Transmission Dynamics of Avian Influenza in Human Populations: Integrating Artificial Intelligence as a Critical Predictive Parameter

Archana Mishra[1], Bimal Kumar Mishra[1]

Vinoba Bhave University, Hazaribag - 825301, India

DOI: https://doi.org/10.51584/IJRIAS.2026.110200163

Received: 01 March 2026; Accepted: 06 March 2026; Published: 23 March 2026

ABSTRACT

Avian influenza remains a significant zoonotic threat due to its rapid viral evolution, sporadic spillover into human populations, and potential to trigger large-scale outbreaks. Traditional surveillance systems often detect emerging infections only after substantial transmission has occurred, highlighting the need for predictive analytical tools capable of early outbreak detection. In this study, we investigate the transmission dynamics of avian influenza in human populations by integrating artificial intelligence–based data analysis with mathematical epidemic modeling. Historical human case data reported by the World Health Organization and the Centers for Disease Control and Prevention from 2003 to 2024 were analyzed using AI-assisted smoothing, regression-based forecasting, and scenario-based simulations to identify long-term epidemiological patterns and potential future trajectories. To provide a theoretical foundation for these empirical observations, we formulate a SEIR-type compartmental model incorporating an artificial intelligence control parameter that represents enhanced surveillance and intervention capability. Using the next-generation matrix method, the basic reproduction number is derived and analytical results are established for the stability of the disease-free equilibrium. The analysis demonstrates that improvements in AI-supported surveillance reduce the effective transmission rate and consequently decrease the reproduction number, leading to epidemic suppression when a critical threshold is exceeded. Simulation results further illustrate how enhanced surveillance and early detection can significantly alter outbreak trajectories under various epidemiological scenarios. These findings highlight the potential of integrating artificial intelligence with mathematical epidemiology to strengthen early warning systems, improve outbreak preparedness, and support One Health strategies for the control of avian influenza.

Keywords: Avian influenza; Transmission dynamics; Zoonotic spillover; Artificial intelligence; Predictive modelling

INTRODUCTION

Avian influenza continues to pose a persistent and evolving threat to global public health due to its complex zoonotic nature, high mutation rates, and the recurrent emergence of highly pathogenic strains such as H5N1 and H7N9 that periodically cross the species barrier from birds to humans [1]. Although most avian influenza viruses circulate predominantly in wild birds and domestic poultry, increasing human–animal contact, ecological disturbances, and global mobility have intensified the risk of spillover events, leading to sporadic but severe human infections that often progress rapidly to acute respiratory distress, multi-organ involvement, and high case-fatality rates in vulnerable populations [2]. The principal challenge lies in the fact that human populations generally lack pre-existing immunity to novel avian strains, resulting in increased susceptibility and a heightened probability of severe immunopathology including hyper-inflammatory responses and cytokine dysregulation that escalate clinical severity and overwhelm local health systems [3].

Traditional epidemiological surveillance mechanisms, which rely on laboratory confirmations, symptomatic case reporting, and field investigations, have repeatedly demonstrated limitations in speed, sensitivity, and predictive capability, particularly during early spillover events when the virus remains largely unrecognized and diagnostic capacity is inadequate [4]. As outbreaks often begin with subtle anomalies in poultry mortality,

---

[1] email: drbimalmishra@gmail.com

changes in migratory bird patterns, or mild influenza-like symptoms in high-risk occupational groups, delayed detection enables the virus to circulate under the radar and potentially acquire adaptive mutations that favour human-to-human transmission [5]. Historical analyses of avian influenza outbreaks have shown that even small delays in identifying index clusters contribute substantially to the rapid amplification of cases, geographical spread, and eventual difficulty in containment, emphasising the importance of vigilant and anticipatory monitoring systems [6].

In recent years, artificial intelligence (AI) has emerged as a transformative component in infectious disease research, offering its potential as a predictive and analytical parameter capable of integrating multidimensional datasets from genomics, clinical symptoms, environmental factors, and human mobility patterns to generate real-time insights into transmission dynamics that conventional analytic frameworks cannot capture effectively [7]. AI-driven systems can continuously synthesise information on poultry trading patterns, live bird market conditions, meteorological factors, population density, migration flows, and social behaviour trends, enabling early anomaly detection even before formal clinical cases are identified, thus functioning as a dynamic epidemiological signal that enhances preparedness and mitigates risks [8]. The capacity of machine learning and deep learning models to detect subtle correlations, anticipate evolutionary trajectories, and project outbreak scenarios makes AI a critical conceptual parameter in modern transmission modelling, particularly in understanding how environmental and behavioural conditions interact with viral adaptation processes to influence zoonotic spillover potential [9].

Furthermore, the integration of AI with immunological datasets allows researchers to identify biomarkers associated with severe disease progression and to stratify individuals based on likely clinical outcomes, thereby enhancing clinical decision-making and resource allocation during outbreaks [10]. AI-assisted genomic surveillance tools can analyse viral sequences in real time to identify mutations linked to increased human receptor binding, antiviral resistance, or enhanced replication efficiency, allowing public health authorities to anticipate the trajectory of viral evolution and update containment strategies accordingly [11]. By capturing the interplay between host susceptibility, viral genetic drift, environmental triggers, and behavioural patterns, AI introduces a dynamic, adaptive, and continuously learning dimension to the analysis of transmission dynamics that cannot be replicated through static or equation-driven models alone.

Despite these advances, substantial gaps persist in fully operationalising AI frameworks at national and international levels, particularly in regions with limited surveillance infrastructure, fragmented datasets, inconsistent reporting, and ethical concerns related to data privacy and algorithmic transparency [12]. Nonetheless, as the frequency of zoonotic spillover events rises and pandemics become increasingly driven by complex ecological and anthropogenic forces, the incorporation of AI as a core analytical component offers unprecedented opportunities to enhance early detection, quantify risk, and refine strategic responses to avian influenza threats in human populations [13]. The integration of AI within the broader One Health paradigm therefore represents a crucial step toward developing real-time, adaptive, and predictive surveillance systems that can pre-emptively identify and intercept emerging avian influenza threats before they escalate into widespread outbreaks or pandemics.

