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Article

Agent-Based Modeling Applications in Agricultural Ecosystems: A concise Review

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Abstract: Agent-based modeling (ABM) is a versatile and important tool for exploring the complexity of agricultural ecosystems. By representing heterogeneous agents such as pests, pollinators, plants, and farmers and their localized interactions, ABMs provide insights into emergent patterns that shape crop productivity and ecosystem services. This concise review highlights major applications of ABMs in agricultural ecosystems, including pest and disease spread, pollination dynamics, vegetation succession, nutrient cycling, and farmer decision-making. Together, these cases demonstrate how ABMs can link micro-level behaviors with system-level outcomes, offering both theoretical understanding and practical management guidance for agroecosystems.

Keywords: Agent-based modeling; Agricultural ecosystems; Pest and disease spread; Pollination

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1. Introduction

Agricultural ecosystems are coupled socio ecological systems in which biological processes and human decisions interact across spatial and temporal scales [21]. Agent based modeling (ABM) has emerged as a powerful approach for representing heterogeneous actors such as pests, pollinators, plants, and farmers and their interactions [1], thereby linking micro level behaviors to emergent, system level dynamics [2].

Relative to statistical or machine learning approaches, ABM offers mechanistic interpretability and natural support for "what if" experimental exploration [22]. In recent years, agricultural ABMs have matured from conceptual prototypes into decision support tools, increasingly reported under standard protocols (e.g., ODD) to enhance transparency and reproducibility [23].

Building on this progress, the present concise review synthesizes key ABM applications in agriculture, with emphasis on i) pest and disease spread, ii) pollination dynamics, iii) vegetation succession, iv) nutrient cycling, and v) farmer decision making. Across these domains, common modeling patterns include spatially explicit landscapes, multi-component sub-models, and scenario analysis that connects process understanding with management insights.

2. Pest and Disease Spread Modeling

ABM is well-suited to capture the complexity of pest and disease dynamics in agroecosystems, which often involve both biological processes and human management. Compared to statistical learning and machine learning methods, ABM offers better interpretability and visualization capabilities.

In 2011, Rebaudo et al. developed an ABM to simulate the spread of an invasive potato pest in Ecuador by combining an ecological sub-model of pest population growth with a social sub-model of farmer behavior [3]. This integrated model allowed examination of how farmers' movements and pest control knowledge influence the regional invasion speed, as shown in Figure 1. The results showed that farmers' long-distance transport

of infested plant material significantly affects pest spread, underscoring the importance of human behavior in epidemiology.

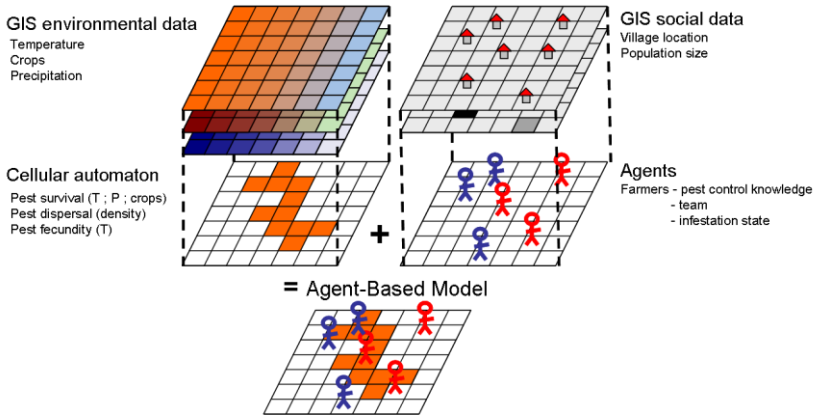

Figure 1. Schematic representation of the model structure

In 2012, Atallah et al. developed a spatially explicit ABM of grapevine leafroll disease that integrates a cellular automaton to represent within-row and across-row transmission [13]. By modeling heterogeneous vines with age-dependent latency and infection stages, the study tested alternative roguing-and-replanting rules, as shown in Figure 2. This work illustrates how ABMs can link epidemiological dynamics with economic outcomes to identify cost-effective disease control strategies.

