



Emergence of Artificial Intelligence in Detection of Avian Influenza Viruses in Birds

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ABSTRACT

Background: Avian influenza viruses (AIVs) are one of the most important viral families on the planet, having considerable health implications for humans, domestic animals and wildlife. Wild birds serve as natural reservoirs for such infections and regular observation of wild bird groups gives crucial data regarding viral development, which is used to build risk evaluation and countermeasures. However, active monitoring systems use a lot of resources, thus improving them for greater efficiency is critical.

Methods: Machine learning (ML), a subset of artificial intelligence, offers statistical learning processes that may be used in disease monitoring systems to acquire new insights. In this study, the researchers focus on the application of gradient boosted trees, a type of machine learning, to estimate the chance of identifying avian influenza viruses from wild bird samples collected during monitoring efforts in the United States.

Result: The study highlights the emergence of new technology, specifically Artificial Intelligence, in the diagnosis of Avian influenza viruses (AIVs) in avian species.

Key words: Artificial intelligence, Avian influenza viruses, Convolutional neural networks, Deep learning, Machine learning, Recurrent neural networks.

INTRODUCTION

Avian influenza viruses (IAVs) target a variety of bird as well as mammalian species, with species selectivity in most cases. AIVs are often found in ecological reservoirs, ducks and shorebirds and they are mostly responsible for subclinical bird illness. Avian influenza viruses infect mammalian hosts including such pigs, humans and other mammals on a sporadic basis and therefore are susceptible of intra - species transmission. Moreover, Avian influenza viruses have a significant possibility of acquiring human-adaptive genomes because to the high rate of variation with segment fusion, posing a high outbreak risk. Swine adjustment especially swine-adapted Avian influenza viruses, in particular, are connected with human outbreaks (Golden *et al.*, 2021). The previous 5 influenza outbreaks were all triggered by avian-origin, swine-origin and reassortant influenza A viruses. As a result, predicting the transmission of bird or pig Avian influenza viruses to humans is critical.

Human-adaptive Influenza a viruses may readily infect and cause illness in people, as well as propagate quickly throughout human civilizations. "H3N2 and H1N1 are the most common human-adaptive Influenza a viruses subtypes that produce outbreaks. Humans are infrequently infected with H5N1, H7N9, as well as other IAV subtypes, but they are not yet capable of spreading in human populations". Numerous viral determinants have been found in laboratory investigations that are linked to IAV human adaptation *via* coordinating receptor binding, controlling the virus's reproduction cycle, including antagonising host immunity. Influenza a viruses, on the other hand, have no universal human adaption factors.

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Virus genome detection of a big data collection, particularly Influenza a viruses, has been assisted by gene sequencing methods as well as machine or deep learning approaches. ML techniques have lately been shown to be useful in a variety of domains, notably virology. Avian

influenza viruses exhibit different host tropism protein profiles, zoonotic danger and sometimes even avian-to-human spread risk, all of which have been identified (Everest *et al.*, 2020). ML approaches have also been used to investigate the host dependency of mononucleotide (nts) as well as tetranucleotide components of influenza viruses. In particular, both computational and experimental studies have pointed to the importance of dinucleotides in viral genomes. Influenza A viruses' pathogenicity and replication are controlled by viral dinucleotides, which are objectives for the host's distinctive immune system (Lam and Pybus, 2018). Computational recognition has also been made of species-specific as well as virus-family-specific dinucleotide sequences. Machine learning techniques have recently been used to reliably predict viral reservoir hosts as well as arthropod vectors based on the dinucleotide content of RNA virus genomes (Alshahrani, 2024; AlZubi, 2023). As a result, we propose that genomic dinucleotide content is yet another important genomic property for influenza viruses, one that is most probably amino acid autonomous as well as might be beneficial in identifying the human adaption feature of Avian influenza viruses.

