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REVIEW

A review of fractional calculus models for avian influenza: Dynamics, memory effects, and control perspectives

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ABSTRACT

Avian influenza is a serious global public health threat, and both humans and animals can be infected. Classical integer-order compartmental models are generally not capable of capturing the complex temporal dynamics of epidemic systems, especially memory-dependent phenomena such as delayed immune response and environmental virus persistence. In this review, we have surveyed the use of fractional calculus in the modeling of avian influenza epidemics with emphasis on disease transmission, memory effects, and intervention strategies. In detail, we consider four fractional operators, namely, the Caputo, Caputo-Fabrizio, Atangana-Baleanu, and fractal-fractional operators, and compare the structures of their kernels and their memory properties. We review progress in data-driven modeling, including calibration to real epidemic surveillance data, seasonal transmission patterns, and fractional optimal control formulations in a One Health framework. Based on the review of 16 studies combining fractional calculus with avian influenza or influenza transmission modeling, consistent evidence is provided that fractional-order models reproduce the real outbreak dynamics better than the classical ones. As far as surveillance data is concerned, the Atangana-Baleanu-Caputo operator yields the fewest prediction errors. Key research gaps are identified, and future directions are proposed, including hybrid fractional-machine learning frameworks for real-time adaptive forecasting.

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1. Introduction

1.1. Epidemiological significance

Influenza is a respiratory infection caused by different types of influenza viruses.[1] The most frequent way these viruses spread is by respiratory droplets. They are highly contagious. There are three primary types of influenza virues: A, B, and C. Type A infects a wide range of hosts, including humans, birds, and other mammals; Type B primarily infects humans; and Type C causes mild respiratory illness mainly in humans.[1–3] In different scientific and engineering domains, mathematical models play an important role in understanding and predicting infectious disease dynamics.[2]

Avian influenza is an infectious disease of birds caused by type A strains of the influenza virus. Most avian influenza viruses do not infect people. However, some can infect individuals and cause illness. The highly pathogenic avian influenza virus, influenza A virus subtype H5N1, was first identified in China in 1996 in geese and in humans after an outbreak in poultry in Hong Kong in 1997.[4] The H7N9 virus is a low-pathogenic avian influenza virus in contrast to H5N1.[5] Another subtype of concern is H9N2, a low-pathogenic avian

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influenza virus that is nevertheless considered a pandemic threat due to its widespread endemicity in poultry across Asia and its repeated zoonotic spillover into humans.[6]

Avian influenza viruses are broadly classified into two pathotypes: low pathogenic avian influenza (LPAI), which typically causes mild clinical signs and reduced egg production in poultry,[7] and highly pathogenic avian influenza (HPAI), which causes severe systemic disease and high mortality rates in infected flocks.[8] Under certain conditions, LPAI strains can mutate into HPAI variants, substantially elevating their pandemic risk.[9]

Avian influenza, particularly the H5N1 and H9N2 subtypes, is a major threat to global health because of its high zoonotic potential and recurrent epidemics in humans and poultry.[10,11] These viruses have been seen to cross species barriers, and the potential for future pandemics indicates the need to understand the processes of interspecies transmission to adopt effective control measures. Mathematical modeling is a useful technique to explain disease transmission and to examine the impact of different treatments such as antiviral medication, immunization, and behavioral changes.[12,13] Credible data to inform public health decisions require realistic models that incorporate the unpredictability of host populations and the time-dependent nature of key biological processes.

1.2. Why fractional models

The main advantage of fractional-order differential equations is that they provide a powerful tool to incorporate memory and hereditary properties of the systems. In integer-order models, these effects are either omitted or difficult to incorporate. Furthermore, fractional models have an additional degree of freedom compared with integer-order models in data fitting.[14] Fractional derivatives can be viewed as continuous interpolations of the integer-order derivatives, and for this reason, they are very useful for analyzing the sensitivity of the epidemic dynamics with respect to the order α. The fractional system converges to its conventional integer-order counterpart as $\alpha \to 1$, which serves as a useful validation benchmark. This continuity property is particularly essential in avian influenza modeling, as the best memory structure may differ between epidemic phases, host populations, and environmental conditions.[15]

Table 1 compares the integer-order and fractional-order epidemic models on several key criteria. Fractional-order models have obvious advantages such as incorporating memory effects for improving data fitting accuracy and providing higher biological interpretability via the fractional order α. But these benefits come at the expense of higher numerical complexity compared to classical integer-order models.

Table 1. Comparison of integer-order and fractional-order epidemic models across key modeling criteria

Criterion	Integer-Order	Fractional-Order
Memory effects	Not captured	Captured via kernel
Data fitting accuracy	Moderate	Higher
Transient dynamics	Exponential	Sub-exponential
Degrees of freedom	Fixed	Extra (order α)
Biological interpretability	Limited	Enhanced
Numerical complexity	Lower	Higher

1.3. Scope of this review

The aim of this review is to provide a comprehensive evaluation of the fractional calculus models for avian influenza. The study has been divided into three main parts: transmission dynamics, memory effects, and control approaches. It also reviews recent advances in data-driven modeling and numerical techniques and outlines important research gaps and future directions in the field. Stochastic integer-order models, agent-based simulations, and purely statistical forecasting approaches are not surveyed, as they are not part of the fractional calculus framework that is the focus of this work.

1.4. Method of literature search

This review was carried out by a comprehensive search of the scientific literature on applications of fractional calculus to epidemic modeling of avian influenza. Relevant studies were identified by searching the major academic databases, such as Scopus, Web of Science, and Google Scholar, with keyword combinations including *fractional calculus and avian influenza*, *fractional-order epidemic model and influenza*, *Caputo derivative and transmission dynamics*, *Atangana-Baleanu operator and zoonotic disease*, and *fractal-fractional and epidemic modeling*.

Relevant research satisfied the following criteria: (i) use of at least one fractional-order operator in a compartmental epidemic model; (ii) direct relevance to avian influenza transmission dynamics or other zoonotic respiratory diseases; (iii) publication in a peer-reviewed journal indexed in Scopus or Web of Science; and (iv) full-text availability in English. The literature search was conducted according to predefined inclusion and exclusion criteria to ensure transparency and consistency in the selection of the reviewed studies. Studies that used only classical integer-order differential equations or those without epidemiological interpretation were rejected.

Additional references were identified by manually checking the reference lists of included studies and recent review publications in the field of fractional epidemic modeling. From this, a final corpus of 16 research papers combining a fractional-order operator with avian influenza or influenza transmission modeling was selected, based on their relevance to the three primary concerns of this review: transmission dynamics, memory effects, and optimal control perspectives. The remaining references cited in this article are foundational (operator definitions and $\mathcal{R}_0$ methodology) or contextual (background epidemiology or fractional models of other diseases discussed in Section 6.3 as directions for future work). The selected studies are from 1996 to 2026 and reflect the evolution of fractional epidemic modeling from early fundamental theoretical concepts[16] to the recent data-driven and machine learning-based frameworks.[15,17]

2. Mathematical and epidemiological foundations

This section presents the mathematical and epidemiological background for the construction of fractional avian influenza models. We begin with classical compartmental structures, then we rationalize the move to fractional-order frameworks, and we conclude with the threshold quantities and the stability conditions that control the epidemic dynamics (**Figure 1**).

2.1. Classical avian influenza compartmental models

Khan *et al.*[18] partition the total bird population N_a into S_a susceptible birds, exposed birds (E_a not yet infectious), and I_a infected birds at any given period t, so that $N_a = S_a + E_a + I_a$. Here, N_h is the population of humans, which is divided into S_h susceptible humans, E_h exposed humans, I_h infected humans, and R_h recovered humans so that $N_h = S_h + E_h + I_h + R_h$. They believe the main source of infection is domestic birds, and the virus does not mutate or transmit between humans. Altaf Khan *et al.*[19] extended this framework to six compartments representing the total population of chickens: susceptible (S), exposed (E), symptomatic (I_s), asymptomatic (I_a), treated (T), and recovered (R). That is, $N(t) = S(t) + E(t) + I_s(t) + I_a(t) + T(t) + R(t)$.

2.2. Why fractional calculus in epidemiology

Fractional-order models allow the introduction of memory and hereditary features into epidemic systems, where the present state of the disease depends on the past history, leading to improved data fitting. This is important for enhancing the accuracy of the predictions and for anticipating the future pattern of the influenza pandemic, which is necessary for policy-making in epidemic control.[15]

A striking example of such an advantage is the study of the AH1N1/09 influenza transmission[20] where the Caputo-Fabrizio fractional derivative proved to be more effective than its integer-order counterpart in reproducing real epidemic dynamics, in particular with respect to the internal memory of the system and its sensitivity to small variations in the derivative order.

2.3. Preliminaries and operator definitions

The four main fractional derivatives used in the reviewed literature on avian influenza are the following operators. Each fractional derivative is presented with the kernel structure, as this directly determines the type of memory that can be captured in epidemic systems.

Definition 1 (Caputo Fractional Derivative[21])**.** *The Caputo fractional derivative of order $\alpha \in (0, 1]$ is defined as:*

$$ {}^{C}D_t^{\alpha} f(t) = \frac{1}{\Gamma(1-\alpha)} \int_a^t (t-s)^{-\alpha} f'(s)\, ds \quad (1) $$

where $\Gamma(\cdot)$ denotes the Euler Gamma function. The power-law kernel $(t-s)^{-\alpha}$ introduces a singular, nonlocal memory structure, making this operator particularly suitable for systems exhibiting long-range temporal dependence.

