorised as positive even when they are truly negative (irrelevant).

Convolutional Neural Network (CNN)

However, CNNs have some limitations when attempting to categorise multiple objects in a single image. They may focus on dominating characteristics and ignore smaller or partially hidden things because of their difficulty with overlapping or occluded objects. Additionally, because CNNs don't explicitly comprehend how objects interact, they can have trouble categorising items with complex spatial relationships.

The CNN model was trained for 100 epochs with images of various viruses for classification. The results showed overfitting curves as shown in the figure. The validation accuracy of the model plateaued at 40% while the

training accuracy reached 100% mark. The loss for validation also increases significantly after the 20th epoch deeming this method of identifying viruses not very useful.

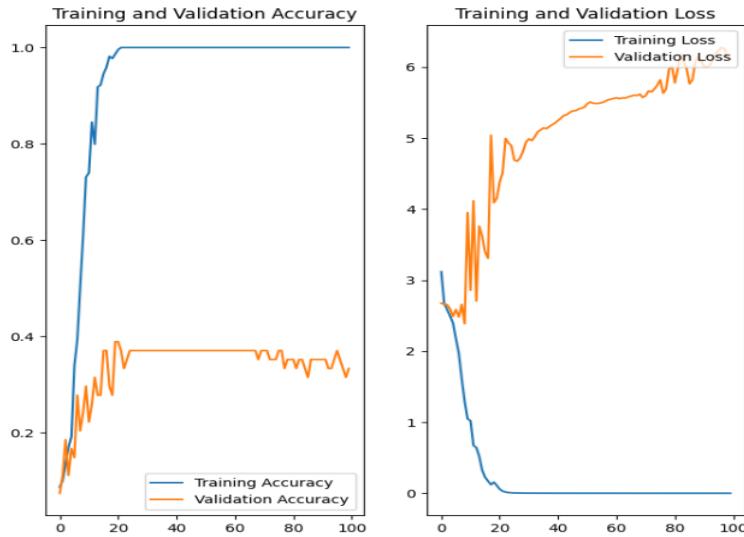


Fig 6.1 Training and Validation curves

You Only Look Once version 8 (YOLOv8)

The YOLOv8 results showed a high degree of satisfaction and outperformed traditional Convolutional Neural Networks (CNNs) in a number of crucial areas. You Only Look Once version 8, also known as YOLOv8, demonstrated enhanced object identification and recognition skills, enabling quicker and more precise real-time processing of still photographs and moving pictures. YOLOv8 consistently outperformed conventional CNNs in comparison because of its cutting-edge design and effective object detection algorithms. YOLOv8 represents an intriguing development in computer vision and deep learning research because it greatly lowered processing time while simultaneously improving item recognition accuracy.