MATERIALS AND METHODS

Novel techniques for quick diagnosis and detection of poultry infectious disease

Technologies for diagnosing infection or sickness in poultry are widely used and may be used to a variety of infectious agents including physiological situations. This part focuses on technology for quick detection of chicken infection, with a particular emphasis on Avian influenza, which is a major developing disease in the livestock industry and the subject of several research initiatives (Cho, 2024). Avian influenza is continually threatening to contaminate farmed poultry and is potential of generating considerable financial losses in the trade because of the the ongoing creation of new influenza viruses via continuous alteration and genetic factor variety, paired with their high frequency in wild bird reservoirs (Hill *et al.*, 2017). Conventional Avian influenza detection in poultry involves labor-intensive procedures such as culture methods accompanied by "real-time polymerase chain reaction (RT-PCR) and enzyme linked immunosorbent tests.

Biosensors for the influenza virus to detect poultry disease

A possible disadvantage of quick screening technologies, especially compared to conventional laboratory procedures, is the absence of assurance while making a diagnosis. Most quick detection tests for human influenza infection, for instance, have poorer sensitivity which could only identify "influenza virus" at the type level, determining if a trial is positive for "influenza A or influenza B". It's necessary to distinguish between elevated/low viral diseases when detecting AIV illness in poultry beyond the viral species level (Reeves *et al.*, 2018). Nonetheless, biosensors with extremely precise detection capabilities are established, with

the ability to detect and identify certain AIV cub categories. Biosensors are tools that can transform the occurrence of a living constituent into a signal that the user can understand.

Biosensors for the influenza virus based on antibodies

Antibodies are the subjects which also have been investigated for practice in the bioreceptor in influenza virus fast sensing devices. "Nidzworski was able to identify several influenza strains using polyclonal antibodies from mice inoculated with influenza M1 protein in an impedance electrochemical spectroscopy biosensor". Because the M1 protein is identical in all Avian influenza viruses, the studies in the previous work hypothesised that this biosensor might identify all Avian influenza viruses (Winker *et al.*, 2007). Resistance biosensors with antibody acknowledgement components exact for peptides generated from the "HA protein" have also been created. H5N1 virus was also more selectively identified in solution employing 2 antibodies: an "anti-H5 antibody" which seized influenza virus in result, accompanied by an electrode mobilised "anti-neuraminidase (N1) antibody". Nonetheless, when Lum's sensor was evaluated with H5N2, but not with H5N3, it gave false positive results, which was most likely owing to common structures between N1 and N2 that were both identified by the anti-N1 antibody. If sensors could be built which are particular for related and harmful forms of influenza virus, this technique might be useful for the poultry sector.

Biosensors for influenza virus based on aptamers

Aptamers are yet another bioreceptor identification component that has been used to identify viral infections in quick methods of screening in the lab. "Aptamers are short oligonucleotide or peptide" patterns with distinct structural components that enable them to attach to big or tiny molecules or macromolecules preferentially. *In vitro* collections of "nucleotide sequences" are produced and evaluated to discover arrangements that recognise a target analyte with higher sensitivity and so this technique has been used to diagnose distinct influenza virus subtypes selectively (Bergervoet *et al.*, 2019). Glycans and antibodies like them because of their strong affinity for their target, compact size, durability and repeatable production. A number of biosensors that use aptamers to detect influenza viruses have been produced, the majority of which are selective for H5N1 diagnosis.

Biosensors for the recognition of influenza virus in poultry

Several of the techniques being explored for influenza biosensors are intended for human point-of-care diagnostics, but same tactics may also be used to poultry. AIVs multiply in the mucosal tissues of avian species, hence biosensors must be able to properly identify the virus from such origins for diagnostic reasons. Furthermore, since certain avian influenza viruses enter the general circulation of hens, identification from serum samples is

critical (Herrick *et al.*, 2013). Some of the many biosensors or fast assays designed for the diagnosis of influenza viruses have been evaluated using biological material from poultry birds.

Biosensors and quick diagnostic assays can help to speed up the diagnosis of poultry illness and infection. Biosensor detection technologies are promising in terms of specificity as well as speed, although such point-of-care systems need manual sampling. After clinical indicators of illness are visible in chicken, biosensors will likely be utilised to substitute lab-based techniques of detection, cutting days or sometimes weeks off it takes to make an authorized analysis. The requirement for physical monitoring, however, is a deterrent to biosensor-centred screening (Beiring, 2013). The ultimate goal is to detect illness in poultry in live time, since valuable time might pass between whenever poultry get affected with a virus and when clinical indications are observed and diagnostic technologies can be deployed. Sensing devices and non-invasive ways of monitoring, like vocalisation assessment and other imaging technology, are now being explored for live diagnosis of infection and illness in chicken. Such detection systems are also advantageous since they reduce the requirement for regular human inspection of chicken houses, lowering the risk of infectious organisms being introduced into flocks.

