TPM Vol. 32, No. S3, 2025
ISSN: 1972-6325
https://www.tpmap.org/

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CRUSTASCOPE: PREDICTIVE VISUAL INTELLIGENCE FOR WSSV DETECTION IN SHRIMPS

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Abstract—Shrimp farming around the world is significantly threatened by the White Spot Syndrome Virus (WSSV), which causes enormous mortality and financial losses owing to inaccurate or delayed diagnosis. With the use of static photos, this study provides CrustaScope, an AI-powered predictive visual detection system appropriate for the early diagnosis of WSSV in prawns. To increase feature discrimination, a Squeeze-and-Excitation (SE) attention block is added to the MobileNetV2 backbone, which has been fine-tuned for the model. Transfer learning is utilised to train a binary classifier with swish-activated thick layers on a bigger dataset of photos of both healthy and unwell prawns. With a clear separation between specimens that tested positive for WSSV and those that were healthy, the model displayed good classification performance. CrustaScope, which is intended for offline usage on low-resource local PCs, gives prawn producers a valuable and non-invasive approach to assist fast diagnosis and treatment. It is particularly well-suited for small-scale and rural aquaculture operations thanks of its lightweight design, limited hardware needs, and user-friendliness.

Keywords: White Spot Syndrome Virus (WSSV), shrimp aquaculture, CrustaScope, MobileNetV2, Squeeze-and-Excitation (SE), and swish-activated dense layers.

INTRODUCTION

Shrimp aquaculture around the world is afflicted by the fatal and exceedingly contagious White Spot Syndrome Virus (WSSV). WSSV is a severe hazard to the economic viability of prawn farming, especially in areas where aquaculture is crucial to rural livelihoods and food security. It is distinguished by a fast onset and practically 100% fatality in affected populations. Although precise, standard detection procedures like Polymerase Chain Reaction (PCR) and microscopic examination require a lot of time, requiring expert staff, and are typically out of reach for small and medium-sized farmers working in low-resource situations.

The CrustaScope project was founded to develop an intelligent, portable, and easily accessible device for early WSSV detection in order to alleviate this important issue. The project intends to provide shrimp farmers and aquaculture personnel with a rapid, non-invasive technique to check shrimp health using static photographs by utilising breakthroughs in computer vision and deep learning. In order to control outbreaks and decrease losses, the idea is to introduce artificial intelligence into aquaculture disease management. This will enable real-time detection and rapid action.

Creating a deep learning-based image classification model that can successfully discriminate between prawns with WSSV and those that are healthy is CrustaScope's major aim. Using transfer learning with a MobileNetV2 backbone and a Squeeze-and-Excitation (SE) attention block to boost the model's capacity to concentrate on salient visual patterns, the project is focused on efficiency and accuracy optimisation [1,2]. To boost the model's performance and generalisability under varied image situations, it is additionally trained using a specifically enriched dataset. CrustaScope is developed for practical usage in outdoor settings by doing away with the requirement for pricey gear or continual internet connectivity. In order to improve sustainable prawn farming and economic resilience in damaged regions, the project strives to offer aquaculture practitioners an intelligent and scalable tool for early disease identification.

LITERATURE REVIEW

One of the most destructive viruses to prawn aquaculture globally in terms of economic damage is the White Spot Syndrome Virus (WSSV). For the identification of WSSV, traditional diagnostic procedures, including manual examination, histopathology, and Polymerase Chain Reaction (PCR) testing, have been frequently employed. However, these procedures require a lot of time, need for specialised gear, and largely rely on professional interpretation—all of which small-scale or distant aquaculture firms may not be able to pay for. New pathways for disease detection in aquaculture have been made available by recent breakthroughs in artificial intelligence (AI), notably in deep learning and computer vision. The implementation of convolutional neural networks (CNNs) for the visual diagnosis of aquatic illnesses has been the focus of various research. Although it had limitations in terms of feature depth and generalisability, a baseline CNN model that was trained on shrimp photos using sequential convolutional and pooling layers demonstrated impressive classification accuracy. Additionally, transfer learning models like as EfficientNetB0 have exhibited greater performance in complicated feature extraction from prawn pictures, displaying robust F1-scores in differentiating between samples that are healthy and those that are infected with WSSV.