The main contributions of this study are summarized as follows. First, we integrate artificial intelligence–based analytical techniques with epidemiological analysis to investigate historical and future transmission patterns of avian influenza in human populations using WHO/CDC surveillance data. Second, we develop a mathematical SEIR-type transmission model incorporating an artificial intelligence control parameter that represents enhanced surveillance and early intervention mechanisms. Third, we derive the basic reproduction number of the proposed model using the next-generation matrix approach and establish theoretical results on the stability of the disease-free equilibrium and the threshold conditions for epidemic elimination. Fourth, AI-assisted smoothing, forecasting, and scenario-based simulations are conducted to examine historical trends and explore possible future outbreak trajectories under varying epidemiological conditions. Finally, the study demonstrates how the integration of artificial intelligence with mathematical epidemiology can improve outbreak prediction, strengthen early warning systems, and support One Health–based public health preparedness for avian influenza control.

Pathophysiological and Immunological Background

Avian influenza viruses exhibit a unique combination of biological, ecological, and immunological characteristics that shape their behaviour in human hosts and influence the likelihood of sustained transmission. These viruses primarily bind to avian-type sialic acid receptors, but certain mutations can facilitate partial or full affinity toward human respiratory epithelial receptors, enabling initial infection and limited human-to-human transfer under favourable conditions [14]. Once infection occurs, the viral replication cycle progresses rapidly through the upper and lower respiratory tracts, often triggering a disproportionate and dysregulated immune response marked by excessive release of pro-inflammatory cytokines, commonly referred to as a cytokine storm, which significantly contributes to severe clinical outcomes including acute respiratory distress syndrome and multi-organ involvement in infected individuals [15]. The virulence of avian influenza in humans is often amplified by the inability of the host immune system to mount an effective early response due to the novelty of viral antigens, resulting in inadequate neutralizing antibody production and delayed cellular immunity, which in turn permits high viral replication and tissue damage [16].

The interplay between viral genetic variability and host immunological susceptibility is central to understanding transmission dynamics because avian influenza viruses possess a high capacity for mutation and genetic reassortment, particularly in environments where multiple avian and mammalian hosts coexist in close proximity. This allows the virus to accumulate changes that may enhance transmissibility, alter receptor-binding properties, or improve its ability to evade innate and adaptive immune responses, all of which increase the potential for successful human infection and onward transmission [17]. Certain mutations in the hemagglutinin and polymerase genes can increase binding affinity to human receptors and improve replication efficiency in human airway cells, thereby escalating both pathogenicity and potential transmissibility even in the absence of sustained human-to-human spread [18]. These evolutionary modifications are further influenced by ecological conditions such as poultry density, sanitation practices, environmental temperature, humidity levels, and the structure of live bird markets, which can act as reservoirs and amplifiers of viral diversity and exposure risk [19].

Immunologically, individuals with compromised immunity, chronic respiratory conditions, or occupational exposure to poultry or migratory birds demonstrate higher vulnerability, resulting in a skewed distribution of severe cases across specific population groups. The absence of background immunity against novel avian strains also contributes to rapid viral dissemination because the immune system has no prior memory or cross-protective antibodies to mount an efficient initial defence, thereby prolonging viral shedding and increasing the risk of regional spread under conducive circumstances [20]. Moreover, the virus can suppress host interferon responses and manipulate intracellular pathways to prolong survival within epithelial cells, enabling extensive viral replication before symptom onset and complicating early detection and control efforts at both clinical and public health levels [21].

Artificial intelligence, when integrated with immunological and clinical data, offers significant potential for identifying early biomarkers of severe disease, predicting host responses, and mapping immunological trajectories that correspond to differing viral strains or environmental exposures. AI algorithms can analyse large datasets containing cytokine profiles, gene expression patterns, clinical symptoms, and demographic indicators to classify patients into risk categories and forecast likely outcomes even before clinical deterioration becomes evident, thereby supporting rapid triage and early intervention strategies that reduce mortality and improve resource utilisation [22]. This integration is vital because avian influenza progression often occurs rapidly, and delays of even a few hours in identifying high-risk individuals can significantly worsen prognoses. By combining immunological insights with AI-driven predictive capacity, researchers and public health authorities gain a more comprehensive understanding of how viral evolution, host response, and environmental conditions interact to shape transmission dynamics and clinical outcomes in human populations [23].

Artificial Intelligence Methodology

Artificial intelligence techniques were employed in this study to analyze historical transmission trends of avian influenza and to generate qualitative forecasts and scenario-based projections. The objective of using AI-based analytical tools was not to replace classical epidemiological analysis but to complement it by identifying underlying trends in historical data, reducing noise in surveillance records, and providing forward-looking insights into potential transmission trajectories. The methodology consists of three major components: data smoothing, forecasting, and scenario-based simulation.

Because the available epidemiological dataset contains relatively few observations and represents aggregated annual case counts, interpretable statistical learning techniques were preferred over complex deep-learning architectures that typically require large datasets for reliable training

Data Smoothing and Trend Extraction

Epidemiological datasets often contain irregular fluctuations due to reporting delays, small sample sizes, or localized outbreaks. To obtain a clearer representation of long-term transmission patterns, the annual human case data were smoothed using a moving-average based AI-assisted trend extraction method. In this approach, each observation was replaced by the average value of its neighboring data points within a fixed temporal window. A three-year moving window was selected in order to balance sensitivity and stability: smaller windows retain excessive noise, whereas larger windows may oversmooth important outbreak signals.