RESULTS AND DISCUSSION

Systems for poultry monitoring based on deep learning

Imaging, segmentation, pre-processing, classification and feature extraction or regression are the steps in traditional ML-based poultry surveillance. It's not easy to do extraction, segmentation, as well as selection engineering. The effectiveness of such algorithms is also impacted by sensor understanding, making them difficult to use on a farm. As illustrated in Fig 1, DL techniques remove these tedious steps by immediately processing images using DNN. So, DL is feature learning (Huettmann *et al.*, 2017). Also, DL models have improved accuracy by avoiding segmentation and feature vector mistakes. Owing to the complexity of the concepts, DL permits substantial parallel processing. So difficult issues can be addressed quickly. Thus, in traditional image processing methods, more study is now focused on optimal network design than on feature extraction.

DL groupings

CNNs, RNN Networks and Pretrained Unsupervised Networks are among the most prominent DL designs discussed in this paper. In principle, each design has a unique potential application and several have already been pre-trained to offer correct categorization in specified areas.

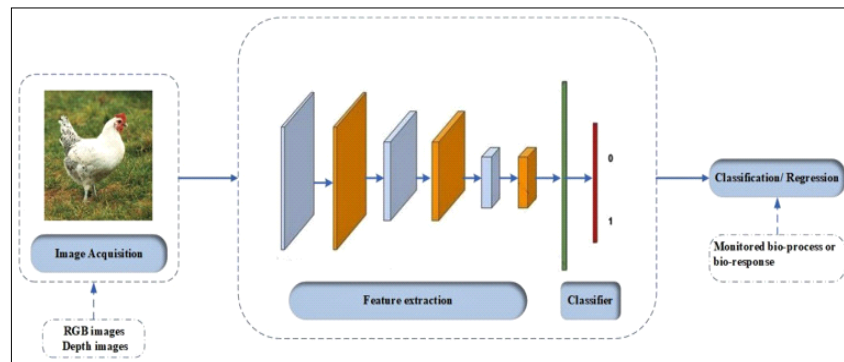


Fig 1: The typical process of chicken monitoring systems based on DL.

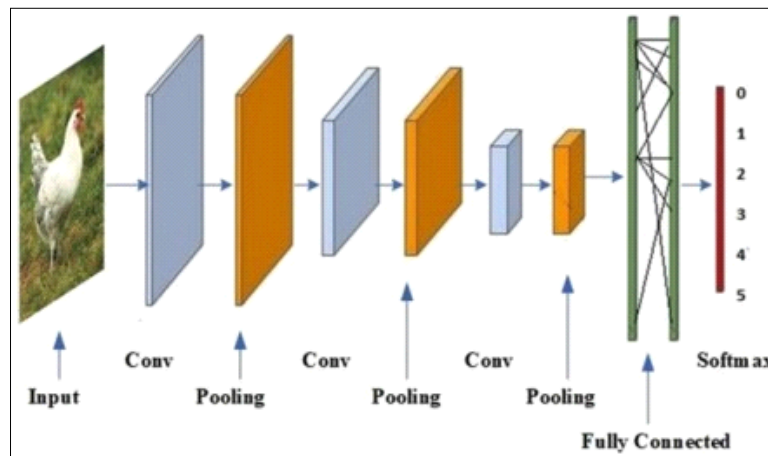


Fig 2: CNN architecture.