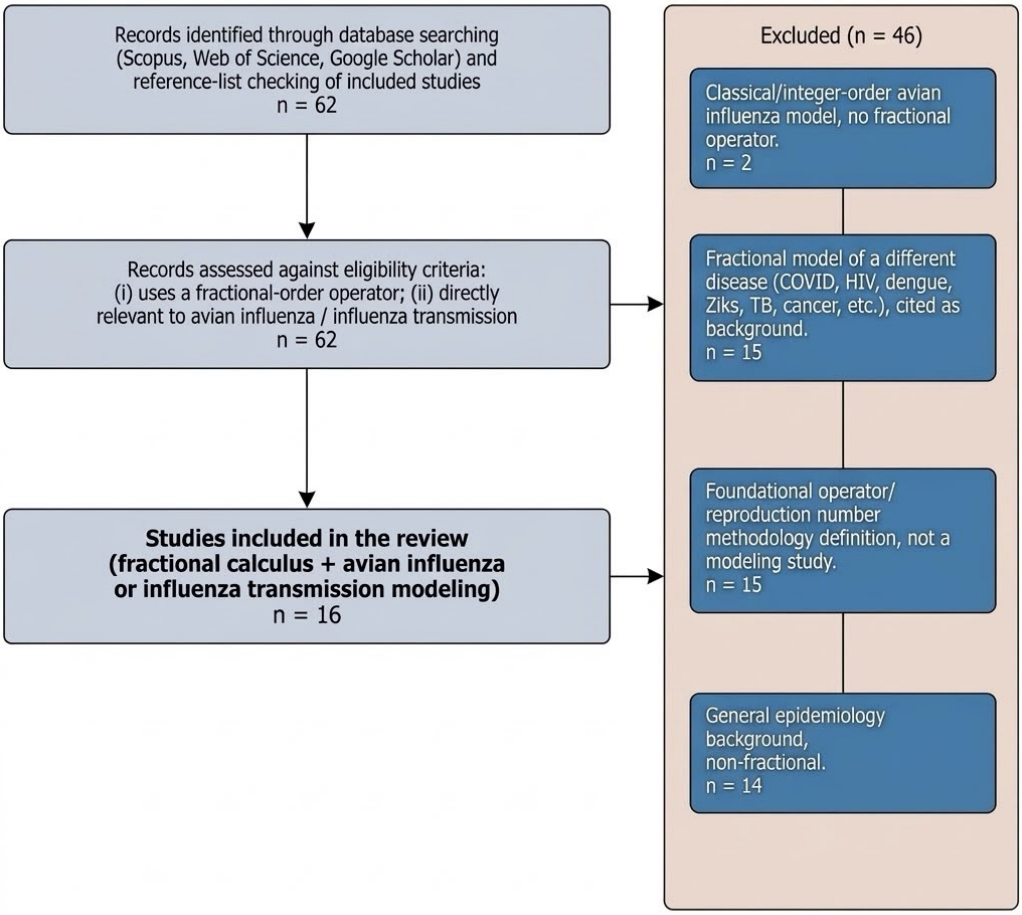


Figure 1. PRISMA flow diagram showing the selection process of studies included in the systematic review[1–18, 21–23, 25, 27–34, 36, 38–42, 45–47, 51, 54, 56–61]

Definition 2 (Caputo-Fabrizio Fractional Derivative[22])**.** *The Caputo-Fabrizio fractional derivative of order $\alpha \in (0,1)$ is defined as:*

$$ {}^{CF}D_t^{\alpha} f(t) = \frac{M(\alpha)}{1-\alpha} \int_a^t \exp\left(-\frac{\alpha}{1-\alpha}(t-s)\right) f'(s) ds \quad (2) $$

where $M(\alpha)$ is a normalization function satisfying $M(0) = M(1) = 1$. The exponential kernel eliminates the singularity present in the Caputo operator, yielding smoother memory decay and improved numerical stability.

Note: The negative sign appears inside the argument of the exponential, ensuring the kernel decays as $(t-s)$ increases, consistent with the fading memory interpretation of this operator.

Definition 3 (Atangana-Baleanu-Caputo (ABC) Fractional Derivative[23])**.** *The Atangana-Baleanu-Caputo fractional derivative of order $\alpha \in (0,1]$ is defined as:*

$$ {}^{ABC}D_t^{\alpha} f(t) = \frac{B(\alpha)}{1-\alpha} \int_a^t E_{\alpha}\left(-\frac{\alpha}{1-\alpha}(t-s)^{\alpha}\right) \times f'(s)\, ds \quad (3) $$

where $B(\alpha)$ is a normalization function satisfying $B(0) = B(1) = 1$, and $E_{\alpha}(\cdot)$ is the one-parameter Mittag-Leffler function defined as:

$$ E_{\alpha}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + 1)}, \quad z \in \mathbb{C} \quad (4) $$

The Mittag-Leffler kernel is both nonsingular and nonlocal, enabling the ABC operator to capture crossover behavior between exponential and power-law memory regimes.

Definition 4 (Fractal-Fractional Derivative with Mittag-Leffler Kernel[24])**.** *The fractal-fractional derivative of order $\alpha \in (0,1]$ and fractal dimension $\beta \in (0,1]$ is defined as:*

$$ {}^{FFM}D_t^{\alpha,\beta} f(t) = \frac{AB(\alpha)}{1-\alpha} \frac{d}{dt^{\beta}} \times \int_a^t E_{\alpha}\left(-\frac{\alpha}{1-\alpha}(t-s)^{\alpha}\right) f(s)\, ds \quad (5) $$

where $\alpha \in (0,1]$ is the fractional order, $\beta \in (0,1]$ is the fractal dimension, and $\frac{d}{dt^{\beta}}$ denotes the fractal derivative. This formulation simultaneously

captures memory effects through the fractional order and structural heterogeneity through the fractal dimension, making it the most general operator considered in this review.

2.4. Biological interpretation of memory

Recent works on fractional epidemic modeling have demonstrated that fractional-order derivatives can capture biologically relevant memory effects, such as delayed immune response, cumulative viral exposure, long-term behavioral adaptability, and environmental persistence of viruses.[16,25] Fractional operators are non-local in time, in contrast to classical intege-order, and have been validated empirically in several infectious disease systems with long-memory transmission processes and sub-exponential growth. Ebrahimzadeh *et al.*[17] demonstrated that the fractional framework leads to better biological interpretability of avian-human influenza transmission and provides more realistic temporal dynamics. Ghanbari *et al.*[26] examined fractional versions of two established avian-human epidemic models, considering the different growth rates of the avian population across both formulations.

2.5. Basic reproduction number

The basic reproduction number $\mathcal{R}_0$ is defined as the expected number of secondary infections generated by a single infectious individual introduced into a fully susceptible population.[27,28] It serves as the principal threshold quantity governing epidemic dynamics.

- If $\mathcal{R}_0 < 1$, the disease-free equilibrium is locally asymptotically stable and the infection cannot sustain itself and dies out.
- If $\mathcal{R}_0 > 1$, the endemic equilibrium exists and the disease persists in the population.

For fractional-order avian influenza models, $\mathcal{R}_0$ is computed using the next-generation matrix (NGM) method originally developed by van den Driessche and Watmough.[28] It has been established that this method remains valid for Caputo-type fractional systems because the equilibrium structure and linearization of the fractional system at the disease-free equilibrium are identical to those of the corresponding integer-order system.[29,30] Formally:

$$\mathcal{R}_0 = \rho(FV^{-1}), \tag{6}$$

where $\rho(\cdot)$ denotes the spectral radius, F is the Jacobian of new infection terms evaluated at the disease-free equilibrium, and V is the Jacobian of the remaining transition terms (recovery, mortality, and progression) evaluated at the same equilibrium.

Under the assumption that the virus does not transmit directly between humans, which holds for the classical avian-human model of Khan *et al.*,[18] the avian and human infection subsystems are decoupled at the disease-free equilibrium, and the next-generation matrix takes a block-diagonal form. Consequently, the overall reproduction number reduces to:

$$\mathcal{R}_0 = \max\{\mathcal{R}_a, \mathcal{R}_h\} \tag{7}$$

where the avian and human components are respectively:

$$\mathcal{R}_a = \frac{\beta_a S_a^0}{\mu_a + \gamma_a}, \qquad \mathcal{R}_h = \frac{\beta_h I_a^*}{(\mu_h + \gamma_h)(\mu_h + \kappa_h)} \tag{8}$$

Although Equation 8 follows the formulation adopted in the referenced study, it is important to distinguish this expression from the classical next-generation matrix (NGM) approach used to derive the basic reproduction number. In the standard NGM framework, $\mathcal{R}_0$ is evaluated at the disease-free equilibrium (DFE), ensuring a consistent threshold parameter for disease invasion. In contrast, the appearance of the endemic equilibrium variable I_a^* in **Equation (8)** reflects the specific modeling assumptions of the original study rather than the conventional NGM formulation. Therefore, this expression should be interpreted within the context of that particular model and not as a universal definition of $\mathcal{R}_0$. This distinction is particularly important in review studies, where different mathematical formulations may employ different derivation procedures while preserving the same epidemiological interpretation. Accordingly, comparisons of reproduction numbers across fractional-order influenza models should primarily focus on their epidemiological significance rather than on differences in their mathematical representations.

where β_a and β_h denote the avian-to-avian and avian-to-human transmission rates, respectively, μ_a and μ_h are the natural mortality rates; γ_a and γ_h are the recovery rates; κ_h is the disease-induced mortality rate in humans; and $S_a^0 = \frac{\Lambda_a}{\mu_a}$ is the disease-free susceptible avian population. Note that the expression for $\mathcal{R}_h$ (see[18]) involves I_a, the avian-infected population at endemic equilibrium, rather than at the disease-free state. This reflects a conditional spillover risk that depends on the established avian prevalence and differs from the standard NGM formulation evaluated entirely at the disease-free equilibrium.