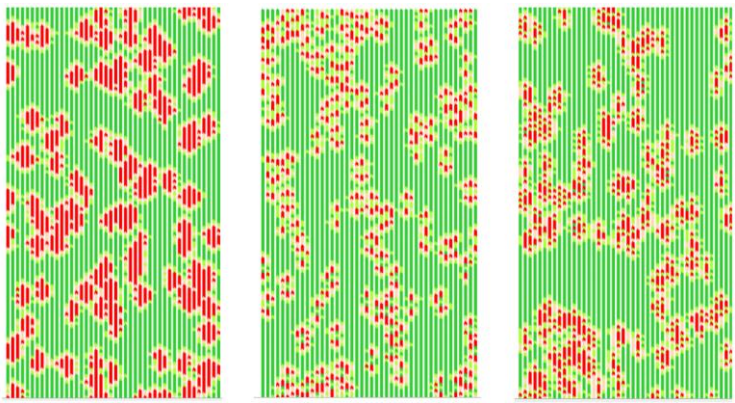

Figure 2. Realizations of the spatial disease diffusion

In 2015, Rebaudo *et al.* developed an agent-based model to investigate how climatic and economic variability shape farmers' adaptive management in pest control [15], as shown in Figure 3. Using field data from the Ecuadorian Andes, they simulated heterogeneous farmers managing the invasive potato tuber moth under scenarios of fluctuating temperature and crop prices. The model incorporated a landscape, pest, economic, and human submodel, with farmer behaviors parameterized by observed typologies ranging from risk-averse to experimenters.

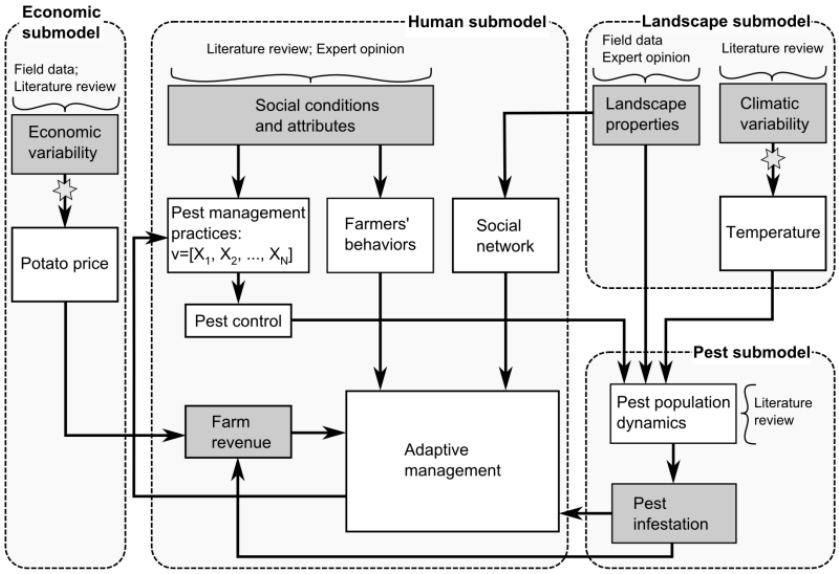

Figure 3. The underlying model is composed of a network of interacting farmers who are capable of learning and adapting to circumstances.

In 2020, Bernoff *et al.* developed a dual framework combining an ABM with partial differential equations to explain the characteristic "dense front with exponentially decaying tail" observed in hopper bands of the Australian plague locust [14]. Their models assume that individual transitions between moving and stationary states depend on local vegetation resources, with stationary locusts feeding and thereby depleting resources, as shown in Figure 4.