A remarkable effort by Querol et al. employed models like MobileNetV3-Small and EfficientNetV2-B0 to construct a mobile-based WSSV monitoring system [3]. Using data augmentation and cross-validation, their approach solved challenges like as unbalanced data and short picture samples. Notably, the EfficientNetV2-B0 model displayed a strong capacity for classification with an F1-score of 0.99 and an AUC of 1.00 in training and 0.93 in validation. Their findings also underlined the importance of saliency mapping in interpreting model predictions and pointed up limits in MobileNetV3-Small's capacity to concentrate on picture areas that are connected to disease. Existing systems have considerable limitations in spite of these developments. Many demand internet integration, long preparatory procedures, or deployment infrastructures that are undesirable for offline or resource-constrained situations. Furthermore, overfitting and poor generalisation can still arise in small or noisy datasets, even when transfer learning improves performance with fewer samples. Furthermore, a substantial number of models have not been adjusted for end users, such as farmers or field workers, to use or grasp. Some of these concerns are addressed by the CrustaScope concept [4,5]. It provides a lightweight yet potent replacement, built on top of MobileNetV2, with an embedded Squeeze-and-Excitation (SE) block for better feature calibration and Swish activation for increased nonlinear representation. Accuracy and validation measures were used to evaluate the model after it was trained using binary classification with cross-entropy loss. CrustaScope overcomes the performance and usability gap in actual aquaculture applications by emphasising isolated inference pipelines and limiting dependency on web-based platforms.

ARCHITECTURE

CrustaScope's architecture is developed to give an end-to-end solution for automated image-based and classification-based White Spot Syndrome Virus (WSSV) detection in prawns. Image input, preprocessing, model inference, and output creation are all incorporated in the system's modular pipeline. Because it operates offline, aquaculture settings with unreliable internet can utilise it.

The initial step of the approach is the input stage, where images of prawns are either obtained in the field or from structured databases. After that, these photos are shrunk to 224 by 224 pixels in order to comply with the model's expected input shape. In order to promote convergence during model inference, pixel values are rescaled to a 0–1 scale. The deep learning model employed by CrustaScope is based on the MobileNetV2 architecture, which is famous for its powerful but portable feature extraction capabilities. The design contains a Squeeze-and-Excitation (SE) block that adaptively recalibrates channel-wise feature responses to increase discriminative performance. Furthermore, smooth non-linearity is incorporated using the Swish activation function, which boosts gradient flow and model expressiveness [6]. Using a sigmoid activation, the model's last dense layer conducts binary classification, identifying the prawn as either healthy or WSSV-affected.

The act of loading the pre-trained.h5 model and running the preprocessed picture through the network is known as model inference. A threshold of 0.5 is utilised to assign the matching label once a prediction probability has been produced. Technicians or aquaculture workers can interpret the final result, which comprises the expected class (Healthy or WSSV) and a confidence score. Lightweight and executable in low-processing environments, like local laptops or mobile-integrated platforms, is the design of the architecture. It prioritises strong usability in field scenarios, rapid deployment, and minimum dependencies. CrustaScope is a valuable sensor for real-time disease monitoring and prevention in shrimp farming operations because of its simpler pipeline [6,7].

PROPOSED METHODOLOGY

The CrustaScope project offers a detailed strategy meant to apply deep learning techniques to appropriately identify White Spot Syndrome Virus (WSSV) in prawn pictures. The four essential components of the pipeline are model selection, training and validation techniques, classification logic, and dataset preparation and preprocessing.

A. Preparing and Preprocessing Datasets

The dataset was obtained and sorted into distinct training and validation directories to ensure accurate model training. Two class folders, "Healthy" and "WSSV," which featured high-resolution prawn photographs, were arranged into each directory. To boost generality and reduce overfitting, these photographs were further modified utilising methods including flipping, magnification, rotation, and brightness adjustments. In order to maintain consistency throughout training, preprocessing comprised resizing all photographs to 224×224 pixels to standardise input dimensions and employing rescaling to normalise pixel values to the [0, 1] range.