It is important to note that while the fractional order α does not alter the value of $\mathcal{R}_0$ itself, it significantly influences the transient dynamics, convergence speed, and oscillatory behavior of solutions approaching equilibrium.[30] The invariance of $\mathcal{R}_0$ with respect to α arises because $\mathcal{R}_0$ is determined by the linearization of the system at the disease-free equilibrium, and the Caputo fractional derivative of any constant equilibrium value is identically zero, leaving the equilibrium conditions unchanged across all $\alpha \in (0, 1]$. Despite this, for $\alpha < 1$, the rate of convergence toward equilibrium is sub-exponential, and the transient infection dynamics are substantially prolonged compared to the integer-order case. This distinction between fractional-order and integer-order models has been confirmed numerically across multiple reviewed studies.[15,26,30]

Table 2 summarizes the basic reproduction number expressions reported by eight of the 16 reviewed studies that derive an explicit, closed-form $\mathcal{R}_0$; the remaining eight studies either did not report a closed-form $\mathcal{R}_0$ or addressed other aspects of the modeling framework.

Table 4 summarizes a set of recommended practices for deriving and reporting the basic reproduction number in fractional-order influenza models. These recommendations are synthesized from the observations made throughout the reviewed literature and aim to improve consistency, transparency, and comparability among future studies employing different fractional operators and modeling frameworks.

Remark 1. *(1) The $\mathcal{R}_0$ expression for Ye et al.,[30] namely $\mathcal{R}_0 = \dfrac{\beta_a K_a}{\mu_a^\alpha + \delta_a^\alpha}$, contains fractional powers of the demographic parameters μ_a and δ_a. This form arises directly from the fractional-order equilibrium conditions under the Caputo framework and does not coincide with the classical integer-order expression, which is recovered only when $\alpha = 1$. Readers should note that this dimensional inconsistency has been discussed in the fractional epidemic modeling literature; see Diethelm[31] for a related discussion of unit consistency in fractional epidemic models.*

(2) The expression $\mathcal{R}_0$ in Rezapour and Mohammadi[20] is expressed in terms of the composite parameter notation as introduced in the original work. The symbols β, δ, κ, and m are not separate biological factors but are composites of transmission, progression, and recovery rates. Full parameter descriptions may be found in.[20]

(3) Khan et al.[24] found no closed form of the basic reproduction number. Instead, the work proves the well-posedness of the fractal-fractional influenza system and tests the Hyers-Ulam (HU) stability, which guarantees stable solutions under moderate perturbations of initial conditions. This analytical approach complements the threshold-based studies to provide a solid stability basis for the two-strain fractional model.

Although heterogeneous formulations of the basic reproduction number are frequently encountered in the reviewed literature, they do not necessarily indicate mathematical inconsistency, since different model structures, compartment definitions, and transmission mechanisms may naturally lead to different analytical expressions. Nevertheless, dimensional consistency and biological interpretability should always be verified before comparing reproduction numbers across different studies. In particular, the next-generation matrix (NGM) approach evaluated at the disease-free equilibrium remains the most widely accepted framework for deriving $\mathcal{R}_0$, providing a standardized threshold parameter with a clear epidemiological interpretation. Therefore, future studies are encouraged to explicitly state the derivation procedure, verify dimensional consistency, and report the underlying assumptions to facilitate meaningful comparisons among fractional-order influenza models.

2.6. Stability analysis

2.6.1. Disease-free equilibrium

For the fractional avian–human influenza compartmental model considered throughout this review, the disease-free equilibrium (DFE) is given by:

$$\mathcal{E}_0 = \left(\frac{\Lambda_a}{\mu_a}, 0, 0, \frac{\Lambda_h}{\mu_h}, 0, 0, 0\right) \tag{9}$$

where Λ_a and Λ_h are the recruitment rates for avian and human populations, respectively.

Theorem 1 (Local Stability of DFE)**.** *The disease-free equilibrium $\mathcal{E}_0$ is locally asymptotically stable if $\mathcal{R}_0 < 1$, and unstable if $\mathcal{R}_0 > 1$.*

Table 2. Summary of basic reproduction numbers across reviewed fractional avian influenza models

Study	Operator(s) Compared	Model	$\mathcal{R}_0$ Expression	Key Finding
Abdoon & Alzahrani[15]	Atangana-Baleanu-Caputo, Caputo-Fabrizio, and Caputo	SEIIR-V influenza model	$\mathcal{R}_0 = \frac{\beta_3(\beta_4\beta_5+\beta_2+\beta_{11})}{(\beta_6+\beta_7+\beta_2+\beta_{10})} \times \frac{1}{(\beta_4+\beta_2+\beta_{11})} \times \frac{1}{(\beta_6+\beta_7+\beta_2)} \times \frac{1}{(\beta_8+\beta_2+\beta_{10})}$	ABC achieved the lowest error against real data; fractional models outperformed the classical model across all three operators compared.
Rezapour & Mohammadi[20]	Caputo-Fabrizio	SEIR (AH1N1)	$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\beta\,\delta\,\kappa}{m}$ ‡	Fractional order controls the numerical dynamics; the disease is controlled when $\mathcal{R}_0 < 1$.
Khan *et al.*[24]	Fractal-Fractional Atangana-Baleanu	Two-strain influenza model with resistant and non-resistant strains	Not explicitly derived.*	The paper focuses on existence, uniqueness, and Hyers-Ulam (HU) stability rather than threshold analysis; a closed-form $\mathcal{R}_0$ was not derived. Fractal-fractional orders influence the dynamics of both resistant and non-resistant influenza strains.
Ghanbari & Gomez-Aguilar[26]	Fractal-Fractional	Logistic growth, incubation period, avian model	$\mathcal{R}_0^{(1)} = \frac{\beta_a K_a}{\mu_a+\delta_a}$ $\mathcal{R}_0^{(2)} = \frac{\Lambda_a\beta_a e^{-\mu_a\tau_a}}{\mu_a(\mu_a+\delta_a)}$	Fractal-fractional operators capture memory effects, self-similarity, and complex infection dynamics.
Ye *et al.*[30]	Caputo	Avian-human with logistic growth	$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\beta_a K_a}{\mu_a^\alpha+\delta_a^\alpha}$ †	The disease-free equilibrium is stable when $\mathcal{R}_0 < 1$; the endemic equilibrium is stable when $\mathcal{R}_0 > 1$.
Asif *et al.*[33]	Atangana–Baleanu (ABC) fractional derivative	Influenza SEITR model with harmonic mean-type incidence rate and treatment class	$\mathcal{R}_0 = \frac{2\beta\delta}{(\delta+\nu)(\phi+\rho+\nu)}$	Sensitivity analysis identifies contact rate β as the dominant transmission driver (normalized sensitivity index +1), while treatment rate ϕ is the most effective control parameter (index −0.89). The ABC derivative captures memory effects and multi-wave patterns better than integer-order models. The Atangana–Toufik numerical scheme demonstrates that increasing treatment rate ω reduces the infected class and expands the recovered class.
Al-Qureshi *et al.*[34]	Atangana–Baleanu (ABC) piecewise fractional; stochastic white noise	HPAI (H5N6) avian influenza with half-saturated incidence and vaccination	Stochastic threshold: $\mathcal{R}_0^s = \frac{2\Xi}{2(\omega+\lambda)+\varphi_3^2}\left(\frac{(1-q)\vartheta_b H_\nu+(1-\phi)q\vartheta_\nu H_b}{\omega H_b H_\nu}\right)$	The piecewise ABC framework outperforms pure deterministic models in capturing crossover behaviors. If $\mathcal{R}_0^s < 1$, infection goes extinct, almost surely (a.s.); if $\mathcal{R}_0^s > 1$, an ergodic stationary distribution exists, and the disease persists. Environmental (white) noise intensity is critical: smaller noise favors persistence, while larger noise drives extinction.