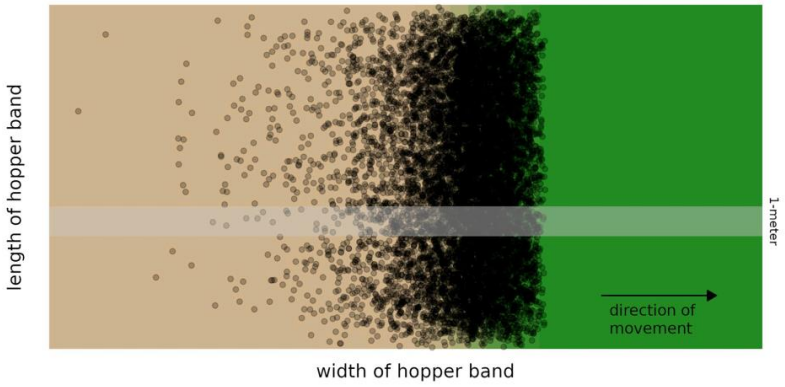

Figure 4. Schematic of a traveling pulse of locusts

3. Pollination Dynamics Modeling

Pollination services in agriculture involve complex interactions between plants, pollinators, and the environment, making them well suited for agent-based modeling. ABMs have been used to explore various facets of pollination [4], including pollinator foraging behavior, plant-pollinator spatial arrangement, and environmental effects on pollination success.

In 2018, Everaars *et al.* [12] developed SOLBEE, an individual-based, spatially explicit model of solitary bees operating on a 1-km² grid landscape, as shown in Figure 5. The model links body size allometrically to foraging traits and simulates a five-stage foraging cycle (forage, move, explore, return, unload). Across 12,000 simulations, results showed that traits dominated: body size largely determined flower-visit rates, while nesting preference governed landscape coverage and foraging distance. Importantly, a simple

proxy—the ratio of nest to foraging habitat—outperformed fragmentation in predicting fitness and pollination outcomes, with visitation saturating near 0.2.

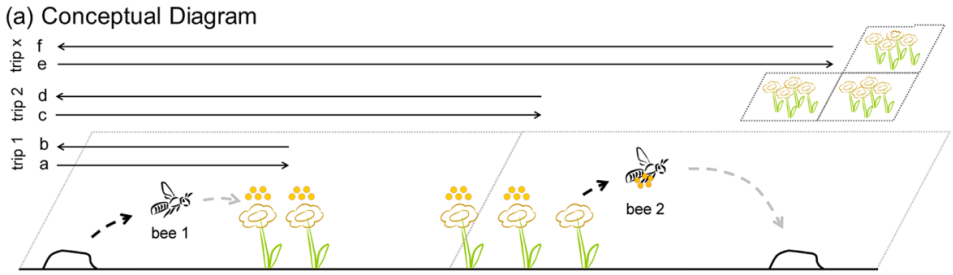

Figure 5. Conceptual diagram, illustrating how landscape grid cells with flowers are used.

In 2018, Qu *et al.* developed an ABM [4] for wild blueberry fields composed of genetically distinct clones pollinated by diverse insects. The model included honeybees, bumble bees, and solitary bees with species-specific foraging traits to assess how pollinator composition and behavior influence fruit set, as shown in Figure 6. Because blueberries are largely self-sterile, the simulation emphasized cross-clone visits across a heterogeneous landscape. By varying clone patch size, pollinator densities, and weather, the authors showed how ABM can reveal optimal species mixes and field arrangements to maximize yield—insights difficult to obtain from field trials alone.