Model	mAP	Precision	Recall
YoloV8	75.4%	72.4%	74.6%

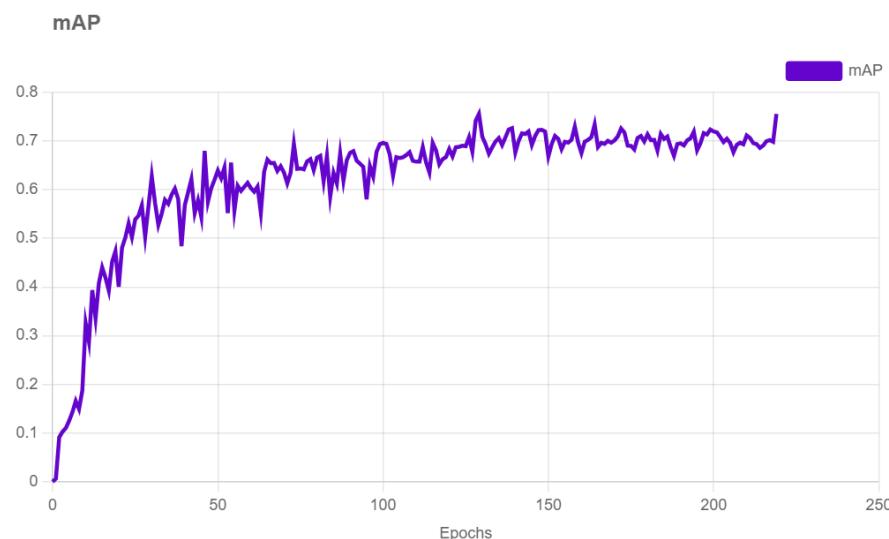


Fig 6.2 mAP vs Epochs

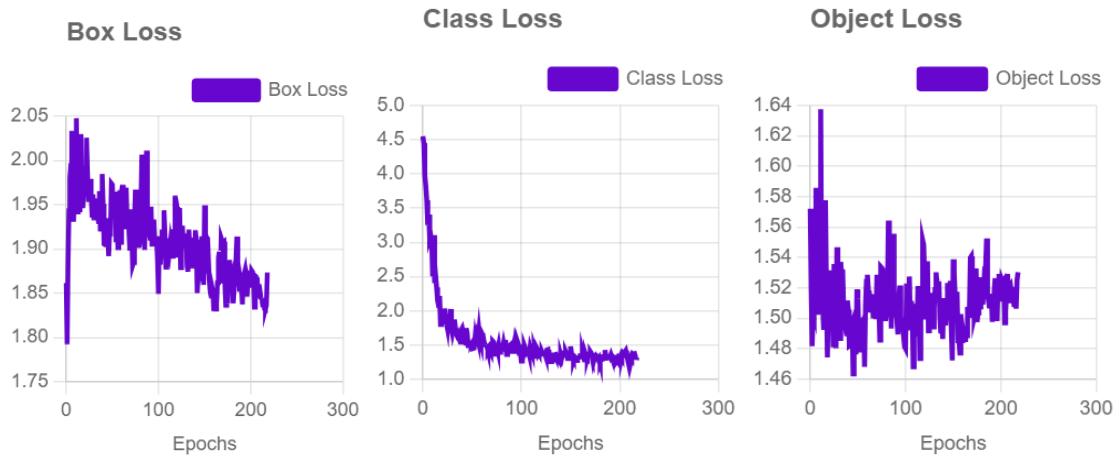


Fig 6.3 Box Loss, Class Loss, Object Loss vs Epochs

As the confidence threshold for classification changes, the F1 confidence curve shows how the F1 score—a gauge of a model's precision and recall trade-off—changes. The links and correlations between various labels or classes in a dataset are visually represented in a labels correlogram, which aids in understanding how labels are related and co-occur in the data.

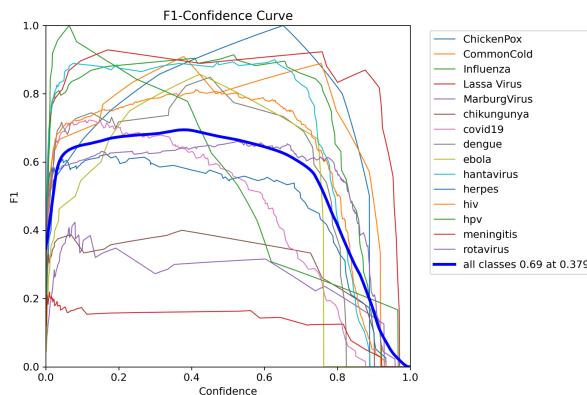


Fig 6.4 F1-Confidence Curve

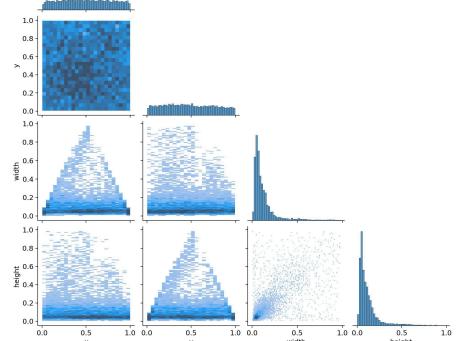


Fig 6.5 labels-correlogram

An illustration of how a model's precision varies at various confidence thresholds is a precision-confidence curve. It aids in determining how precision and confidence are traded off in categorization or prediction tasks. The trade-off between precision and recall (sensitivity) for various classification thresholds is visually represented by a Precision-Recall curve. It offers perceptions on how effectively a model balances memory and precision as the classification threshold shifts.