(*Cont'd...*)

Table 3. (*Continued*)

Study	Operator(s) Compared	Model	$\mathcal{R}_0$ Expression	Key Finding
Yaagoub *et al.*[35]	Caputo fractional derivative D^α	Three-strain influenza (A, B, C) with treatment protocols	Strain-specific reproduction numbers: $\mathcal{R}_i = \frac{\gamma\beta_i(1-\eta_i)}{\delta(\phi_i+\delta)}$ for $i = A, B, C$; and $\mathcal{R}_0 = \max\{\mathcal{R}_A, \mathcal{R}_B, \mathcal{R}_C\}$	The disease-free equilibrium is globally asymptotically stable (GAS) when $\mathcal{R}_0 \leq 1$. Each single-strain endemic equilibrium is GAS when its $\mathcal{R}_i > 1$ and the others ≤ 1. The fractional derivative order does not alter stability but accelerates convergence to equilibrium as α decreases. Treatment parameters η_i markedly diminish the prevalence of all three strains.

Remark 2. *The proof follows from the Matignon stability criterion,*[32] *which was originally established for linear fractional differential systems and has since been widely adopted in fractional epidemic modeling:*[30]

$$|\arg(\lambda)| > \frac{\alpha\pi}{2} \tag{10}$$

This condition is verified when $\mathcal{R}_0 < 1$, confirming local asymptotic stability of $\mathcal{E}_0$.

2.6.2. Endemic equilibrium

When $\mathcal{R}_0 > 1$, a unique endemic equilibrium $\mathcal{E}^*$ exists:

$$\mathcal{E}^* = (S_a^*, E_a^*, I_a^*, S_h^*, E_h^*, I_h^*, R_h^*) \tag{11}$$

Theorem 2 (Global Stability of Endemic Equilibrium)**.** *If $\mathcal{R}_0 > 1$, the endemic equilibrium $\mathcal{E}^*$ is globally asymptotically stable.*

Remark 3. *The proof is established via a suitable Lyapunov function of the form:*

$$\mathcal{V}(t) = \sum_i c_i \left(x_i - x_i^* - x_i^* \ln \frac{x_i}{x_i^*} \right), \tag{12}$$

For $V(t)$ to be globally asymptotically stable, the following two criteria should be satisfied: (i) $V(t) \geq 0 \forall t$ and $V(t) = 0$ only at E^*; (ii) ${}^C D_t^\alpha V(t) \leq 0$ along all trajectories of the fractional system and ${}^C D_t^\alpha V(t) = 0$ only at E^*. These constraints are justified by the fractional Lyapunov stability theorem of Caputo systems; see[30] *for the full derivation.*

Recent developments in fractional calculus have considerably expanded the range of applications of fractional operators beyond epidemiological modeling. For example, the Caputo–Fabrizio fractional integral has recently been employed to establish Hermite–Hadamard type inequalities for non-convex functions, providing new theoretical contributions to fractional analysis and integral inequalities.[36] In another direction, fractional-order concepts have been applied to network science through fractional percolation on random graphs, offering novel insights into network robustness, vulnerability, and phase-transition behavior in complex systems.[37] These advances highlight the versatility of fractional operators and further motivate their application to complex biological systems, including avian influenza dynamics.

3. Fractional operators used in avian influenza

Various fractional operators have been used for avian influenza modeling, yielding different mathematical features and epidemiological interpreta-

tions. Here we recall their formal definitions and compare their kernel structures, singularity features, and applicability for capturing distinct memory regimes in epidemic systems.

Before reviewing each operator's application to avian influenza modeling, we recall their precise mathematical definitions. Let $f : [a, b] \to \mathbb{R}$ be an absolutely continuous function and $\alpha \in (0, 1]$ the fractional order.

Table 4. Recommended guidelines for deriving and reporting the basic reproduction number ($\mathcal{R}_0$) in fractional-order influenza models

Criterion	Recommendation
Derivation method	Whenever applicable, derive $\mathcal{R}_0$ using the next-generation matrix (NGM) approach to ensure consistency with the standard epidemiological framework.
Equilibrium point	Evaluate $\mathcal{R}_0$ at the disease-free equilibrium (DFE). Expressions involving endemic equilibrium variables should be clearly justified and interpreted within the context of the original model.
Dimensional consistency	Verify that all terms in the analytical expression of $\mathcal{R}_0$ are dimensionless and mathematically consistent before reporting or comparing results.
Biological interpretation	Clearly explain the epidemiological meaning of each transmission pathway contributing to $\mathcal{R}_0$ and relate the mathematical expression to the underlying disease dynamics.
Cross-study comparison	When comparing different influenza models, emphasize the epidemiological interpretation and modeling assumptions rather than relying solely on the analytical form of $\mathcal{R}_0$.
Reporting standards	Explicitly state the derivation procedure, model assumptions, parameter definitions, and validation strategy to facilitate reproducibility and meaningful comparison across studies.

2.7. Effect of fractional order on stability

A distinctive feature of fractional-order epidemic models is the dependence of convergence dynamics on the fractional order α. As $\alpha \to 1$, the fractional system recovers the classical integer-order behavior. For $\alpha < 1$, solutions exhibit the following characteristics:[15,30]

- **Sub-exponential convergence** toward equilibrium, resulting in prolonged transient phases.
- **Memory-dependent oscillations** that reflect accumulated historical exposure effects.
- **Slower epidemic peaks** with extended decay phases, more consistent with observed avian influenza outbreak patterns.[15,30]

These properties make fractional-order models particularly valuable for long-term epidemic forecasting, where classical models systematically underestimate the persistence of infection dynamics.

2.8. Caputo-based models

Ye *et al.*[30] investigated a fractional-order avian-human influenza epidemic model with logistic increase of avian population. The theoretical results are verified by numerical simulations. The authors proved the existence, uniqueness, non-negativity and positive invariance of the solutions as well as the conditions for global asymptotic stability of both the disease-free and endemic equilibrium points.

The avian-human system is formulated using Caputo fractional approach. The avian population is divided into susceptible and infected birds, while the human population is divided into susceptible, infected, and recovered humans. Avian population increase is regulated by logistic factors, while epidemiological interactions are governed by transmission, spillover, recovery, and mortality characteristics across species. Importantly, the Caputo operator induces nonlocal memory in time, allowing the model to account for lagged immunological phenomena and cumulative exposure histories that are characteristic of avian influenza spillover systems.

Building on their earlier work,[38] Ye *et al.*[30] further developed the Caputo-based fractional avian influenza framework by incorporating logistic population growth for the avian compartment. In this research, the authors proposed a fractional-order

epidemic model for avian influenza dynamics in 2019. Detailed numerical simulations were performed to verify the model against theoretical predictions. The results validated the capability of the Caputo operator to recreate the sub-exponential growth and extended decay phases typical of real avian influenza outbreaks, providing the numerical and analytical basis on which the logistic-growth extension of[30] was subsequently created.

A related Caputo-based work by González-Parra *et al.*[14] used a fractional-order SEIR-type model to simulate the epidemic of influenza A (H1N1) at the population level. The authors showed that the numerical results of the nonlinear fractional model agree closly with to the real H1N1 surveillance data by using the Grünwald-Letnikov discretization approach. Most importantly, the study revealed that the fractional order α may be tuned to precisely adjust the epidemic curve, thus capturing the sub-exponential growth and the plateau phase better than the integer-order equivalent. This study strengthens the general argument for the use of Caputo-based models in avian influenza scenarios, in particular to replicate outbreak trajectories in situations with limited data.

2.9. Caputo-Fabrizio fractional models

In a recent study,[20] the mathematical model for AH1N1/09 influenza transmission[39] was studied with the Caputo–Fabrizio fractional derivative because recent studies have shown that fractional-order derivatives are more suitable than integer-order derivatives for simulating real phenomena, including internal memory effects. In the numerical part, they obtained results using the integer derivative and compared them to study the differences between the fractional- and integer-order outcomes of the model. They calculated the reproduction number and the equilibrium points of the system and then used numerical simulation to investigate the behavior of the system around these points. Because the integer-order derivative changes only in unit steps, it does not allow analysis of the effect of small perturbations in the derivative order on model outcomes. Rezapour *et al.*[20] obtained outputs of the fractional-order model for different values of the derivative order and studied the effect of the derivative order on the results.

The Caputo-Fabrizio fractional derivative extends influenza compartmental modeling by substituting the singular power-law kernel with a nonsingular exponential memory structure. In the SEIR model, the parameters of the susceptible, exposed, infectious, and recovered classes represent transmission, incubation, and recovery parameters, and the fractional order represents the degree of the historical infection effect. This smoother memory representation enhances numerical stability and enables greater sensitivity analysis of the epidemic evolution for minor perturbations of the derivative order. Although nonsingular exponential kernels have their merits, other works pursued even richer long-memory features offered by the Mittag-Leffler-based operators.

Evirgen *et al.*[40] provided another contribution to the Caputo-Fabrizio framework. They analyzed the dynamics of influenza A by introducing varying contact rates for different population subgroups. This heterogeneous contact structure is a key enhancement over previous CF models such as[20] which assumed uniform mixing throughout the population. The assumption of varied contact rates between subgroups allows the model to better depict the heterogeneity of transmission observed in avian influenza settings, in particular, the different degrees of exposure among poultry workers, live bird market vendors, and the general human population. Under this setting, the smooth exponential memory decay of each contact pathway is determined separately by the Caputo-Fabrizio derivative, which produces richer epidemic curves than those obtained under homogeneous mixing assumptions.