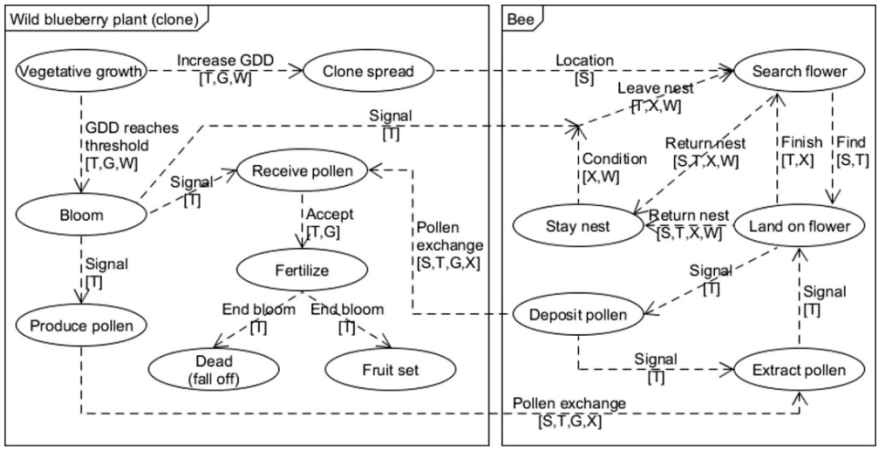

Figure 6. Conceptual model of wild blueberry cross-pollination composed of key ecological processes

In 2023, Cao *et al.* developed a spatially explicit Strawberry Pollination Simulation Model (SPSM) on the GAMA platform, representing honeybees as foraging agents and each strawberry flower as a receptive entity in a bounded greenhouse layout. This paper [5] used SPSM to test bee density and hive distribution, tracking every bee, flower, pollen grain, and fruit, as shown in Figure 7. Results showed a saturation beyond ~1 bee per plant, and that more even hive placement improves fruit quality and overall pollination efficiency. Continuous bee activity also mitigates stigma receptivity constraints, helping explain why bee pollination outperforms manual pollination.

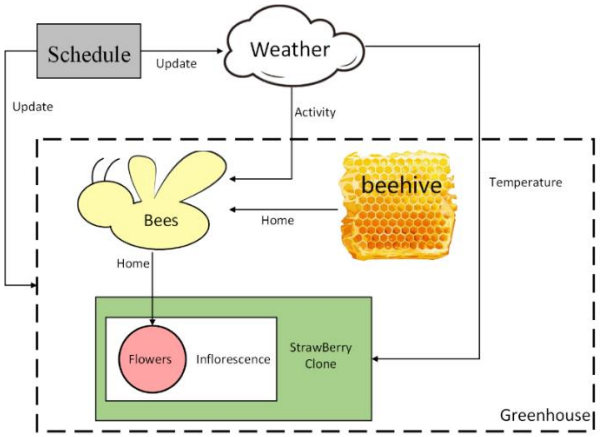

Figure 7. Entities and their interactions for strawberry pollination

Building on the same SPSM framework, Cao *et al.* [6,7] extended the model with a state machine representation of bee flight and multiple cultivars, to evaluate field design (i.e.interplanting) and staggered planting strategies in 2024, as shown in Figure 8. Simulations favored alternating rows of different cultivars within the same bed to enhance cross-pollination, and suggested staggering planting by ~5 days to reduce peak bloom competition for bee visits and increase average berry weight.

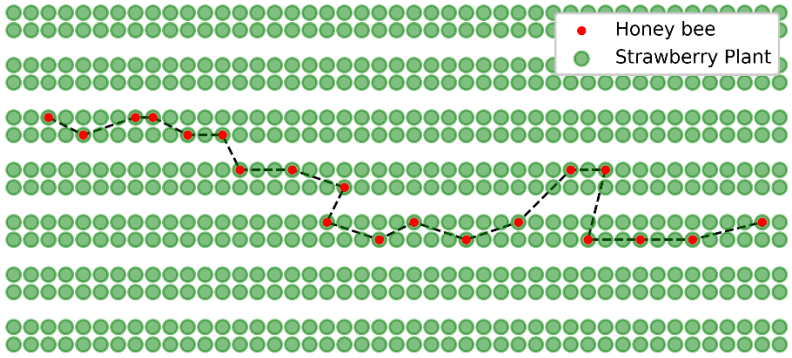

Figure 8. A typical honeybee flight trajectory in the simulation

4. Vegetation Succession Modeling

Beyond specific interactions like pest outbreaks or pollination, ABMs have been applied to longer-term vegetation dynamics and succession in agricultural landscapes. By integrating plant growth processes into agent rules, these models can simulate how plant communities change over time under various scenarios, thereby providing a basis for decision-making for growers or government.