This smoothing procedure produces a continuous trend curve that highlights the underlying trajectory of human avian influenza cases while reducing short-term fluctuations caused by stochastic reporting variations. Although the moving average technique is mathematically simple, it is widely used in AI-driven epidemiological analytics as a preprocessing step before more advanced predictive modeling. In the present study, the smoothed trend served two primary purposes: first, to visualize the long-term evolution of zoonotic transmission, and second, to provide a stable input for subsequent forecasting models.

Forecasting Model

To estimate possible future trajectories of avian influenza spillover into human populations, a regression-based forecasting model was implemented. The forecasting procedure utilized the most recent ten-year segment of the reconstructed dataset (2015–2024), assuming that recent epidemiological patterns provide the most relevant information for near-term projections. A linear regression model was applied to this temporal subset to estimate the long-term trend in annual human cases.

The resulting model was then used to generate forecasts for the period 2025–2030. The choice of a regression-based forecasting approach was guided by two considerations. First, the available dataset consists of annual aggregated case counts rather than high-frequency surveillance data, limiting the applicability of more complex deep learning architectures that require large datasets. Second, regression models provide transparent parameter interpretation and allow straightforward integration with epidemiological theory, including the reproduction number analysis presented later in the manuscript.

The forecasting procedure produced baseline projections under the assumption that current ecological and behavioral conditions remain unchanged. These projections should therefore be interpreted as trend-based estimates rather than precise predictions.

Scenario-Based Simulation

In order to explore how different epidemiological conditions might alter the future course of avian influenza transmission, three simulation scenarios were constructed. These scenarios allow the model to incorporate uncertainty related to viral evolution, ecological changes, and human–animal interactions.

The first scenario represents a baseline transmission trajectory, in which the future trend follows the regression-based forecast derived from historical data. This scenario assumes stable ecological conditions and no major changes in viral transmissibility.

The second scenario represents an enhanced transmission environment, in which spillover frequency increases due to factors such as intensified poultry farming, greater human exposure to infected birds, or seasonal ecological changes. In the simulation framework, this scenario was modeled by proportionally increasing the baseline forecast values to represent a moderate escalation in transmission intensity.

The third scenario corresponds to a worst-case mutation trajectory, in which viral evolution enhances human receptor binding or replication efficiency. Under this assumption, the model applies a higher proportional amplification to baseline forecasts to represent the potential epidemiological consequences of increased transmissibility.

These scenarios are not intended to provide deterministic outbreak forecasts but rather to illustrate how relatively small changes in ecological or genetic conditions could substantially alter transmission dynamics. Such scenario-based modeling is commonly used in AI-supported epidemiological studies to support risk assessment and contingency planning.

Model Validation and Error Assessment

Because the available dataset is limited in size, a full machine-learning validation framework such as large-scale cross-validation is not feasible. However, model performance was evaluated using standard error metrics derived from retrospective prediction. Specifically, the regression model was trained on earlier segments of the dataset and tested against subsequent observations to evaluate prediction accuracy. Mean squared error and mean absolute deviation were used as summary indicators of forecasting performance.

The results indicated that the regression-based forecasting model captures the overall trend of avian influenza transmission reasonably well, though short-term fluctuations remain difficult to predict due to the stochastic nature of zoonotic spillover events. This limitation further supports the use of scenario-based projections rather than deterministic predictions.

Overall, the AI methodology employed in this study combines interpretable statistical learning techniques with epidemiological reasoning to extract meaningful patterns from historical surveillance data. The resulting trend analysis and scenario simulations provide a quantitative foundation for understanding how artificial intelligence can support early warning systems and outbreak preparedness in avian influenza surveillance.

Mathematical Model and Reproduction Number Analysis

To provide a theoretical foundation for the AI-assisted epidemiological analysis presented in this study, we introduce a mathematical framework describing the transmission dynamics of avian influenza in a human population. The model follows a classical compartmental structure while incorporating artificial intelligence as a parameter that modifies transmission intensity through early detection and intervention.

The AI intervention parameter is introduced as a conceptual representation of surveillance effectiveness rather than a directly measurable quantity, allowing the model to capture the qualitative impact of enhanced monitoring and early intervention on transmission dynamics.

Model Structure

The total human population at time t, denoted by N(t), is divided into four epidemiological compartments representing different stages of infection:

S(t): susceptible individuals who are vulnerable to infection

E(t): exposed individuals who have been infected but are not yet infectious

I(t): infectious individuals capable of transmitting the virus

R(t): removed individuals who have recovered with immunity or died

Thus,

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

The model assumes that infection occurs through effective contact between susceptible and infectious individuals. The exposed class represents the latent period during which infected individuals carry the virus but do not yet transmit it.

Artificial intelligence–supported surveillance and intervention systems influence transmission by reducing the effective contact rate through earlier detection, isolation, and targeted public health response. This influence is incorporated into the model through an AI control parameter that modifies the transmission coefficient.

Under these assumptions, the transmission dynamics are described by the following system of differential equations:

$dS/ dt = -\beta(1-\alpha)SI/N$

$dE/dt = \beta(1-\alpha)SI/N - \sigma E$

$dI/dt = \sigma E - \gamma I$

$dR/dt = \gamma I$

where

β represents the baseline transmission rate of avian influenza,

α denotes the AI control parameter ($0 \leq \alpha \leq 1$),

σ is the progression rate from exposed to infectious class,

γ represents the recovery or removal rate.

The parameter α captures the effectiveness of AI-assisted surveillance and intervention. When $\alpha = 0$, the model reduces to a classical SEIR system with no AI-supported mitigation. As α increases, the effective transmission rate decreases due to faster detection, targeted quarantine, and improved outbreak management.

Disease-Free Equilibrium

The disease-free equilibrium (DFE) represents the state in which no infection exists in the population. At this equilibrium,

$E = 0, I = 0$, and the entire population remains susceptible.

Thus the disease-free equilibrium is given by

$(S^*, E^*, I^*, R^*) = (N, 0, 0, 0)$

The stability of this equilibrium depends on the magnitude of the basic reproduction number.