2.10. Atangana-Baleanu and Mittag-Leffler Kernels

To address the criticism that the Caputo-Fabrizio kernel lacks true nonlocality, Atangana and Baleanu proposed a novel, improved formulation of a fractional derivative (see[41]) utilizing the Mittag-Leffler function as a non-local and non-singular kernel. The memory is precisely described by the Atangana-Baleanu-Caputo (ABC) fractional derivative.[42] The most notable applications of the ABC operator are found in.[43] However, crossover from conventional to sub-diffusion and crossover from stochastic process to power law can both be described by this generalized Mittag-Leffler kernel. Furthermore, a major disadvantage of such operators in these situations is that the kernel is unable to identify crossover from deterministic to stochastic settings or from stochastic to deterministic contexts.[44,45]

In the dynamics of avian influenza, the Atangana-Baleanu operator combines nonlocal dependence with a nonsingular Mittag-Leffler kernel, thus providing a fuller representation of long-term memory. This allows the model to better describe crossover epidemic phenomena, such as the transition from a fast deterministic spreading phase

to a delayed sub-diffusive persistence phase. This adaptability is particularly pertinent to highly pathogenic avian influenza systems because previous exposure patterns greatly influence delayed spillover, environmental persistence, and recurrent outbreaks. Recent work has generalized these kernels to piecewise fractional formulations, leading to more abrupt transitions between deterministic and stochastic epidemic phases.

The Atangana-Baleanu definition is among the most effective formulations of fractional derivatives for modeling real-world problem.[26] These fractional operators were defined as a convolution integral utilizing a nonsingular Mittag-Leffler kernel. This nonsingular convolution structure enables the operator to preserve the entire history of the system's state and is particularly ideal for modeling biological processes with memory that progressively accumulates over time. This is particularly relevant for epidemiological modeling since it enables the system to memorize previous infection states in a smooth and nonsingular manner, which is closer to real biological memory processes.

In another generalization of the ABC operator for influenza modeling, a study in 2025[33] incorporated a harmonic mean-type incidence rate into the Atangana-Baleanu-Caputo fractional framework. This incidence rate was shown to be more efficient than the usual bilinear or saturated incidence functions in capturing the saturation of the transmission at high prevalence. The authors calculated the disease-free and endemic equilibria and obtained the basic reproduction number. A sensitivity analysis was performed to rank the model parameters in terms of their impact on $\mathcal{R}_0$. The most sensitive parameters were found to be the transmission rate and the recovery rate, and the ABC fractional order α has a significant effect on the convergence speed toward both equilibria, in agreement with the general trend found in the studies reviewed in Section 3.1.

2.11. Fractal-fractional operators

Fractal-fractional operators are a modern generalization of the classical theory of fractional calculus, unifying fractional derivatives and fractal geometry. This hybrid formulation provides a more flexible characterization of complex systems, especially those with irregular structure and mixed temporal dynamics. In contrast to classical fractional operators based solely on memory effects, fractal-fractional models also describe spatial and structural complexity through fractal dimensions.

The fractal-fractional derivative describes the processes occurring in natural and man-made fractal systems more precisely, such as irregular growth patterns, rough surfaces, and self-similar structures. This operator has wide applications in several disciplines. In physics, it has been used to analyze diffusion in fractal media, electrical conductivity in fractal networks, and wave propagation in fractal geometries.[24] These features make fractal–fractional models particularly suitable for epidemiological systems with irregular and heterogeneous transmission patterns and population structures.

These operators are typically constructed mathematically by the convolution of generalized kernels (e.g., Mittag-Leffler, exponential, and power-law functions) with fractal derivatives,[24] which makes it possible to describe many kinds of memory and scaling characteristics in a single model. This approach is more appropriate for portraying real-world biological systems where disease transmission may be irregular and non-uniform among populations and situations.

From an epidemiological perspective, the fractal-fractional approach is particularly beneficial for modeling viral diseases such as influenza, in which contact structures, environmental exposure, and host interactions are fundamentally complex. These models are more realistic than classical integer-order and ordinary fractional models because they consider memory effects as well as structural variability.

2.12. Piecewise and stochastic fractional operators

Al-Qureshi *et al.*[34] showed that the stochastic process has a threshold value R_0^s that can be used to predict mean persistence and eradication of the virus. Moreover, they constructed a sequence of admissible Lyapunov candidates to prove that there exists an ergodic stationary distribution for the stochastic form of the system studied here for $\mathcal{R}_\prime^\int > 1$.

The inclusion of time delays in fractional operators provides an extra dimension of dynamical richness. In a 2025 study,[46] a multi-delay avian influenza model for H7N9 with incubation period, reporting delay, and fractional-order memory was constructed. The authors analyzed the Hopf bifurcation at the endemic equilibrium and demonstrated that the interplay between the delay period and fractional order α determines whether the system converges smoothly or exhibits extended oscillations around the endemic state. This bifurcation

behavior has immediate epidemiological implications for avian influenza: prolonged oscillations correlate with recurring outbreak cycles found in H7N9 surveillance data and smooth convergence to progressive endemicity. Thus, the delay-fractional model provides a more subtle explanation of outbreak recurrence than either pure delay or pure fractional models can give alone.

The idea of a piecewise differential/integral formulation was later proposed by Atangana and Seda.[47] They further extended their initial idea of simulation by proposing piecewise modeling. In this work, they provide a novel way to emulate epidemiological problems with crossover propensities, which could be the future of modeling.[20] In fact, fractional differential equations have been shown to model global events with high accuracy.[29]

In particular, for avian influenza, piecewise fractional formulations are useful for depicting abrupt shifts resulting from market closures, chicken culling campaigns, environmental disinfection, or rapid seasonal spillover episodes. Variable memory regimes between epidemic phases are more adequate for describing the true temporal heterogeneity of highly pathogenic epidemics. In addition to the design of the operator, the epidemiological realism of fractional avian influenza models is highly sensitive to the biological representation of the transmission channels.

2.13. Comparison of fractional operators

As summarized in **Table 5**, the mathematical characteristics of each fractional operator are closely related to its epidemiological behavior. Power-law kernels retain stronger historical memory, often resulting in delayed epidemic peaks and prolonged outbreak duration. In contrast, exponential kernels primarily reflect recent system states, leading to faster stabilization of epidemic dynamics. Mittag–Leffler kernels provide an intermediate memory mechanism that balances long-term memory with numerical stability, whereas fractal–fractional operators further account for multiscale transmission processes and heterogeneous disease spread. Consequently, the choice of fractional operator should be guided not only by its mathematical formulation but also by the epidemiological characteristics of the disease being modeled.

Table 5. Mathematical properties of fractional operators used in avian influenza modeling and their epidemiological implications

Operator	Kernel type	Singular	Nonlocal	Fractal dimension	Epidemiological implications
Caputo	Power-law	Yes	Yes	No	Delayed epidemic peak, prolonged outbreak duration, and strong long-memory effects.
Caputo–Fabrizio	Exponential	No	No*	No	Faster epidemic stabilization, smoother temporal evolution, and emphasis on recent system states.
Atangana–Baleanu	Mittag–Leffler	No	Yes	No	Balanced memory effects, realistic epidemic decay, and improved predictive performance.
Fractal–Fractional	Mittag–Leffler + Fractal	No	Yes	Yes	Captures multiscale transmission dynamics and heterogeneous disease spread while preserving memory effects.

The nonlocal classification of the Caputo-Fabrizio (CF) operator remains debated. Hristov *et al.*[48] have argued that because the CF kernel is an exponential function, which is a solution of a first-order ODE, the operator is effectively equivalent to a local derivative and does not possess genuine nonlocal memory in the fractional sense. This contrasts with the Atangana-Baleanu operator, whose Mittag-Leffler kernel is nonlocal by

construction. Practitioners should be aware of this distinction when selecting the CF operator for long-memory epidemic systems.

Abdoon *et al.*[15] compared the effectiveness of fractional models using Atangana-Baleanu-Caputo, Caputo-Fabrizio, and Caputo with the predictive performance of integer-order models on weekly influenza cases using data from the Kingdom of Saudi Arabia. The main originality of this work is the introduction of the Atangana-Baleanu-Caputo fractional model for influenza forecasting, which incorporates epidemic memory and leads to higher accuracy than previous models. These models effectively captured the peak and decline of influenza cases. These results suggest that fractional-order models are superior to classical integer-order models for the prediction of influenza dynamics.

Overall, the choice of a fractional operator considerably affects the depiction of memory effects and the consequent epidemic dynamics, stimulating further study of physiologically plausible transmission mechanisms (**Figure 2**).

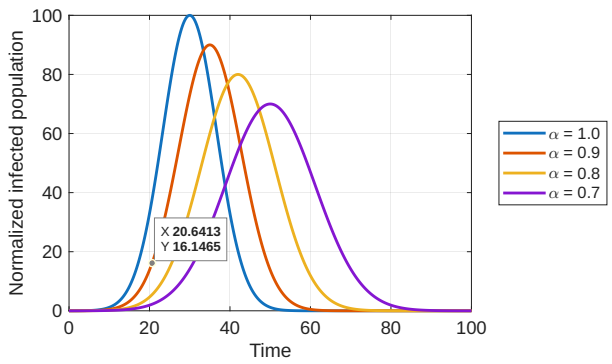


Figure 2. Illustrative effect of different fractional orders on epidemic dynamics. As the fractional order decreases, the epidemic peak is delayed, the outbreak duration is prolonged, and the decay phase becomes slower due to the long-memory characteristics of fractional-order models.