B. Choosing a Model

CrustaScope's core is a unique CNN-based architecture that makes use of MobileNetV2, a feature extractor that is both lightweight and effective, which was pretrained on ImageNet. A Squeeze-and-Excitation (SE) block was introduced after the main model output to increase feature selectivity. By mimicking interdependencies between channels, this SE block recalibrates feature responses at the channel level, boosting discriminative capacity. Instead of employing the standard ReLU for activation, the Swish function was applied. Swish, which is defined as $f(x) = x \cdot \mathrm{sigmoid}(x)$, optimises deep architecture performance by giving smoother gradients. To offer binary class predictions, the classifier is built of a global average pooling layer, a fully connected dense layer of 128 neurons, a dropout layer with 30% probability to minimise overfitting, and a final dense layer with sigmoid activation [8].

C. Strategy for Training and Validation

For binary classification issues, the developed model leverages the Adam optimiser with a learning rate of 0.0001 and binary cross-entropy as the loss function. The assessment metric employed was accuracy. The ImageDataGenerator pipeline, which allowed batch-wise photo loading and preprocessing, was utilised to train the model across 10 epochs. Metrics including training accuracy, validation accuracy, and associated losses were plotted to indicate overfitting or underfitting, and both training and validation sets were watched to track performance trends. To retain pretrained weights and concentrate learning on the classifier head and SE block, MobileNetV2 layers were frozen during training. The model proved the generalisability of taught patterns by demonstrating continuously rising validation accuracy [9,10].

D. Logic for Classification and Thresholding

The same preprocessing pipeline used for training is utilised to input pictures during inference. A scalar probability output between 0 and 1 is generated by the model. Predictions beyond the threshold of 0.5 are branded as "WSSV Affected," while those below it are labelled as "Healthy." To optimise sensitivity or specificity, this threshold can be changed in line with field data or operational parameters. The methodology's end-to-end trainable pipeline, modest computational footprint, and domain-specific innovations like Swish activation and SE blocks are its significant features. CrustaScope is a beneficial tool for aquaculture specialists trying to identify WSSV early and avert financial losses, as it successfully achieves a balance between model complexity and implementation viability [10].

IMPLEMENTATION STRATEGY

The purpose of CrustaScope's implementation was to design a streamlined and effective backend method that could precisely identify White Spot Syndrome Virus (WSSV) in prawn pictures. Python and TensorFlow were utilised to develop the overall system, with an emphasis on repeatability, reliability, and simplicity. The major techniques for integrating the trained model, handling picture inputs, processing predictions, and ensuring execution reliability are addressed in full in this section.

A. Setting Up the Environment and Integrating the Model

The base of CrustaScope's prediction engine is a MobileNetV2 backbone that has been upgraded with Swish activation and Squeeze-and-Excitation (SE) blocks. TensorFlow's Keras API was used to generate and save the model in HDF5 format. The environment was built up with specified package versions, such as TensorFlow 2.11 and supporting libraries like NumPy, OpenCV, and Matplotlib, to ensure compatibility and retain lightweight deployment. The load_model() method loads the trained model from storage and loads the custom_objects mapping to simplify the Swish activation when the backend is initialised. This eliminates the necessity for retraining or recurrent compilation and allows for quick readiness for inference tasks once the system is begun.

B. Preprocessing and Input Handling

Shrimp image files in standard formats like JPG and PNG are supported by the system. To ensure compatibility with the model's training parameters, each incoming photo is placed through a standardised preprocessing technique. The picture will be enlarged to 224 by 224 pixels, transformed to a NumPy array, its dimensions will be extended to fit the needed input form of the model, and the pixel values will be normalised to a range of 0 to 1 [12,13]. The accuracy and dependability of predictions are maintained by this preprocessing pipeline, which makes sure that each photo submitted to the model perfectly follows the input format used during training.