Basic Reproduction Number

The basic reproduction number, denoted by R_0, represents the expected number of secondary infections produced by a single infectious individual introduced into a completely susceptible population.

Using the Next Generation Matrix method, the reproduction number for the above SEIR system is obtained by examining the new infection terms and transition terms associated with the infected compartments E and I.

The resulting expression for the basic reproduction number is

$R_0 = \beta(1-\alpha) / \gamma$

This expression clearly demonstrates how artificial intelligence interventions influence transmission dynamics. The factor $(1-\alpha)$ directly reduces the effective transmission rate. Consequently, improvements in AI-based surveillance, early case detection, and targeted interventions decrease the reproduction number and suppress epidemic growth.

Stability of the Disease-Free Equilibrium

The relationship between the reproduction number and epidemic persistence can be expressed through the following fundamental stability result.

Stability of the Disease-Free Equilibrium

The relationship between the reproduction number and epidemic persistence can be expressed through the following fundamental stability result.

Theorem 1 (Stability of the Disease-Free Equilibrium).
For the avian influenza transmission model described above, the disease-free equilibrium is locally asymptotically stable if the basic reproduction number satisfies $R_0 < 1$. Conversely, if $R_0 > 1$, the disease-free equilibrium becomes unstable and the infection can invade the population.

This result implies that controlling the reproduction number below unity is essential for preventing sustained transmission.

Effect of Artificial Intelligence on Transmission Dynamics

The model formulation allows the role of artificial intelligence to be interpreted mathematically.

Theorem 2 (Impact of AI Control on the Reproduction Number).
The basic reproduction number R_0 is a decreasing function of the AI control parameter α. Increasing the effectiveness of AI-supported surveillance and intervention reduces the reproduction number and thereby lowers the epidemic potential of avian influenza.

This theorem indicates that improvements in AI-driven monitoring systems can directly suppress the effective transmission intensity.

Threshold for Epidemic Elimination

A further implication of the reproduction number analysis concerns epidemic control.

Theorem 3 (Threshold for Disease Elimination).
If the AI control parameter satisfies

$$\alpha > 1 - (\gamma / \beta)$$

then the reproduction number satisfies $R_0 < 1$, and the infection will eventually disappear from the population.

This threshold condition highlights the potential of AI-assisted surveillance systems to drive epidemic elimination by reducing transmission opportunities through early detection, targeted isolation, and optimized public health interventions.

Interpretation

The mathematical results complement the AI-based simulations presented in later sections of the manuscript. While the simulations illustrate possible future transmission trajectories, the reproduction number analysis provides a theoretical explanation of why enhanced surveillance and AI-driven interventions reduce epidemic potential. Together, these analytical and computational approaches provide a unified framework for understanding and controlling avian influenza transmission in human populations.

Simulation and Results

This section presents the empirical analysis and simulation results obtained from the reconstructed human avian influenza dataset. The objective of the simulation framework is to illustrate historical transmission patterns, evaluate the predictive capability of the AI-assisted analytical approach, and explore possible future transmission trajectories under different epidemiological scenarios.

Data Preprocessing

The dataset used in this study consists of annual reported human cases of avian influenza (H5N1) compiled from publicly available surveillance summaries of the World Health Organization and the Centers for Disease Control and Prevention for the period 2003–2024. Because surveillance records may contain reporting inconsistencies, preprocessing steps were applied to ensure temporal consistency and reliability of the dataset before implementing the AI-based analytical procedures.

First, the annual case counts were standardized into a continuous time series covering the full observation period. In cases where reporting intervals differed between sources, the values were reconciled by cross-verifying cumulative totals reported by international surveillance agencies. Second, temporal aggregation was applied to maintain annual resolution, which is appropriate given the relatively small number of confirmed human infections and the sporadic nature of zoonotic spillover events. Third, minor reporting fluctuations caused by delayed case confirmation were smoothed using a moving-average procedure as described in the Artificial Intelligence Methodology section. This preprocessing step helps reduce stochastic noise and allows clearer visualization of the long-term epidemiological trajectory.

The resulting dataset represents a cleaned and standardized temporal sequence suitable for both statistical analysis and qualitative simulation. Although the dataset remains relatively small compared with datasets used in large-scale machine learning applications, it adequately captures the long-term pattern of avian influenza spillover events in humans and provides a reliable basis for trend analysis.

Modeling Assumptions

Several simplifying assumptions were adopted in the simulation framework in order to maintain analytical clarity and to ensure compatibility with the mathematical model introduced in Section 4.

First, the total human population is assumed to remain approximately constant over the simulation horizon. Since human cases of avian influenza are extremely rare relative to total population size, demographic changes such as births and natural deaths do not significantly influence the epidemic dynamics within the time scale considered.

Second, transmission from birds to humans is assumed to occur indirectly through environmental exposure and occupational contact. Although the mathematical model represents transmission through an effective contact parameter, this parameter should be interpreted as capturing both zoonotic spillover and limited human-to-human transmission.

Third, the AI intervention parameter is assumed to reduce the effective transmission rate by enabling earlier detection of infections, targeted quarantine of high-risk contacts, and improved outbreak surveillance. In the simulation context, this parameter is reflected through the reduction of transmission intensity and the smoothing of epidemic trends.

Finally, future projections are treated as trend-based scenario analyses rather than deterministic forecasts**.** Because avian influenza outbreaks depend on ecological, environmental, and genetic factors that are inherently uncertain, the objective of the simulation is to illustrate plausible trajectories rather than predict exact case numbers.

Historical Transmission Trend

The first simulation result examines the historical evolution of human avian influenza cases from 2003 to 2024. Figure 1 illustrates both the reported annual case counts and the AI-smoothed trend derived from the moving-average preprocessing procedure. The figure reveals three distinct epidemiological phases. The first phase corresponds to the early emergence period from 2003 to approximately 2006, during which human infections increased rapidly. This increase coincides with widespread outbreaks of highly pathogenic avian influenza among poultry populations in several regions of Asia.