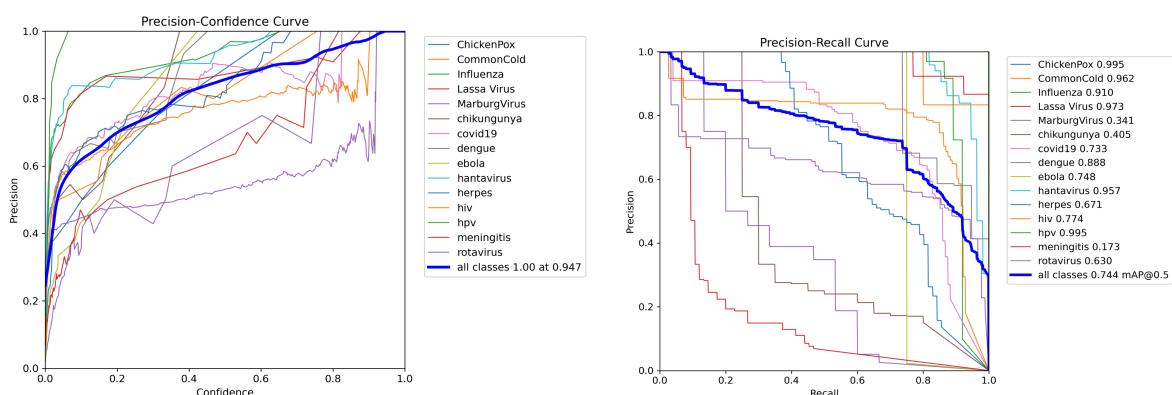


Fig 6.6 Precision Confidence Curve

A recall-confidence curve demonstrates how a model's recall (sensitivity) evolves when the categorization confidence threshold changes. It aids in assessing how recollection and confidence in categorization tasks relate to one another.

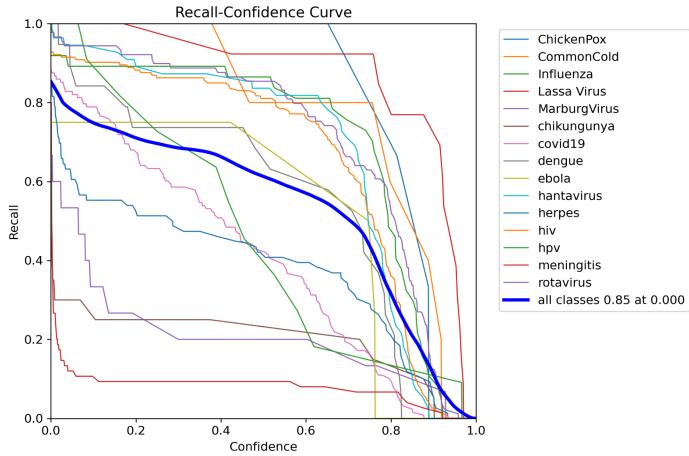


Fig 6.8 Recall Confidence Curve

In Figure 6.8, all more YOLO-v8-related curves on loss and metrics are shown.