3. Memory-driven transmission dynamics

The mathematical features of fractional operators are well known, but the epidemiological relevance is in the representation of actual biological transmission pathways. This section considers three related routes by which memory effects alter avian influenza dynamics: cross-species spillover, behavioral modulation, and environmental persistence.

3.1. Cross-species spillover dynamics

The Caputo-based avian–human influenza model bifurcates the system into infected and noninfected bird populations and susceptible, infected, and recovered human populations. This structure allows the model to capture transmission among bird reservoirs and zoonotic spillover into the human population. The model also takes into account the course of human illnesses through recovery and disease-induced mortality processes, in addition to direct transmission between birds.[30] The avian component also models biologically accurate population management, allowing the system to simulate sustained avian reservoir dynamics and the eventual impact on human epidemics. The compartmental approach, in general, provides a physiologically valid basis to study cross-species avian influenza transmission under memory-dependent dynamics.

Ebrahimzadeh[17] formulated a general fractional-order avian-human influenza model simultaneously including environmental transmission, nonlinear behavior-driven incidence functions, and two interacting virus strains. Most existing models mainly take into account one or two of these mechanisms. Futhermore, Ebrahimzadeh[17] developed a unified mathematical framework that embraces all the relevant epidemiological components. Moreover, the adoption of Caputo-type fractional derivatives allows the model to consider memory-dependent biological phenomena, which are usually disregarded in standard integer-order models, such as delayed recovery, persistence of virus in the environment, and past exposure. This novel combination fills a major gap in the literature on modeling influenza and provides a more practical basis for evaluating the dynamics of zoonotic transmission and developing optimal control methods.

The transmission mechanism of avian influenza is zoonotic in nature and explicitly links infected bird reservoirs and human infections through repeated exposure pathways. These spillover processes are particularly pertinent to live poultry markets, poultry farms, and bird-handling environments where regular interaction with diseased birds greatly increases the likelihood of cross-species transmission. From a fractional modeling viewpoint, the inclusion of memory effects in this route is particularly essential since the risk of human infection is generally driven by cumulative exposure histories rather than discrete contacts.

A fractional zoonotic model[49] in 2025 further develops this cross-species concept with three new strategies on the animal side to control the disease: sterilization of animal reservoirs, restriction of access to food to reduce animal congregation, and reduction of the frequency of human-animal interaction, in addition to the standard ABC fractional derivative. Existence and uniqueness are

proved through stability analysis using the Banach fixed-point theorem and the Picard iterative method, and robustness against small perturbations is ensured by the Hyers-Ulam stability. In the live poultry market context, where the main drivers of zoonotic spillover risk are animal density and frequent human-animal interaction, sterilization and congregation-restriction regulations are particularly essential from an avian influenza perspective.

3.2. Memory-dependent transmission modulation

The model in[17] contains a nonlinear behavioral response mechanism to incorporate psychological adaptation and awareness in the human population, following the approach of fear-effect incidence functions discussed in.[18] Effective contact rates drop dynamically with increasing infection frequency through the reflection of defensive reactions such as social distancing, improved hygiene, and reduced exposure, thereby bridging epidemiological dynamics with human perception and decision-making.

The mechanism is particularly significant for fractional avian influenza models since the transmission intensity is rarely controlled solely by the existing infection levels. In contrast, contact behavior in poultry farms and live bird markets is highly influenced by cumulative exposure history, delayed awareness, and increasing adaptation to risk. Fractional memory operators intrinsically account for this progressive modulation, resulting in more realistic epidemic waves with deferred peaks and protracted decay periods. Memory-shaped contact behavior is not the only mechanism sustaining delayed spillover waves. Several studies point to the importance of environmental reservoirs and persistent exposure pathways.

3.3. Environmental and behavioral persistence

In natural ecosystems, the spread of the disease is aided by local wild birds, and the spread of infection is mostly driven by migrating birds.[8] The virus can also be transmitted to local hens via ingestion of infected feces, which promotes the transmission of the disease via the oral route.[50] Three epidemiologically distinct compartments each contribute to disease transmission: humans, poultry, and contaminated environments.

Environmental persistence is a major factor in delayed outbreak recurrence in avian influenza systems. Secondary waves of infection may be sustained by the persistence of the virus in poultry waste, contaminated farm surfaces, and market environments, even when the primary avian outbreak appears to be contained. These environmental reservoirs, along with the lagged human behavioral relaxation observed after periods of heightened awareness, provide long-memory feedback loops that are easily captured by fractional operators. This makes fractional models particularly useful for explaining extended zoonotic risk and recurring spillover events.

Zahra *et al.*[51] presented a new approach to extend this environmental persistence theme, in which ambient air pollution is explicitly treated as a long-memory environmental driver in a fractional SEIIHRD framework using the ABC derivative. This formulation allows the memory kernel of the ABC operator to capture the persistent impacts of chronic exposure to pollution on immunosuppression and inflammation in human respiratory susceptibility, thus offering a biological explanation for high influenza transmission during the period of high pollution. The model differentiates between moderate and severe infections, resulting in a more realistic depiction of the healthcare burden. Numerical simulations demonstrate that a reduction in the fractional order α extends the duration of outbreaks by prolonging the sub-exponential decay phase and has direct implications for the design of sustained public health interventions in industrialized or high-pollution zoonotic risk zones.

4. Data-driven and farm-level dynamics

The practical value of fractional epidemic models lies in their ability to reproduce real outbreak patterns. This section discusses studies developing fractional avian influenza models using empirical data, including farm-level calibration, seasonal transmission patterns, and the numerical methods employed for parameter estimation and model validation.

4.1. Farm-level fractional dynamics

Abdoon *et al.*[15] showed the significance of incorporating real epidemiological data into fractional models to improve forecast accuracy. Calibration of models using weekly infection data allows for the description of the real course of outbreaks and the evaluation of the efficacy of competing modeling approaches. These data-driven frameworks enable more reliable analysis of the disease dynamics and provide a realistic basis for evaluating the effectiveness of the model in real-world scenarios.

Real farm data from Bangladesh are used to fit the model, and corresponding parameter values

are determined. Graphical results are provided by the authors to show that the disease can be eradicated for different model parameter values. They proved that the disease can be treated by combining medication and vaccination, utilizing real farm data, and assuming a vaccine efficacy of 80%.[19]

Farm-level fractional models provide a biologically rich description of avian influenza epidemics, differentiating between the progression of illness within a flock, asymptomatic transmission, the response to therapy, and the dynamics of recovery. The main benefit of these is the direct use of actual poultry surveillance data that allows for model calibration at the scale of actual transmission. This precision is critical for understanding persistent farm reservoirs, delayed reinfection, and cumulative memory effects that occur with repeated seasonal exposure.

4.2. Seasonal and real-data memory patterns

Avian influenza (AI) is a viral infectious disease that primarily affects birds but can occasionally infect humans, as documented in outbreak reports from East China.[52] Migrating birds are crucial to the spread of the infection,[8] and local wild birds contributed to the spread of the disease within their native environment. The disease can also be transmitted by the oral-fecal route if local birds ingest contaminated excrement.[50] As introduced in Section 1.1, the distinction between LPAI and HPAI subtypes is epidemiologically significant for seasonal modeling, since HPAI viruses generate sharper and higher epidemic peaks with faster mortality dynamics.

The fractional-order models have been more effective in reproducing the real influenza outbreak patterns, notably in capturing the time and amplitude of epidemic peaks.[15] The memory effects in these models enable them to capture delayed transmission responses and accumulated exposures, thereby more realistically modeling the growth and decay stages of infection curves. Thus, fractional approaches are very beneficial the research on seasonal outbreaks and the characterization of recurrent epidemics.

These findings were supported by a recent study[53] that validated a seasonal fractional SVEIHR model (susceptible, vaccinated, exposed, infected, hospitalized, and recovered) using real influenza surveillance data from the Ministry of Health of the Kingdom of Saudi Arabia for 2021. When the Caputo fractional operator was included in the model formulation, a better fit to the measured seasonal peaks was obtained compared to the corresponding integer-order model, and the fractional order α was seen to act as a fine-tuning parameter for the memory strength of the seasonal transmission cycle. This conclusion provides direct support for the claim made in Section 3.1 about the systematic outperformance of fractional models over classical formulations in generating delayed and asymmetric epidemic curves observed in real surveillance datasets.

Xing *et al.*[54] used real data to build a dynamical model and found that seasonal temperature changes played a significant role in the transmission of avian influenza. Wild bird migration is an important factor in seasonal fluctuations that play a role in the transmission of AI in chickens. A mathematical model, fed with real data collected over time from infected farms, reflects the seasonal patterns of AI, showing annual, semiannual, or both patterns. Based on the annual peak in their 12-month data, the researchers concluded that the AI dynamics under annual seasonality posed a considerable risk of spilling over to other species. The authors analyzed the seasonal trend of AI to identify the high-risk periods. The risk is high and seasonal. It lasts for four months, from November to February, and peaks in January.