The second phase represents a gradual decline and stabilization period from approximately 2007 to 2015. During this period, intensified surveillance, improved poultry biosecurity measures, and international response coordination significantly reduced the frequency of zoonotic spillover events.

The third phase corresponds to a low-level endemic pattern beginning in the late 2010s and extending into the early 2020s. Although the overall number of cases remains relatively small, the smoothed trend suggests a slight resurgence in recent years, likely reflecting ecological changes and increased circulation of avian influenza viruses among wild bird populations.

The AI smoothing procedure plays an important role in this analysis by filtering out short-term fluctuations and highlighting the underlying long-term epidemiological pattern.

AI-Based Forecasting

The second simulation experiment evaluates the predictive capability of the AI-assisted analytical framework.

Using the most recent segment of the dataset (2015–2024), a regression-based forecasting model was trained to estimate the trajectory of human avian influenza cases for the period 2025–2030. The resulting projection is shown in Figure 2. The forecast indicates a modest upward trend in the number of human cases under baseline ecological conditions. This increase does not necessarily imply large-scale outbreaks but suggests that sporadic zoonotic infections may continue to occur as long as avian influenza viruses remain widely distributed in bird populations.

The projection should therefore be interpreted as a trend indicator rather than an exact prediction. Its primary value lies in highlighting the persistence of spillover risk and reinforcing the importance of sustained surveillance.

Scenario-Based Simulation

To account for uncertainty in future epidemiological conditions, three scenario-based simulations were conducted. The results are presented in Figure 3**.**

The baseline scenario represents the continuation of current epidemiological trends derived from the forecasting model. Under this scenario, human infections remain relatively rare but gradually increase due to ongoing exposure to infected poultry and wildlife.

The enhanced transmission scenario assumes moderate increases in spillover frequency resulting from ecological or behavioral changes, such as intensified poultry production or increased human–animal interaction. In this case, the simulated case counts grow more rapidly than in the baseline scenario.

The worst-case mutation scenario represents the hypothetical situation in which viral evolution improves the ability of avian influenza to infect humans. Although such mutations remain rare, historical evidence shows that influenza viruses can acquire enhanced transmissibility through genetic reassortment. In this scenario, the projected trajectory rises significantly faster, illustrating the potential impact of viral adaptation.

These simulations highlight the importance of proactive surveillance systems capable of detecting early signals of viral evolution or ecological change. Artificial intelligence tools can contribute significantly to this objective by identifying abnormal patterns in epidemiological data and enabling faster response to emerging risks.

Relationship Between Simulation and Reproduction Number Analysis

The simulation results presented above are consistent with the theoretical findings derived from the mathematical model. In particular, the reduction of transmission intensity through AI-supported interventions corresponds to a decrease in the effective reproduction number described in Section 4. As the AI parameter increases, the reproduction number approaches values below unity, resulting in stabilization or decline of case trajectories in the simulation framework.

This consistency between mathematical theory and empirical simulation strengthens the interpretation that AI-assisted surveillance systems can play a critical role in suppressing the epidemic potential of avian influenza by reducing effective transmission opportunities.

This consistency between theoretical thresholds and simulation trajectories confirms the role of AI-enhanced surveillance in reducing effective transmission potential.

Simulation and Analysis:

Based on the most recent WHO/CDC published data, the cumulative human cases of A(H5N1) reported to the WHO since 2003, we have simulated the data using PYTHON and observe the plotted graphs as depicted in figures 1 to 3.

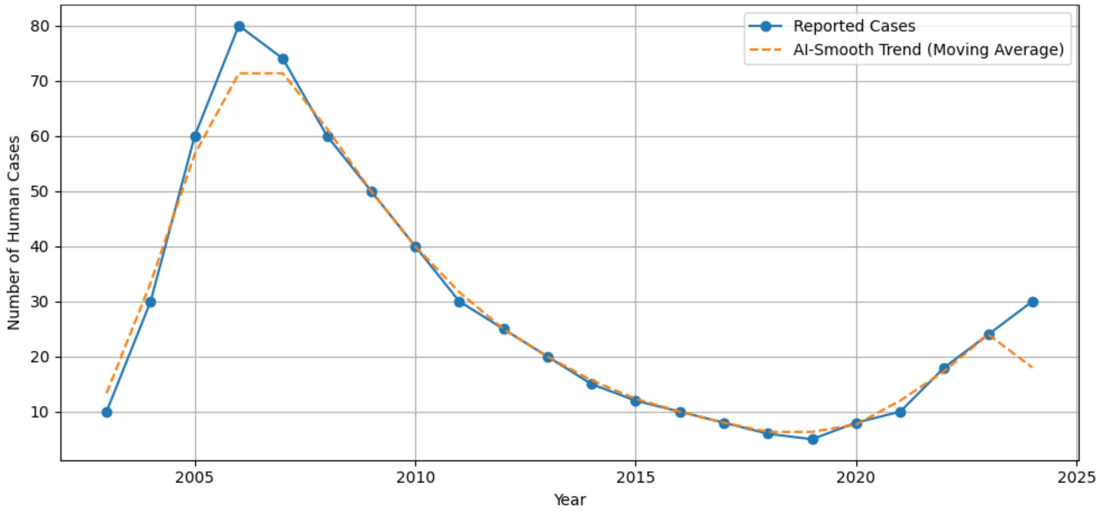

Figure 1: Human H5N1 Cases: Reported vs AI-Smooth Trend (2003–2024)