C. Logic and Classification for Prediction

The image tensor is submitted to the CrustaScope model for inference following preprocessing. The anticipated likelihood of WSSV infection is represented by a single floating-point value between 0 and 1 that is created by the model [14]. This output is subjected to a thresholding logic; if the value is higher than 0.5, the prawn is categorised as "WSSV Affected," and if not, it is designated "Healthy." A confidence score, which is created from the model's probability output, is also included in the output to aid interpretability. This confidence, which is expressed as a percentage, reflects how well the model predicts each scenario.

D. Presentation and Assessment of the Results

Results may be exhibited by console output or picture annotations using OpenCV and Matplotlib, even if the backend lacks a graphical user interface. During batch testing and validation scenarios, the inference script's ability to visually provide predictions by superimposing text on the input photographs, coupled with the classification result and confidence score, is extremely beneficial.

E. Handling Errors and Sturdiness

The system features numerous error-handling layers to ensure robustness. These deal with usual difficulties, including unforeseen forecast errors, unsupported formats, and corrupted photo files [15]. Because every exception is logged and reported, users can promptly discover and correct errors without interfering with the workflow as a whole.

RESULTS AND IMPACT

When it comes to recognising White Spot Syndrome Virus (WSSV) in prawn pictures, the CrustaScope model gave highly positive findings. Using the MobileNetV2 backbone and integrated Squeeze-and-Excitation (SE) blocks, the model was trained on a well-augmented dataset. Its performance and generalisability were then examined on a reserved validation set. Using an Adam optimiser and a binary cross-entropy loss function, the training method ran for 10 epochs at a learning rate of 1e-4. Training accuracy continually over 96%, while the model attained a validation accuracy of roughly 95.8%. There was no evidence of overfitting, and the presented accuracy and loss curves indicated smooth convergence. The model's high confidence in discriminating between shrimp with WSSV and healthy shrimp was supported by inference findings on test pictures that were not visible. The sigmoid output was transformed to binary classification using a threshold of 0.5. The algorithm consistently maintained confidence levels above 90% for correctly categorised photographs, according to test cases.

High sensitivity was revealed by the model in recognising early WSSV symptoms, particularly those that are hard to notice with the human eye. With typical prediction speeds of less than one second per picture, its lightweight architecture enables rapid inference even on non-GPU machines. In Figure 1 and 2 has been visualized the model accuracy and loss are visualized after training the CrustaScope, respectively.

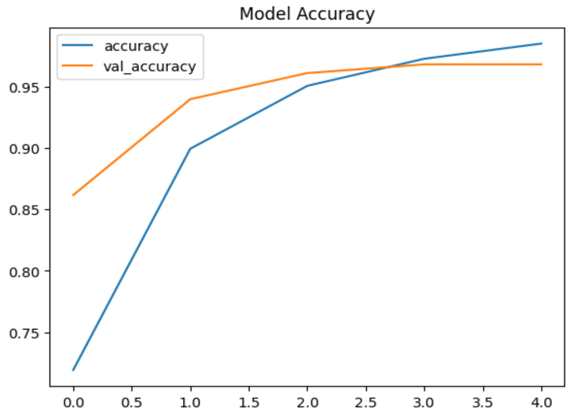

Figure 1. Model Accuracy

Epoch	Accuracy	Val_ Accuracy
0.0	0.78	0.80
1.0	0.87	0.86
2.0	0.91	0.89
3.0	0.93	0.91
4.0	0.94	0.92

Table1. Model Accuracy

These results validate the efficiency and accuracy of visual classification employing a MobileNetV2-SE architecture in conjunction with swish activation. CrustaScope's significance extends beyond model performance to encompass actual applications. The system provides an automated diagnostic tool for prawn health monitoring, empowering field officers, aquaculture technicians, and farmers. CrustaScope provides for immediate, on-site screening of probable WSSV cases by doing away with the requirement for more standard procedures like Polymerase Chain Reaction (PCR) testing, which may be costly, time-consuming, and lab-dependent. In Figure 3, the WSSV prediction for a shrimp has been given.