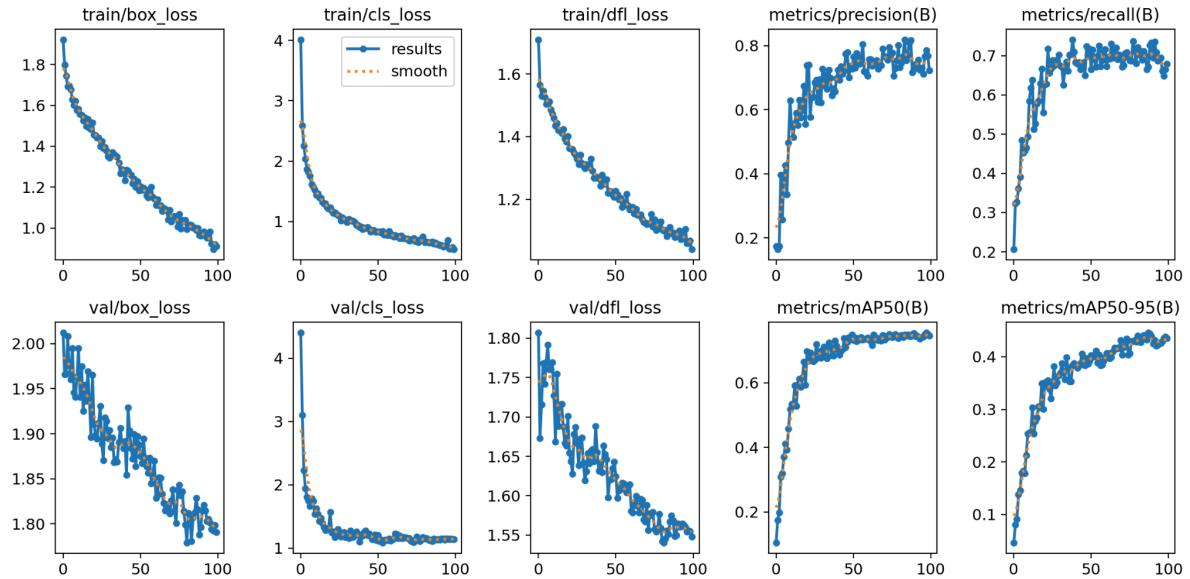


Fig 6.9 loss and metrics curves

The processes of building and training bounding boxes in batches, followed by our model's validation and prediction phases, are shown in the photos below.