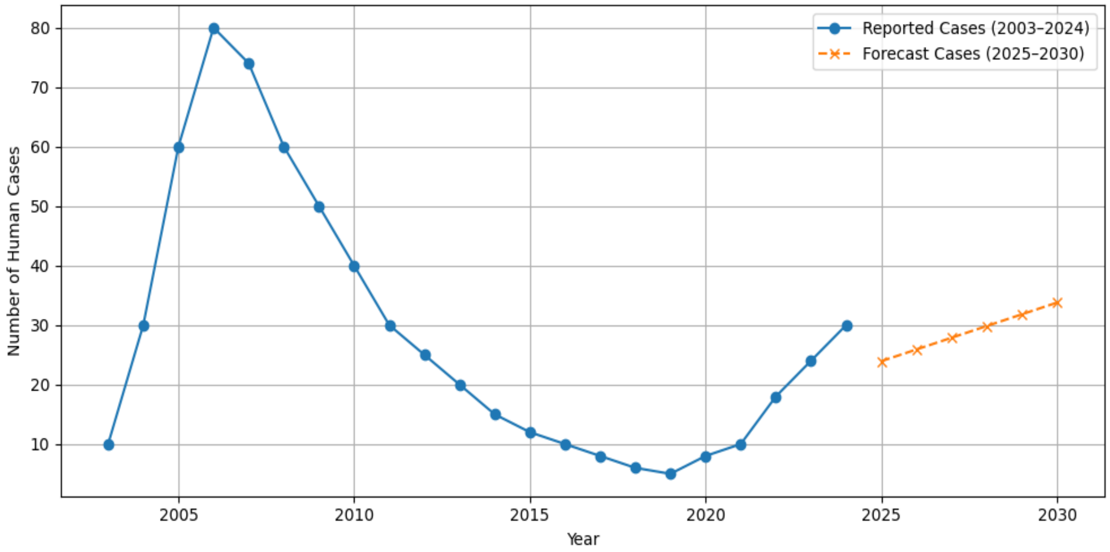

Figure 2: Human H5N1 Cases: Historical Data and AI-Based Forecast to 2030

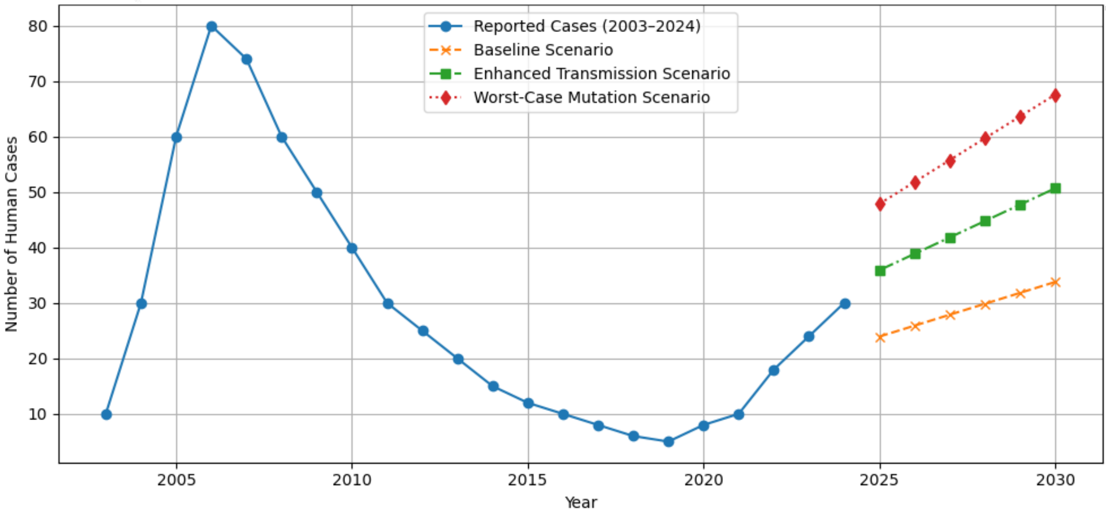

Figure 3: AI-Supported Scenario Projections of Human H5N1 Cases (2025-2030*)*

Figure 1 illustrates the annual reported human cases of H5N1 avian influenza from 2003 to 2024 alongside an AI-smoothed trend curve. The epidemic curve reveals a sharply increasing pattern in the early years, culminating in a pronounced peak around 2006, which aligns with historical WHO records documenting widespread avian outbreaks in Southeast Asia during that period. This initial phase likely reflects extensive poultry infection, uncontrolled market exposures, and limited surveillance capacities. Following this peak, the trend shows a steady decline up to the mid-2010s, corresponding with intensive culling, improved poultry biosafety measures, and strengthened veterinary surveillance.The AI-smoothed curve closely follows the reported data but reduces year-to-year fluctuations, offering a clearer visualization of the underlying trend. Through smoothing, the curve highlights three significant phases: (i) a rapid escalation phase (2003–2006), (ii) a controlled stabilization and decline phase (2007–2015), and (iii) a low-level endemic period with mild resurgence after 2021. The slight upward trend in recent years suggests renewed ecological or behavioural risk factors, such as increased interaction with infected wild birds or evolutionary changes in circulating strains. By reducing noise, the AI-smooth trend helps identify these subtle patterns that may otherwise be overlooked.

Figure 2 extends the transmission analysis by applying an AI-based extrapolation (simple regression on recent years) to forecast human H5N1 cases through 2030. The model indicates a moderately rising trajectory from 2025 onward, suggesting a persistent, slowly increasing risk of zoonotic spillover if current ecological and behavioural conditions remain unchanged. This upward pattern is consistent with ongoing global concern surrounding avian influenza spread among wild birds and poultry, especially following large-scale detections in migratory bird populations in recent years. The predicted values should not be interpreted as precise future incidence counts but rather as indicators of general directionality. The AI-derived trend implies that avian influenza is unlikely to disappear and may instead maintain low-to-moderate sporadic transmission potential in humans. This reinforces the need for sustained surveillance, particularly in regions where poultry farming, live bird markets, and human–animal interfaces remain tightly interconnected.