NNs

The most widely used structure in machine learning and computer vision analysis is CNNs. "Convolutional Neural Networks are a multi-layered network" that really can study attributes of a goal and detect it autonomously. Convolutional, pooling, non-linear activation, as well as fully linked layers are among the neural layers that make up this system (Humphries *et al.*, 2018). Every layer converts the input to the outcome for neuron start, leading to a successful fully-connected layers and the charting of a source to a 1D characteristic space. In contrast to traditional neural networks, convolutional neural networks use convolution in its place of regular matrix increase in its coatings. Parameter sharing as well as sparse connections are the two basic characteristics of Convolutional Neural Networks. The architecture of Convolutional Neural Networks is seen in Fig 2.

For feature maps, CNN uses convolutional layers to correlate the actual picture. "The Rectified linear unit layer (ReLU) enhances training efficiency and non-linearity of feature maps (inputs) by using a function". The pooling layer shrinks the input volume. Therefore, the pooling layer only affects the input volume's width and height. This process is called down-sampling or subsampling. This reduces processing cost in subsequent layers and avoids overfitting. The completely linked layers transform 2D image features to 1D feature vectors.

ResNets are a result of complicated challenges in CNN architectures. Every coating is a purpose established to be run on a source, with the inclined output possible of response to prior levels through shortcut networks (Jiao *et al.*, 2016). ResNets are more accurate, need less weight and are very modular. They may also be used to determine a network's depth. The primary drawbacks of Deep Residual Networks are that deeper networks make mistake identification tougher. A narrow network may also result in ineffective learning (Lugito *et al.*, 2022; Sharun *et al.*, 2024).

The VGGNet has a conventional convolutional network topology, with max-pooling, convolutional, as well as activation layers before fully linked categorization layers. MobileNet is a mobile-optimized version of the Xception framework. SqueezeNet is a strong DL design for low bandwidth systems (Swayne *et al.*, 2006). It uses a CNN design but has half the variables of AlexNet and is as accurate as AlexNet on ImageNet. It is a multi-layer capsule technique that deepens the nesting or underlying structure of CNNs. It's utilised for picture identification since it's resistant to geometric distortions. So it can handle orientations, spins, as well as translations well.

RNNs

RNN, Attention, as well as Long/Short Memory are examples of systems which can grip time-series data (LSTM). RNNs are a network where present result is dependent on both current data input and prior data processing. As a result, Recurrent neural networks are used in areas like translation

software, voice generation, including natural language interpretation where the order wherein data is given is critical. Every piece of calculated data is saved and used to create the final result. Therefore, based on the prior inputs in the set of data, the same input might produce multiple results. Since the same job is done for each component in the sequence, the Recurrent neural networks are known too as recurrent (Gulyaeva *et al.*, 2017). This results in the formation of various "fixed-size output vectors", with the concealed vector field changed for each input. As a result, Recurrent neural networks captures both consecutive and time-dependent data relationships. The Bidirectional Recurrent neural networks as well as the Encoder-Decoder Recurrent neural networks are 2 kinds of RNN. Recurrent neural networks draw implications from the current data fact in a series comparative to both upcoming and prior data points, hence the productivity of a "BRNN" is dependent on both previous and upcoming outcome. The EDRNN can convert variable-length output sequences from input data patterns. "Additional hidden state layers, more layers between both the hidden layer layer as well as the output layer, non-linear hidden units between the input layer as well as the hidden state layer, or even all 3 may be used to make Recurrent neural networks deeper".

PUNs

Unsupervised classification is used to train the hidden layers of pre-trained models Unsupervised Networks in order to obtain correct dataset matching. The layers are taught autonomously and sequentially, with each layer's input being the previously learned layer. After every layer has been pre-trained, the entire system is fine-tuned using supervised learning. "Autoencoder, Generative Adversarial Networks (GAN), as well as Deep Belief Networks are examples of PUNs (DBNs)".