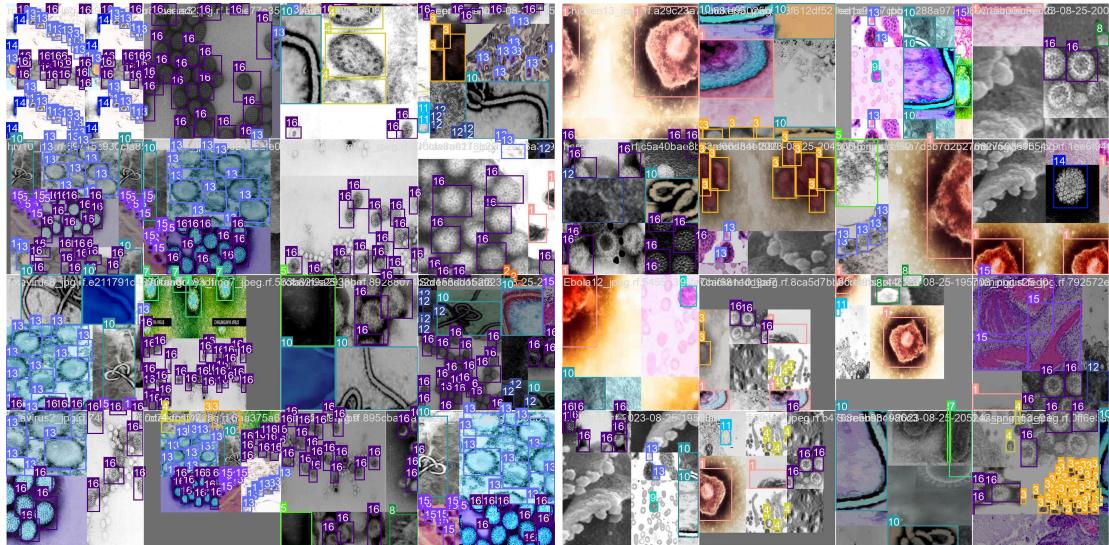


Fig 6.10 Training batch-0

Fig 6.11 Training batch-1

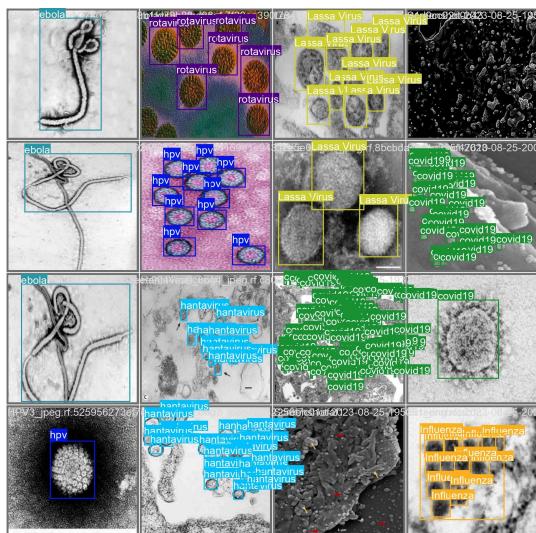


Fig 6.12 Validation batch-1 labels

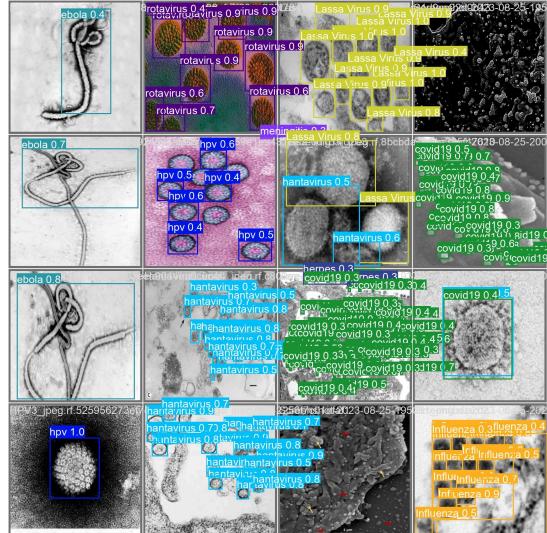


Fig 6.13 Validation batch-1 prediction

You Only Look Once version 5 (YOLOv5)

For our object detection task, we used YOLOv5, but regrettably we did not get the required outcomes. Despite our best efforts, the model's performance fell short of what we had hoped for, which prompted us to look into alternate strategies and tweak our implementation to increase precision and dependability.

When evaluating the balance between precision and recall in object recognition, the F1-confidence curve in the YOLOv5 results is essential. It sheds light on how well the model performs when given different confidence criteria for its predictions. In order to optimise the model's performance and strike the ideal balance between false positives and false negatives in object detection tasks, one can use this curve to identify the ideal threshold that maximises both precision and recall.

For better understanding the model's performance across several item categories or labels, a labels correlogram in YOLOv5 findings is helpful. It enables you to see how accurately the model recognises particular items within an image dataset. This correlogram can help you identify the classes that the model struggles with and those that it performs well in, allowing you to make targeted tweaks or adjustments to improve object detection and categorization in your application.

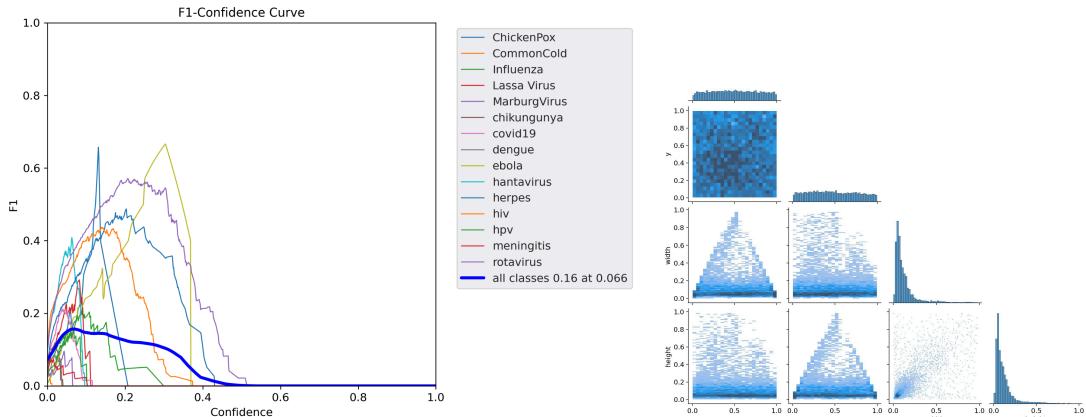


Fig 6.14 F1-Confidence Curve (YOLOv5)

Fig 6.15 Labels-Correlogram (YOLOv5)

The YOLOv5 results' precision-confidence curve is a crucial tool for evaluating the model's dependability at various confidence thresholds. It gives a visual picture of how changing the confidence threshold affects the accuracy of object detections. Users can utilise this curve to make well-informed choices regarding how precision and recall are traded off. By examining this curve, you may choose a suitable confidence threshold that fits the needs of your particular application, ensuring that you strike a balance between detection accuracy and the necessary level of confidence for your use case.