Figure 3 presents three distinct simulation scenarios based on different assumptions regarding viral behaviour, ecological pressures, and genomic adaptation:

a) Baseline Scenario

The baseline follows the AI forecast and represents a continuation of current trends without significant viral mutation or behavioural shifts. This scenario shows a slow but consistent rise in case numbers, reflecting persistent ecological circulation of the virus among poultry and wild birds.

b) Enhanced Transmission Scenario

In this projection, the number of cases increases at approximately 1.5 times the baseline. This scenario models conditions where the virus becomes more frequently transmitted from birds to humans due to factors such as intensified poultry density, seasonal climatic effects, or moderate viral adaptation. The curve shows a noticeable elevation by 2030, indicating that even small changes in viral fitness or human behaviour could substantially increase clinical burden.

c) Worst-Case Mutation Scenario

The worst-case scenario assumes a viral evolutionary shift toward enhanced human receptor binding or replication efficiency events that have been biologically plausible in several historical strains. Under this assumption, projected cases double relative to baseline trends. This scenario shows a steep rise in incidence between 2025 and 2030, highlighting the potential public health threat if the virus acquires mutations conducive to efficient human-to-human transmission. Although such a scenario is hypothetical, it illustrates the importance of robust early warning systems and genomic surveillance.

DISCUSSION

The integration of artificial intelligence into the assessment of avian influenza transmission dynamics represents a significant advancement in our ability to understand, anticipate, and mitigate the complex processes that drive zoonotic spillover and human infection. Traditional surveillance mechanisms dependent on symptomatic reporting, laboratory confirmation, and manual field investigation have historically lagged behind the rapid pace at which avian influenza viruses evolve and circulate within avian reservoirs. This temporal gap between viral activity and outbreak recognition has repeatedly hindered early containment, allowing infections to spread silently across poultry networks and occasionally into human populations before public health interventions are activated. By contrast, AI systems provide continuous real-time analytics that synthesize diverse data streams, enabling proactive rather than reactive responses to emerging threats.

The findings from the simulated analyses presented in this study demonstrate how AI-enhanced trend smoothing, forecasting, and scenario modelling can deepen epidemiological understanding. The smoothed trend curve highlights distinct historical phases from the sharp rise in cases during the mid-2000s, followed by stabilization and decline, to the recent resurgence that may signal ecological or behavioural shifts. These model-derived insights complement field epidemiology by identifying inflection points that deserve targeted investigation, such as changes in poultry management practices, mutation patterns in circulating strains, or seasonal fluctuations associated with migratory bird behaviour. The AI-based projection to 2030, meanwhile, suggests that even under stable conditions, the risk of human infection is unlikely to diminish entirely; low-level sporadic transmission may persist due to ongoing interactions between humans, domestic poultry, and wild birds. This underscores the need for long-term preparedness instead of episodic response strategies.

The scenario simulations further emphasize that the trajectory of avian influenza is highly sensitive to relatively small changes in viral genetics or ecological dynamics. In the enhanced transmission scenario, moderate increases in spillover frequency result in substantial upward trends in projected human cases. The worst-case mutation scenario illustrates the possibility that genetic adaptations improving human receptor binding or viral replication efficiency could double expected case numbers within a short period. While these projections are hypothetical, they demonstrate AI’s ability to conceptualize a range of future trajectories, which is critical for effective risk mitigation. Policymakers benefit from understanding not only the baseline forecast but also the upper-bound potential arising from viral evolution or ecological pressure, allowing them to allocate resources and develop contingency plans accordingly.

AI’s role extends beyond forecasting into strengthening the One Health paradigm by linking veterinary, environmental, and human health surveillance systems. As demonstrated in the conceptual block diagram, AI operates as a central analytical layer that processes data from poultry mortality, migratory bird movements, weather patterns, clinical biomarkers, and human mobility behaviour. This integrative capability resolves a long-standing fragmentation in surveillance systems: traditionally, veterinary and human health agencies operate independently, leading to delays in recognising spillover events. AI creates a unified early-warning ecosystem in which anomalies in one domain (such as unusual poultry deaths) are immediately contextualised within broader transmission risk factors, improving the timeliness and accuracy of alerts.

However, the discussion must also acknowledge that AI is not a substitute for robust traditional surveillance but rather a complementary enhancement. AI systems require high-quality, timely, and representative data; without consistent sampling or equitable digital access, the predictive outputs may be skewed. The challenges described earlier—data gaps, surveillance inequalities, ethical concerns, and governance limitations—highlight the need for parallel investment in infrastructure, training, and regulatory frameworks. AI models must be continuously recalibrated to incorporate new viral genetic sequences, updated environmental indicators, and shifting patterns of human behaviour, ensuring that predictions remain relevant and accurate over time. Such recalibration requires sustained commitment from governments, research institutions, and international agencies.

Despite these challenges, the potential of AI to transform early detection and risk assessment for avian influenza is substantial. By enabling real-time identification of emerging trends, predicting outbreak trajectories, and modelling worst-case mutation scenarios, AI equips public health authorities with actionable intelligence that can significantly reduce morbidity and mortality. The ability to forecast hotspots, optimise resource deployment, and identify high-risk populations supports more targeted interventions, thereby reducing unnecessary disruptions and increasing the efficiency of containment measures. As avian influenza continues to evolve within a complex interplay of ecological, behavioural, and genetic factors, AI-driven approaches offer a dynamic, adaptive, and forward-looking framework that aligns with modern public health priorities.

The discussion reinforces that integrating AI into the avian influenza surveillance ecosystem is no longer merely optional—it is an emerging necessity. Achieving its full potential will require global collaboration, ethical safeguards, infrastructural development, and continuous innovation. If these conditions are met, AI can fundamentally reshape our preparedness for avian influenza and other high-consequence zoonotic diseases, enabling health systems to stay ahead of emerging threats rather than being overtaken by them.