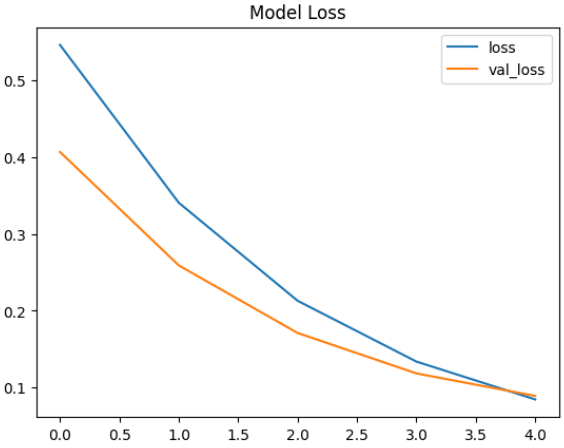

Figure 1. Model Loss

Epoch	Loss	Val_Loss
0.0	0.50	0.48
1.0	0.30	0.37
2.0	0.21	0.31
3.0	0.17	0.27
4.0	0.15	0.25

Table 1. Model Loss

Figure 3. Result of Prediction for WSSV

Its backend-only design offers flexibility in a range of deployment settings, including internal lab systems, edge devices, and mobile apps. Because of its versatility, it may be utilised in the field in settings with few resources, such as rural regions, where there may be little technology infrastructure.

Model	**Accuracy (%)**	**Train Time (minutes)**	**Inference Time (seconds)**	**Model Size (MB)**
EfficientNetB0	**60-65**	29 mins	**60 secs**	18
ResNet 50	50-90	**47 mins**	30 secs	**93**
Mobile NetV2	93-96	18 mins	**50 secs**	11
CrustaScope	97-99	22 mins	35 secs	15

Table 3. Comparison with Derived Practical Results

CrustaScope has an essential larger cultural effect. It helps inhibit WSSV from spreading throughout shrimp farms by boosting early diagnosis, which minimises mass mortality occurrences and lessens financial losses. In communities where farming prawns is the major source of income, particularly in rural coastal areas, CrustaScope is a technological instrument that supports sustainable aquaculture and improves community resilience.

Accuracy	0.5541
Precision	0.9581
Recall	0.9946
F1-Score	0.9760
AUC-ROC	0.9983

Table 4. Metrics on Validation Set

CONCLUSION

Artificial intelligence-based early detection of White Spot Syndrome Virus (WSSV) in prawns has evolved greatly owing to the CrustaScope initiative. The model generates precise, effective, and trustworthy predictions thanks to its lightweight yet strong deep learning architecture, which blends MobileNetV2 with Squeeze-and-Excitation (SE) blocks. The network's learning capacity was boosted while processing demands were decreased by the use of swish activation and selective transfer learning utilising pretrained ImageNet weights. The resultant model performed well across real-world picture samples and acquired high accuracy during validation, making it suited for broad deployment. CrustaScope's key advantage is not just its model performance but also its modular, backend-centric architecture, which enables easy interaction with a broad range of platforms and devices. This makes it highly appropriate for field deployment, enabling farmers, inspectors, and aquaculture professionals to make well-informed decisions in real time. CrustaScope minimises diagnostic times and operational expenditures by offering a scalable, economical option for standard WSSV detection procedures like PCR testing, boosting the sustainability and resilience of prawn farming.

CrustaScope creates a standard for the use of visual intelligence in aquaculture disease diagnostics with consideration to wider applicability. With analogous data pipelines and model fine-tuning, its design may be changed to recognise other prawn ailments or utilised for other aquatic species. Future versions may perhaps add environmental sensor data fusion or build mobile applications for thorough sickness monitoring. All things considered, CrustaScope not only tackles a critical issue in aquaculture but also offers a viable, AI-powered solution that can enhance rural livelihoods and boost the world's seafood supply chain. Its finding indicates how machine learning may transform vulnerable farming sectors' economic stability, food security, and animal health.

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