The Precision-Recall Curve in the YOLOv5 findings is crucial for assessing the model's performance, particularly when there is a class imbalance or when you want to give precision or recall priority based on the requirements of your application. This curve shows graphically how precision and recall trade off as the confidence level is changed. It aids in choosing the ideal threshold that strikes the ideal balance between precision and recall, ensuring that your object identification system satisfies particular performance goals and specifications.

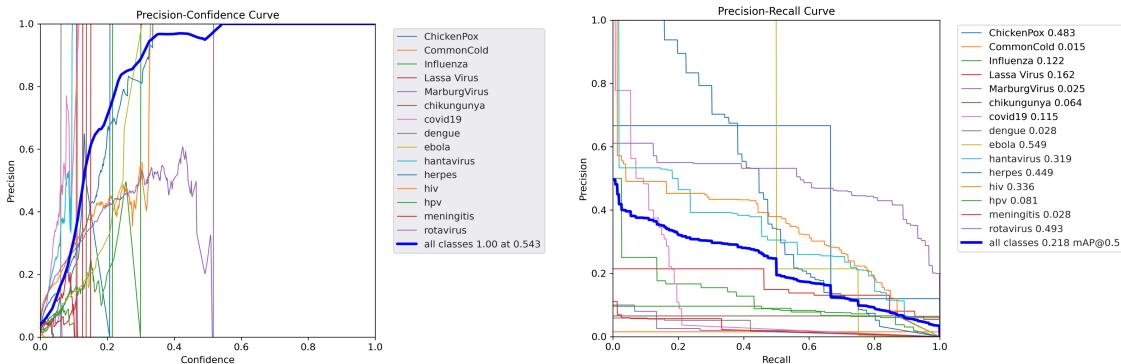


Fig 6.15 Precision-Confidence Curve (YOLOv5)

Fig 6.16 Precision-Recall Curve (YOLOv5)

The YOLOv5 findings' Recall-Confidence Curve is a useful tool for evaluating how recall varies with various confidence criteria. The model's capacity to find instances of items at various confidence levels is shown by this graph. Selecting a threshold that provides the necessary amount of recall while minimising false positives is made easier by analysing this curve.

For assessing how effectively the model handles many instances of the same object category within an image, the Labels vs. Instance Curve is crucial. It sheds light on the model's consistency in identifying and differentiating between instances of the same class. The model's accuracy in detecting and categorising several objects of the same category can be improved by looking at this curve.

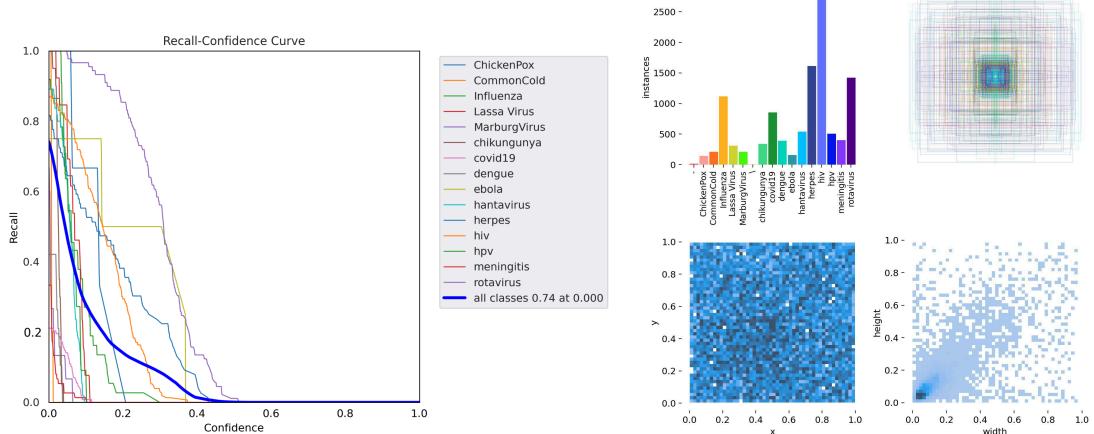


Fig 6.17 Recall- Confidence Curve (YOLOv5)

Fig 6.18 Labels vs Instances (YOLOv5)

The processes of building and training bounding boxes in batches, followed by our model's validation and prediction phases, are shown in the figures below.