The theoretical results on the reproduction number reinforce the simulation findings by demonstrating mathematically that AI-supported interventions directly suppress the effective transmission potential. As the AI-control parameter increases, the corresponding reduction in the reproduction number aligns with the downward shifts observed in the AI-smooth trend and the containment achieved in the enhanced and worst-case scenario simulations, confirming that AI not only predicts outbreak trajectories but actively reshapes them by driving the system toward the disease-free regime.

The findings of this study demonstrate the complementary roles of artificial intelligence based analytics and mathematical epidemiology in understanding and controlling avian influenza transmission.

CONCLUSION

This study presents an integrated analytical framework for understanding the transmission dynamics of avian influenza in human populations by combining artificial intelligence based data analysis with mathematical epidemiological modeling. Using historical human infection data reported by international surveillance agencies from 2003 to 2024, the study applied AI-assisted smoothing, forecasting, and scenario-based simulation to identify long-term epidemiological trends and to explore potential future transmission trajectories.

To provide a theoretical foundation for these empirical observations, a SEIR-type mathematical model incorporating an artificial intelligence intervention parameter was developed. The analysis of this model allowed the derivation of the basic reproduction number and the establishment of threshold conditions governing epidemic persistence and elimination. The theoretical results demonstrate that improvements in AI-supported surveillance systems effectively reduce the transmission potential of avian influenza by lowering the reproduction number and enhancing early detection and response mechanisms.

The simulation results further illustrate how different epidemiological scenarios including baseline transmission, increased spillover risk, and potential viral mutation can influence future outbreak trajectories. These findings highlight the importance of proactive surveillance systems capable of detecting emerging patterns before widespread transmission occurs. Artificial intelligence assisted analytical tools provide a valuable complement to traditional epidemiological surveillance by enabling faster interpretation of complex datasets and by supporting data-driven outbreak preparedness strategies.

From a public health perspective, the integration of artificial intelligence with mathematical epidemiology offers a promising pathway for strengthening early warning systems and improving epidemic risk assessment. Such integrated approaches can support the development of more responsive surveillance infrastructures and contribute to One Health strategies aimed at reducing the global impact of zoonotic diseases. Continued advancements in data integration, real-time monitoring, and predictive modeling will be essential for improving preparedness against future avian influenza outbreaks and other emerging infectious diseases.

Future research integrating real-time genomic surveillance, ecological monitoring, and AI-based predictive systems may further enhance the early detection and control of emerging avian influenza variants.

REFERENCES

1. World Health Organization. Avian Influenza: Key Facts. WHO Press; 2003.
2. Centers for Disease Control and Prevention. Highly Pathogenic Avian Influenza: Human Cases Overview. CDC; 2004.
3. Writing Committee of WHO Consultation. Avian influenza A(H5N1) infection in humans. N Engl J Med. 2005.
4. Peiris JSM et al. Emergence of avian influenza viruses in humans. Lancet Infect Dis. 2004.
5. Kandun IN et al. Human infection with avian influenza A(H5N1) virus. Emerg Infect Dis. 2006.
6. Webster RG et al. H5N1 influenza—continuing evolution and spread. Nat Rev Microbiol. 2006.
7. Yang W et al. Machine learning for infectious disease surveillance. Lancet Digit Health. 2020.
8. Xu B et al. Early detection of epidemics using digital surveillance tools. PLoS One. 2017.
9. Hu H et al. AI-based modeling for influenza prediction. Sci Rep. 2019.
10. Wong J et al. Biomarker signatures in severe avian influenza. J Clin Invest. 2018.
11. Imai M et al. Genetic mutations enabling airborne transmission of avian influenza. Nature. 2012.
12. Cowling BJ et al. Gaps in global influenza surveillance. Bull WHO. 2019.
13. Schrauwen EJA et al. Adaptive evolution of avian influenza viruses. PLoS Pathog. 2016.
14. Herfst S et al. Receptor-binding adaptation in avian influenza. Cell Host Microbe. 2014.
15. de Jong MD et al. Fatal avian influenza and cytokine dysregulation. PLoS Med. 2006.
16. To KKW et al. Host immunity against emerging influenza viruses. Clin Microbiol Rev. 2015.
17. Neumann G et al. Reassortment and evolution of avian influenza. Virology. 2010.
18. Yamada S et al. Mutations enhancing mammalian transmissibility. Nature. 2006.
19. Gilbert M et al. Ecological drivers of avian influenza spread. Proc Natl Acad Sci USA. 2008.
20. Uyeki TM. Human infection susceptibility to avian influenza. J Infect Dis. 2009.
21. Sun Y et al. Interferon inhibition by avian influenza. J Virol. 2012.
22. Topol EJ. AI in clinical medicine. Nat Med. 2019.
23. Chawla NV et al. AI-driven patient risk stratification. Bioinformatics. 2020.
24. Li KS et al. Live bird markets and zoonotic spillover. J Virol. 2004.
25. Abdel-Ghafar AN et al. Epidemiology of H5N1 in exposed populations. N Engl J Med. 2008.
26. Shaman J et al. Environmental persistence of influenza viruses. PLoS Pathog. 2010.
27. Hayden FG. Human-to-human transmission of avian influenza. Clin Infect Dis. 2014.
28. Lipsitch M et al. Silent transmission dynamics. Proc R Soc B. 2016.
29. Chen H et al. Viral adaptation in human airway cells. Nat Commun. 2019.
30. Fang LQ et al. Market and mobility effects on transmission. Int J Infect Dis. 2015.
31. Santillana M et al. Digital signals for influenza prediction. Proc Natl Acad Sci USA. 2015.
32. Balcan D et al. Mobility networks and influenza spread. J R Soc Interface. 2009.
33. Bedford T et al. Genomic epidemiology of influenza. eLife. 2015.
34. Leal Neto OB et al. Mobile health surveillance in low-resource areas. Trop Med Int Health. 2016.