In an unsupervised setting, an ANN uses a back - propagation procedure technique. The input is compacted into a latent-space depiction, as well as the extracted features are identical to or nearly identical to the input values. They're widely used in anomaly identification

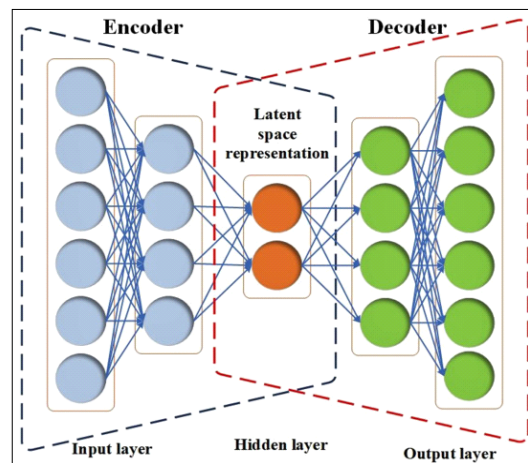


Fig 3: The autoencoder architecture.

situations, such as financial transaction detecting fraud. As illustrated in Fig 3, the network consists of encoder and decoder components (Hiono *et al.*, 2015). Because of discontinuity in the latent feature representations, autoencoders cannot be used as a generative model. As a result, variational autoencoders were developed as a possible option. Instead of one vector, the encoder produces two. This feature allows the “decoder to decode” standards with minor changes in the same input.

Convolutional, Vanilla, Multilayer, as well as Regularized autoencoders are the four primary forms of autoencoders. The vanilla autoencoder is the most basic, consisting of a “single hidden layer neural network”. A multilayer autoencoder has more hidden layers than a standard autoencoder. Convolutional is a kind of autoencoder that uses convolutional layers rather than fully linked layers. Finally, the Normalized autoencoder improves efficiency by using a particular loss function.

Table 1: Data augmentation methods.

Descriptions	Data augmentation techniques	
	Method	Classification
Conversion of the RGB colour space to HSV, TIN, CMY and LAB colour spaces.	Color space transformation	Photometric transformations
By combining k closest neighbours to construct new instances in lower-dimensional representations in high-level layers, noise, extrapolating and interpolating are possible.	Feature space	Deep learning-based augmentation
The creation of fake instances from a dataset with properties that are comparable to those of the original dataset.	Generative adversarial network (GAN)-based	
Using Neural Style Transfer, combining pictures and geometric alterations, a neural network is pre-programmed to learn augmentations.	Meta-learning schemes	
The use of adversarial attacking in a competitor network to learn picture augmentations that cause misclassifications in the rival classification network.	Adversarial training	
Manipulates the sequential representations throughout a CNN, <i>i.e.</i> , one image's style may be transferred to another while the original information is preserved.	Neural style transfer	
Rotating a picture by ± 8 degrees around its centre.	Rotation	Geometric transformations
To prevent positioning bias in the data, shift pictures left, right, up, or down.	Translation	
Isolating a single colour channel, such as R, G, or B and manipulating colour histograms (brightness)	Color	
Vertical and horizontal mirroring	Flipping	
Reducing the supplied image's size	Cropping	
Using a Gaussian noise matrix to inject a matrix of random values (Gaussian distribution).	Noise in jection	
Masks a $n \times m$ patch of a picture with either 0 seconds, 255 seconds, mean pixel values, or random values.	Dropout regularization	Random erasing
Averaging the pixel values of photos to create a new image.	Mixing images together	Mixing images
Use a high contrast vertical or horizontal edge filter to sharpen the image's edges.	Sharpening	Kernel filters

GANs include the concurrent learning of two Deep learning that compete with one another. During training, the generator generates fresh examples by modelling a transform mechanism. The differentiator, on the other hand, determines whether an instance comes from the producer or the testing dataset, with the former optimising the classification process mistake and the latter optimising the gap between the produced and training data. As a result, the 2 channels are considered regarded as rivals (Le Trung *et al.*, 2020). As a result, the entire network advances with each training iteration. Since of Generative Adversarial Networks' capacity to replicate any supply of the information in any field, they are frequently used in machine learning, particularly in picture production, as well as speech, literature and music.

Like variational encoders, GANs have the benefit of not requiring predictable bias, allowing for rapid training the model in a semi-supervised context. Unfortunately, one of the key disadvantages of GANs is that the generator and discriminator's functionality are critical to the model's effectiveness and if one component fails, the entire system fails. Furthermore, because to the two-model training, training GAN is operationally costly and takes a long time.