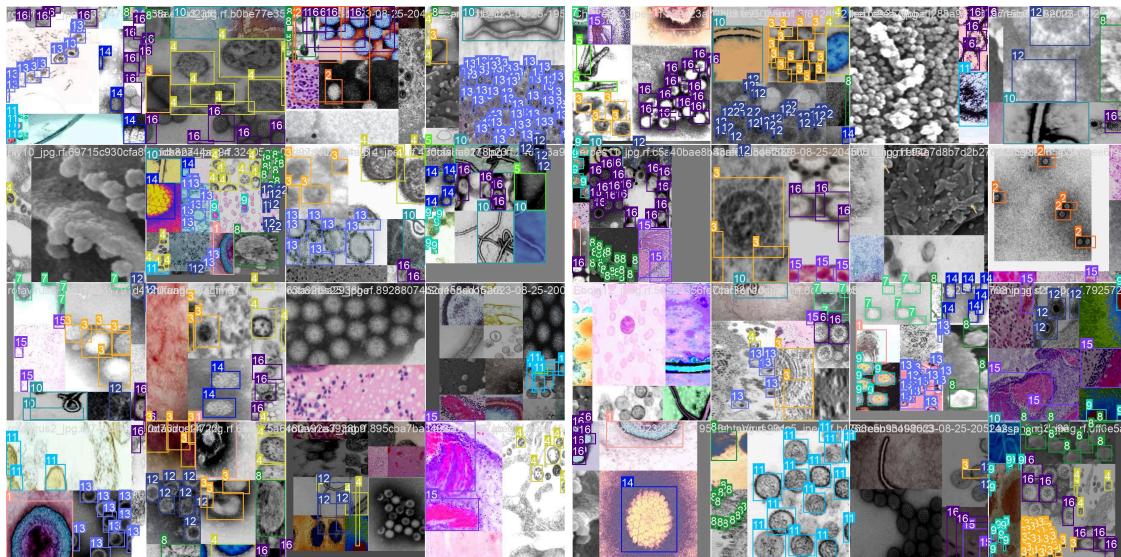


Fig 6.19 Training batch-0

Fig 6.20 Training batch-1

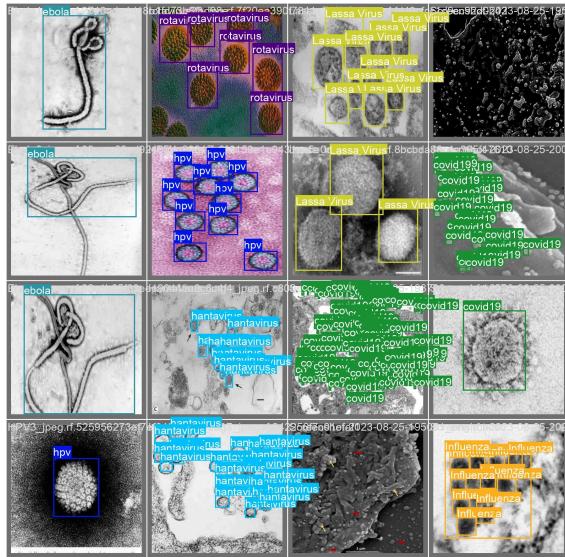


Fig 6.21 Validation batch-1 (YOLOv5)