Numerical simulations show a good correlation between the obtained results and the predicted results. Ghanbari *et al.*[26] studied the numerical solutions of different fractional and fractal-fractional avian influenza epidemic models using the trapezoidal product-integration rule and Lagrange interpolations. The present work is devoted to the analysis of logistic growth models with fractional derivatives of Liouville-Caputo and Atangana-Baleanu type that describe the incubation times. They studied the existence and uniqueness of solutions. They carried out several numerical simulations to show the effectiveness and reliability of these methods for simulating fractional differential equations. This underlines the relevance of robust numerical implementations when applying fractional models to real epidemiological systems, in particular for estimating memory effects and parameter sensitivity.

Seasonal forcing adds further memory to the dynamics of avian influenza, linking present outbreaks to past patterns of climate and husbandry. Fractional-order formulations are particularly well suited to describing these delayed seasonal recurrences because of their intrinsic long-memory dependence over several cycles of transmission. This facilitates the analysis of persistence patterns,

farm-level reinfection, and repeated winter peaks in poultry surveillance datasets.

4.3. Numerical schemes and parameter sensitivity

The selection of a numerical scheme is of crucial importance for the accuracy of fractional epidemic models since typical integer-order solvers cannot simply be applied to nonlocal fractional operators. The studies examined used several discretization methods, with different trade-offs between accuracy, stability, and computational cost.

The authors calculated the fractional derivatives of the model using the Grünwald–Letnikov technique and the Caputo operator. From their analysis, they concluded that the nonlinear fractional-order epidemic model is suitable for generating numerical results that agree well with real data on influenza A (H1N1) at the population level.[14]

The choice of numerical approximation strongly influences on the interpretation of fractional avian influenza dynamics, especially when the order of the derivative and the memory strength are derived from real data. Robust parameter sensitivity analysis can be achieved using Grünwald–Letnikov discretization, L1 schemes, and forward–backward sweep techniques while preserving biologically relevant temporal memory. Such methods are crucial for translating fractional epidemic theory into realistic outbreak forecasts and control strategies. Moreover, recent studies have demonstrated the usefulness of new numerical methods for solving fractional and fractal-fractional models. Interpolation-based approaches, such as Lagrange polynomial schemes,[24] have been effectively applied to ensure stability and accuracy in the simulation of nonlocal epidemic systems.

In a recent study,[15] fractional epidemic models are generally evaluated using quantitative error measures such as the root mean square error (RMSE) and the mean absolute error (MAE). These measures offer a systematic approach to evaluating how accurately the model's predictions match real data. Empirical results show that fractional-order models consistently yield lower error values than classical ones, confirming their higher predictive power. In particular, models based on the Atangana–Baleanu operator have been shown to generate the most accurate results among the investigated approaches.

Table 6 summarizes the principal validation strategies and predictive performances reported in representative fractional-order influenza studies. Although different datasets and evaluation methodologies were employed, including RMSE, MAE, numerical analysis, and real-data fitting, these studies demonstrate that fractional-order formulations can provide a flexible framework for describing epidemic dynamics by incorporating memory effects. In studies involving real epidemiological data, fractional models often showed improved agreement with observations compared with their corresponding integer-order counterparts.

Although the reviewed studies demonstrate the potential of fractional-order models to reproduce observed epidemic dynamics, several important challenges remain in data-driven modeling. In particular, parameter identifiability should be carefully assessed, since different parameter combinations may produce similar epidemic trajectories, thereby reducing the uniqueness and reliability of the estimated models. Moreover, epidemiological surveillance data are frequently affected by measurement errors, underreporting, reporting delays, and random fluctuations, making robustness to noisy data an essential consideration during model calibration. Consequently, sensitivity analysis, uncertainty quantification, and identifiability assessment should accompany parameter estimation procedures to improve model validation, enhance predictive reliability, and facilitate meaningful comparisons among different fractional-order formulations.

Among the 16 papers analyzed in **Table 7**, the most frequently selected fractional operators were the Caputo derivative (7 studies), Atangana–Baleanu derivatives (3 studies), Caputo–Fabrizio derivatives (2 studies), and fractal–fractional formulations (2 studies). One study evaluated multiple operators (Caputo, Caputo–Fabrizio, and Atangana–Baleanu); one used a piecewise stochastic Atangana–Baleanu formulation; and one did not specify the fractional operator. In terms of application domain, the majority of the studies focused on influenza or avian influenza transmission, with only one addressing a generic zoonotic disease framework. Moreover, only 4 studies (25%) tested their models against real epidemiological or surveillance data, while the remaining studies were mainly theoretical or numerical. These results suggest that the Caputo derivative is still the preferred choice for fractional influenza modeling and that data-driven model calibration is relatively rare.

Table 6. Comparative summary of representative fractional-order influenza models discussed in this review

Reference	Fractional Operator	Validation	Key Outcome
González-Parra *et al.*[14]	Caputo	Real outbreak data	Fractional dynamics improved the agreement with influenza outbreak observations compared with the classical model.
Abdoon and Alzahrani[15]	Caputo, CF, ABC	RMSE, MAE	The ABC operator showed superior fitting accuracy among the investigated fractional operators.
Khan *et al.*[19]	Caputo	Data-driven analysis	The model provided existence and stability results and was calibrated using poultry farm data.
Ghanbari and Gómez–Aguilar[26]	Fractal–Fractional	Numerical analysis	The fractal–fractional framework incorporated memory effects through power and Mittag–Leffler kernels.
Ye *et al.*[30]	Caputo	Dynamic analysis	Fractional dynamics incorporated memory effects and influenced epidemic evolution.
Alsubaie *et al.*[53]	Caputo	Real surveillance data (Saudi MOH, 2021), seasonal model fit	The Caputo operator gave a better fit to measured seasonal peaks than the integer-order model; the fractional order α acted as a fine-tuning parameter for the memory strength of the seasonal transmission cycle.

Table 7. Classification of the reviewed corpus of 16 studies by fractional operator, epidemiological domain, and use of real data

Reference	Operator	Domain	Real data
González-Parra *et al.*[14]	Caputo	Influenza (H1N1)	Yes
Abdoon and Alzahrani[15]	Caputo, CF, ABC (comparison)	Influenza	Yes
Ebrahimzadeh[17]	Caputo	Avian-human influenza	No
Khan *et al.*[19]	Caputo	Avian influenza (poultry)	Yes
Rezapour and Mohammadi[20]	Caputo–Fabrizio	Influenza (AH1N1/09)	No
Khan *et al.*[24]	Fractal–Fractional (ABC-kernel)	Influenza (two-strain)	No
Ghanbari and Gómez–Aguilar[26]	Fractal–Fractional	Avian influenza	No
Ye, Lin and Xu[30]	Caputo	Avian-human influenza	No
Ye and Xu[38]	Caputo	Avian influenza	No
Evirgen *et al.*[40]	Caputo–Fabrizio	Influenza A	No
Asif *et al.*[33]	Atangana–Baleanu	Influenza	No
Al-Qureshi *et al.*[34]	Piecewise/stochastic (ABC)	Avian influenza (HPAI)	No
Althubyani *et al.*[49]	Atangana–Baleanu	Zoonotic (general)	No
Zahra, Li and Al-Ahmari[51]	Atangana–Baleanu	Influenza	No
Alsubaie *et al.*[53]	Caputo	Influenza (seasonal)	Yes
Yaagoub, Farah and Ahmad (2025)[35]	Caputo	Influenza (three-strain)	No

5. Control perspectives and One Health strategies

To bring fractional epidemic models into workable public health policies, frameworks that embed memory-dependent intervention dynamics are required. In this section, we discuss fractional optimal control formulations, the One Health paradigm as an integrated intervention framework, and important research gaps that still need to be addressed in future work.

5.1. Fractional optimal control insights

The five time-dependent management measures considered are vaccination, treatment for both human strains, culling of infected birds, environmental decontamination, and public awareness campaigns. Ebrahimzadeh[17] developed an optimal control framework with a cost functional that minimizes both financial and health expenses. A more realistic representation of intervention timing is obtained using fractional optimal control frameworks, as the effectiveness of immunization, treatment, culling, and awareness campaigns depends significantly on delayed biological and behavioral reactions. Memory-aware control strategies are particularly useful for long-lasting zoonotic outbreaks.

The fractional optimal control problem is formally governed by the Pontryagin Maximum Principle generalized for fractional order systems. The corresponding optimality conditions give rise to a system of fractional adjoint equations that must be solved together with the state equations, usually using forward-backward sweep numerical methods. The fractional order α directly enters into the adjoint system so that the optimal control trajectories are themselves memory-dependent, a feature absent from classical integer-order control formulations and one that is especially relevant for interventions such as vaccination campaigns, where the timing and cumulative coverage history both affect effectiveness.

The optimal management of H7N9 avian influenza with numerous time delays is studied in.[46] They impose control measures such as stopping live bird market activities, killing sick poultry, and isolating humans. The research shows that delay-aware control should be launched earlier than conventional fractional optimal control, because the system response to the intervention is also susceptible to the incubation and reporting lags of the delay structure.

For example, the sensitivity of optimal control trajectories to the memory strength is demonstrated in,[51] where applying fractional optimal control to an ABC influenza model with environmental contamination shows that the intervention durations must be significantly extended for smaller fractional orders. This result carries an important practical message: public health planners designing vaccination or culling campaigns for avian influenza should take into account the historical memory of previous outbreaks when deciding the intervention timelines, since memory-weak systems $\alpha \to 1$ may significantly underestimate the required duration of sustained control.