Pre-processing of image

Prior the picture is provided as a source to the Deep Learning model, it undergoes pre-processing. The most popular picture pre-processing approach for adapting the image to the Deep Learning model supplies is image downsizing. Some other important pre-processing operation is data labelling, which involves the establishment of bounding boxes. Information labelling is often done by hand in order to use a bounding box to identify the ground truth. To construct the boundary boxes and retrieve their co-ordinate coordinates, labelling software including such Labelling is used (Elith *et al.*, 2008). Ground truth labelling is an important stage in categorization jobs since it offers a foundation for evaluating the proposed detector's effectiveness. The aforementioned approaches are the most common strategies used in poultry tracking Deep Learning modelling systems. Some other pre-processing processes include picture subdivision, which highlights the ROI and so facilitates Fang's learning experience. To lessen the influence of disturbance in the dataset, background reduction or foreground pixel separation might be used.

Data growth

To attain an acceptable convergence for greater identification accuracy while avoiding over-fitting, Deep Learning systems requirement a large amount of training information. As a result, a data augmentation approach is used to enlarge the training information by transforming it dynamically without affecting its categorization. The entire number of photos utilised in training will be " $(k + 1)$ -fold" of the entire dataset if k is the number of augmentation strategies employed. Furthermore, the picture modification successfully expands the training set without requiring a huge augmented

training set to be stored (Dugan, 2012). The information increase strategies used in the deep learning dispensation data are listed in Table 1.

DL applications

Deep learning models have been used in poultry surveillance systems for a variety of purposes, including behaviour categorization, tracking, detecting unwell birds and classifying droppings. Using colour and depth photos, Pu created a Convolutional Neural Networks sensor to characterise chicken flock activities at the feeders (Bocharnikov and Huettmann, 2019). Heat stress in chickens was monitored using a Faster R-CNN Convolutional Neural Networks chicken movement detector in combination with the "temperature-humidity index (THI)". As the basic CNN, the sensor used the "Zeiler and Fergus network". The chicken movement was identified by applying minimum length finding and colour feature matching algorithms to monitor the fowl's position between frames. Since it is an end-to-end target identification technique, the finding swiftness of "YOLO v3" is quicker than that of previous two-stage target detection algorithms (Liu, 2018). Wang demonstrated a real-time behaviour detection system. With a mean accuracy rate of 94.72 per cent, our system was able to recognise six chicken actions. Zhuang and Zhang (2019) proposed an enhanced SSD for ill broiler identification.

CONCLUSION

As the demand for poultry grows, chicken farms will be pushed to expand in size and quantity of birds. The need for higher output will encourage producers to be more effective and reducing losses will be critical. However, densely crowded chicken farms will probably raise the risk of infection-related losses. Simply said, standard illness and infection monitoring methods will not enough whether prospect output targets are to be met. In its place, rapid recognition technologies that continuously screen poultry for illness may be used to supplement current infectious illness diagnosis and diagnostic systems. Rapid real-time monitoring can rapidly inform and find providers in the event of a problem. Biosensors will also give manufacturers with a precise diagnostic that is done on-site. Producers benefit greatly from the mixture of early diagnosis and quick diagnosis since it enables urgent treatment to be performed to avoid the transmission of sickness to other birds, hence avoiding possible losses that would have happened if conventional techniques had been utilised. Since these equipment become more ubiquitous on farms, they will also give data that may aid in the prediction of developing chicken illnesses. Web-based, ecological, including geographical data, in addition to farm-generated information, will become more significant for collecting and integration in predictive analytics. To account for the amount and diversity of data, as well as the necessity for actual analysis, the dynamic data that will be incorporated in such systems will necessitate big data analytics platforms.

Multiple hurdles await the application of technology in the poultry production business that improve identification, detection, including prediction of infectious illnesses, yet they will be needed to meet future production levels.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

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Authors' contributions

All authors contributed toward data analysis, drafting and revising the paper and agreed to be responsible for all aspects of this work.

Data availability

The data analysed/generated in the present study will be made available from the corresponding authors upon reasonable request.

Availability of data and materials

Not applicable.

Use of artificial intelligence

Not applicable.

Declarations

Authors declare that all works are original and this manuscript has not been published in any other journal.

Conflicts of interest

The authors declare that they have no conflict of interest.

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