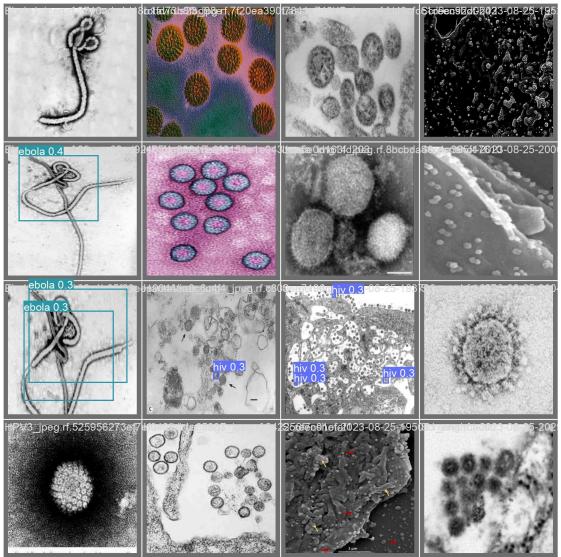


Fig 6.22 Validation batch predictions (YOLOv5)

In Figure 6.23, all more YOLO-v5-related curves on loss and metrics are shown.

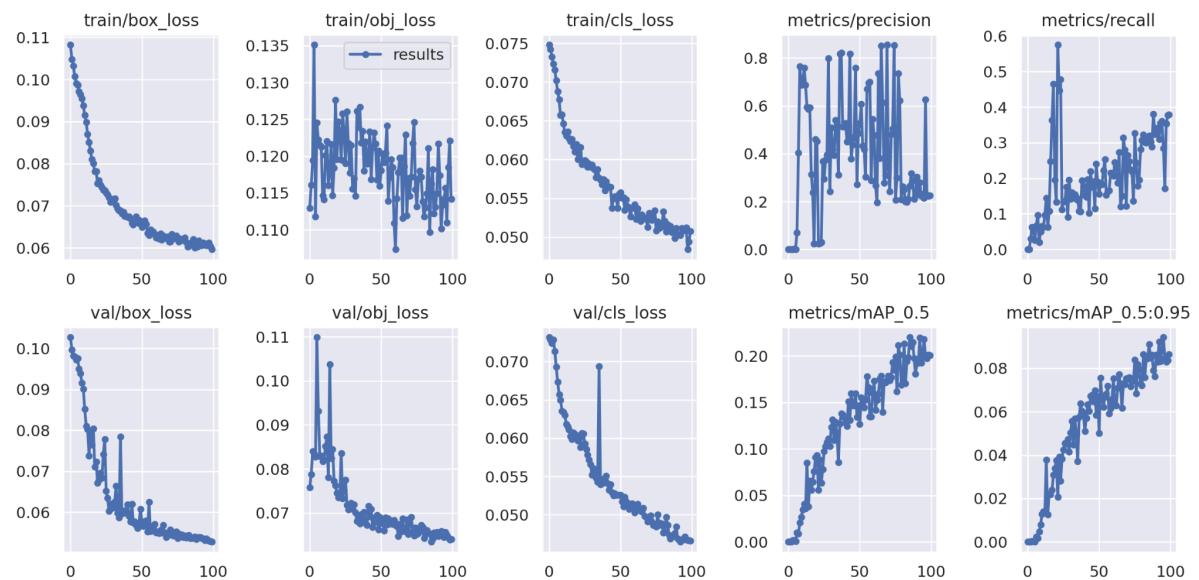


Fig 6.23 loss and metrics curves

Conclusion:

In conclusion, the combination of virology and machine learning has enormous potential for improving our understanding of and resistance to viruses. The project's goals demonstrate a futuristic method of classifying and identifying viruses. We want to revolutionise the discipline of virology by developing a virus detection device capable of precisely recognising viruses under a microscope and applying YOLO for real-time analysis. The combination of technology and virology not only makes it possible to analyse viruses quickly and effectively but also addresses the urgent need to predict viral evolution, improving public health protection.

In order to conduct thorough viral analysis, the project's multi-class classification training for the YOLO model is essential. Its adaptability to a variety of settings is further ensured by its toughness in handling differences in virus shape, staining methods, and image quality. Its applicability in diverse research and diagnostic applications

is improved by the focus on building a model that can generalise to previously unrecognised data and virus strains.

Last but not least, the development of a scalable system to handle expanding datasets demonstrates a forward-looking strategy, recognising the likelihood of running into more infections and amassing more photos in the near future. In conclusion, this combination of virology and machine learning not only promises to advance our understanding of virus classification, but also provides us with the means to proactively counter the threats posed by these potent agents of change as they arise, ultimately improving the protection of public health.

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