5.2. One Health intervention perspective

Three epidemiologically distinct compartments contributing to disease spread were added: humans, poultry, and a contaminated environment. One of the main advantages of contemporary fractional avian influenza models is their compatibility with the One Health paradigm, where birds, humans, and contaminated environments are considered dynamically connected reservoirs. Such a holistic view is essential for formulating viable intervention techniques beyond host-only control.

The One Health framework, acknowledged explicitly by the WHO, FAO, and OIE as a tripartite approach to managing zoonotic diseases, provides the conceptual basis for combining avian, human, and environmental surveillance into a single intervention plan.[55] The One Health control philosophy is operationalized on the animal side in,[49] where the fractional ABC framework is utilized to analyze interventions targeting the animal reservoir directly rather than the human population alone. This animal-reservoir-first approach is consistent with the One Health tripartite paradigm[55] and shows that fractional memory operators can quantify the delayed effectiveness of animal-side interventions on downstream human infection rates—a modeling capability that is absent from classical integer-order One Health frameworks.

5.3. Research gaps and future control directions

A fundamental limitation of the current literature is the lack of defined criteria to select the most appropriate fractional operator for specific avian influenza contexts. Few studies systematically analyze the predictive performance of the Caputo, Caputo–Fabrizio, Atangana–Baleanu, and piecewise stochastic operators using shared outbreak datasets, yet all of them provide effective memory representations.

A related methodological gap concerns dimensional consistency in fractional $\mathcal{R}_0$ expressions: when fractional powers appear in demographic

parameters, the resulting threshold quantity may lack a clear epidemiological unit interpretation.[31] Establishing standardized derivation conventions for $\mathcal{R}_0$ in fractional systems remains an open problem.

Furthermore, to enhance the predictive responsiveness and mathematical robustness of future avian influenza models, researchers should leverage recent methodological breakthroughs across various fractional-order epidemiological and sociobiological systems. For instance, advanced parameter identification and optimal control techniques developed for Caputo fractional diabetes frameworks[56] offer a solid template for optimizing intervention costs under high parameter uncertainty.

Similarly, the successful deployment of fractal-fractional derivatives calibrated with real-world clinical data in tuberculosis transmission dynamics[57] provides an invaluable computational road map for modeling the structural heterogeneity and seasonal variability of avian influenza strains.

Additionally, innovative investigations into biological and behavioral systems—such as tumor dynamics under the Caputo operator,[58] alcoholism models subject to demographic variations via nonsingular kernel derivatives,[59] and social behavioral adaptations like giving up smoking within nonsingular frameworks[60]—demonstrate the immense versatility of non-singular and non-local memories. Incorporating these cross-disciplinary innovations into future avian influenza research will significantly improve the characterization of complex crossover phenomena, localized cross-species spillover, and the dynamic relaxation of human risk awareness following major epidemic waves.

Future control-oriented research should extend to adaptive policies based on environmental contamination indicators, real-time poultry surveillance, and changing human behavior, in addition to deterministic intervention schedules. Such memory-aware techniques are anticipated to better manage re-emerging farm-associated outbreaks and delayed spillover waves. Another interesting direction is to merge fractional epidemic models with machine learning, Bayesian inference, and physics-informed neural networks. This allows us to immediately estimate quantities such as the derivative order, hidden memory kernels, and time-varying control parameters from acquired data.[15] Such hybrid frameworks could be very helpful in enhancing epidemic forecasting and intervention optimization, particularly in complex settings where diseases are spread from animals to people. Such hybrid approaches represent a promising frontier for improving the real-time responsiveness and predictive accuracy of fractional epidemic frameworks in zoonotic disease management.

Another active frontier is multi-strain fractional modeling. Recently,[35] a five-compartment fractional order model for a three-strain influenza outbreak with a treatment strategy for each strain was suggested. Using the next-generation matrix approach, separate basic reproduction numbers $\mathcal{R}_A, \mathcal{R}_B$, and $\mathcal{R}_C$ are obtained. Four equilibrium points are identified, and their stability is investigated. A major unresolved problem for future fractional modeling work will be to extend this three-strain framework to avian influenza scenarios where co-circulating LPAI and HPAI strains, together with possible mutant variations, may interact simultaneously.

Recent studies have further demonstrated that fractional order epidemic models apply to a wide range of infectious diseases. For instance, Dharmalingam *et al.*[61] analyzed a fractional Zika virus model using semi-analytical techniques and investigated effective intervention strategies. Their results reinforce the versatility of fractional-order formulations and illustrate that the mathematical methodologies discussed in this review are not limited to avian influenza but can be successfully extended to other epidemiological systems.

Finally, a methodological gap that pervades all the reviewed models is the limited use of global sensitivity analysis techniques such as the Partial Rank Correlation Coefficient (PRCC) method.[62] Most of the reviewed studies only report local sensitivity of $\mathcal{R}_0$ to individual parameters. The incorporation of PRCC-based global sensitivity analysis into fractional models of avian influenza would enable researchers to identify parameters with global impact on epidemic outcomes under uncertainty, providing more robust guidance for targeted interventions and allocation of surveillance resources. We see a partial realization of this strategy in,[33] where sensitivity analysis of the basic reproduction number under the ABC operator reveals the relative importance of transmission and recovery parameters, offering an initial template for PRCC-style ranking in fractional influenza models.

6. Conclusion

This paper provides a detailed analysis of fractional calculus frameworks in the mathematical modeling of avian influenza, with specific attention to transmission dynamics, memory-dependent behavior, and intervention approaches. The synthesis of evidence from 16 analyzed studies yields the following unified findings.

Avian influenza outbreaks have complex temporal dynamics, and fractional-order models are more suitable than integer-order models. Fractional models, employing nonlocal memory operators, are able to capture sub-exponential epidemic growth, longer transient phases, and delayed peak timing, which are regularly missed by classical integer-order models.[15,30]

Fractional operators have clear biological interpretations: the Caputo derivative is characterized by a power-law kernel, which reflects the long-range temporal dependence; the Caputo-Fabrizio operator has an exponential kernel, which corresponds to a slower decay of memory; and the Atangana-Baleanu operator has a Mittag-Leffler kernel, which enables crossover dynamics between epidemic phases of deterministic and sub-diffusive types.[22,26] Fractal-fractional formulations offer more flexibility, as they allow for the simultaneous capture of memory effects and structural heterogeneity through the fractal dimension parameter, making them suitable for modeling irregular population contact structures and heterogeneous environmental exposure.[24]

The data-driven evidence consistently supports the superiority of fractional frameworks over classical models. Models based on the Atangana-Baleanu-Caputo operator have the lowest RMSE and MAE values for real influenza surveillance data, demonstrating their higher prediction accuracy compared to the Caputo and Caputo-Fabrizio alternatives.[15] Fractional models fitted to real poultry monitoring data from Bangladesh show that disease eradication is possible under realistic vaccination scenarios at the farm level. An 80% vaccine effectiveness is adequate to reduce $\mathcal{R}_0$ below unity.[19] Seasonal forcing studies also indicate a persistent high-risk transmission window from November to February, with January having the largest spillover risk, emphasizing the need for memory-aware scheduling of seasonal interventions.[54] Reliable outbreak forecasts from fractional epidemic theory rely on robust numerical methods such as the Grünwald–Letnikov discretization, L1 methods, and Lagrange polynomial interpolation.[14,26]

Fractional optimal control models provided a more realistic description of intervention dynamics by naturally incorporating delays in biological and behavioral reactions into the control model. The optimality conditions, obtained by means of the Pontryagin Maximum Principle extended to fractional-order systems, give rise to memory-dependent adjoint equations whose solutions include the accumulated history of previous interventions, which is not the case in classical integer-order control problems. The One Health paradigm,[55] where avian, human, and environmental compartments are considered as dynamically connected reservoirs, provides the most comprehensive basis for the design of memory-aware zoonotic disease control methods.[17]

Despite these achievements, there are a number of critical research gaps. First, there is a need for systematic comparative research with shared outbreak records, as there are no standard criteria for identifying the most suitable fractional operator for a given avian influenza environment. Second, thedimensional consistency of $\mathcal{R}_0$ expressions under fractional equilibrium conditions, where demographic parameters may have fractional exponents, requires a formal resolution.[31] Third, the application of global sensitivity analysis approaches, such as the Partial Rank Correlation Coefficient (PRCC) approach,[62] is still limited in fractional epidemic models, which limits us the ranking of factors according to their impact on outbreak dynamics. Finally, the integration of fractional epidemic models with machine learning, Bayesian inference, and physics-informed neural networks is a promising direction for real-time parameter estimation, adaptive forecasting, and intervention optimization in complex zoonotic contexts.[15]

In conclusion, fractional calculus has become an invaluable tool for constructing realistic and biologically interpretable models of avian influenza dynamics. The combination of fractional frameworks with machine learning, real-time surveillance data, and adaptive control theory offers enormous potential for improving epidemic prediction and intervention design against the ongoing dangers of zoonotic influenza.

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Author contributions

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Availability of data

No datasets were generated or analyzed during the current study. All results are based on theoretical analysis and numerical simulations. The MATLAB codes used to generate the numerical results are available from the corresponding author upon reasonable request.

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