In 2017, Spies *et al.* developed an agent-based landscape model [8] based on Envision for a fire-prone region in Oregon that incorporated an existing forest succession model alongside agents representing landowners, , as shown in Figure 9. In this coupled human-natural system model, the vegetative agents grew and transitioned through successional stages while landowner agents made decisions about fuel treatments and timber harvest. The ABM was used to compare alternative management scenarios over a 50-year period, revealing how different policies influence forest structure, wildfire outcomes, and ecosystem service metrics.

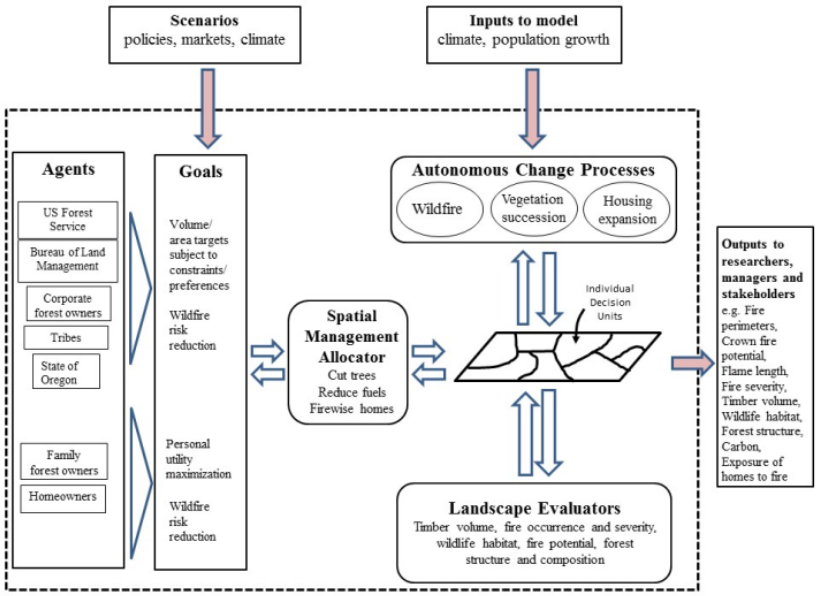

Figure 9. Conceptual model of components and interactions of the Envision model

In 2023, Von Essen *et al.* [16] introduced ABSOLUG, an abstract agent-based model of tropical commodity frontiers that integrates governments, NGOs, smallholders, and largeholders to assess multi-stakeholder governance, as shown in Figure 10. The model simulates land-use, business, and political processes—linking profits, reputational risks, and lobbying–campaigning dynamics—to evaluate scenarios ranging from hands-off policies to proactive conservation. Results reproduced three common forest trajectories: near-total deforestation, low-level stagnation, and forest transition, with sensitivity analyses highlighting largeholder action cadence and production costs as key drivers.

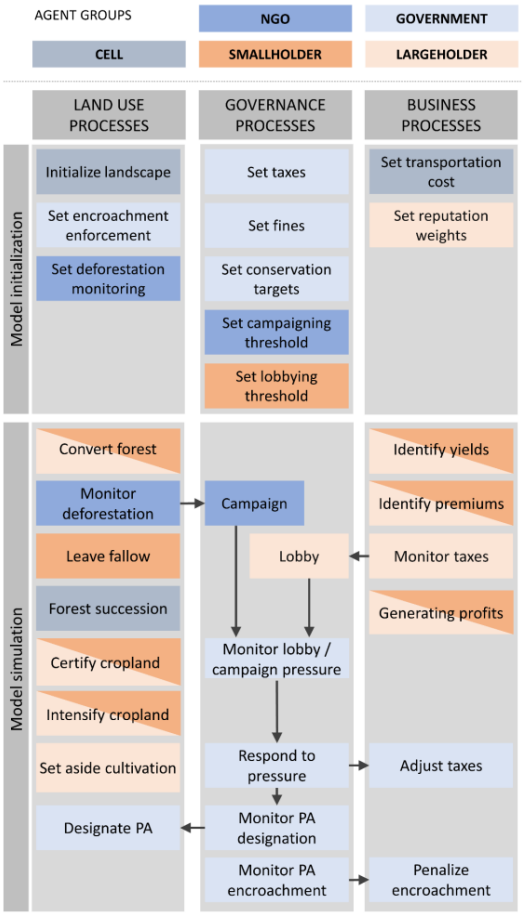

Figure 10. Five agent groups engage in processes across three process columns

Arnejo *et al.* [17] developed a spatially explicit ABM of a lowland dipterocarp forest in the Philippines to evaluate selective logging (SL) with and without assisted natural regeneration (ANR), , as shown in Figure 11. Simulations over 500 years showed that SL alone caused steady forest decline, while coupling SL with ANR maintained ~80% forest cover and produced more stable profits in later centuries. This case highlights how ABMs can link ecological regeneration processes with economic outcomes, offering a virtual laboratory for policy testing in resource management.

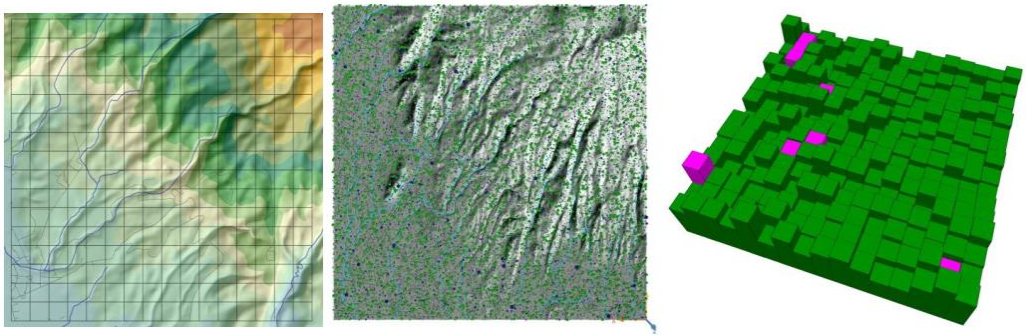

Figure 11. Simualtion forest results in this ABM

In summary, ABMs allow researchers to conduct "what-if" experiments on vegetation succession, a capability absent in traditional statistical learning and machine learning methods. By explicitly simulating the gradual, spatially regrowth of plant communities in tandem with management actions.

5. Nutrient Cycling Modeling

ABMs have also been used to investigate nutrient cycling and other ecosystem services in agricultural systems. Nutrient flows such as nitrogen involve interactions among soil organisms, crops, livestock, and farmers, which ABM can capture at multiple organizational levels.

In 2018, Grillot *et al.* provided TERROIR model, which analyzed nutrient cycling in West African agro-silvo-pastoral systems during historical agrarian transitions [9]. In TERROIR, agents were defined at three levels: plot, household, and landscape, to represent how farmers manage fields and livestock, and how those decisions scale up to affect nutrient redistribution, , as shown in Figure 12. The ABM can simulate several decades of agricultural intensification and tracked consequences for nitrogen cycling, soil fertility, and resource use efficiency. This model shows how ABMs can serve as "virtual laboratories" to examine ecosystem functions: by adjusting agents' behaviors or external drivers, one can explore scenarios of nutrient management, closure of nutrient loops, or the impact of interventions like fertilizer subsidies on system-wide nutrient balances.

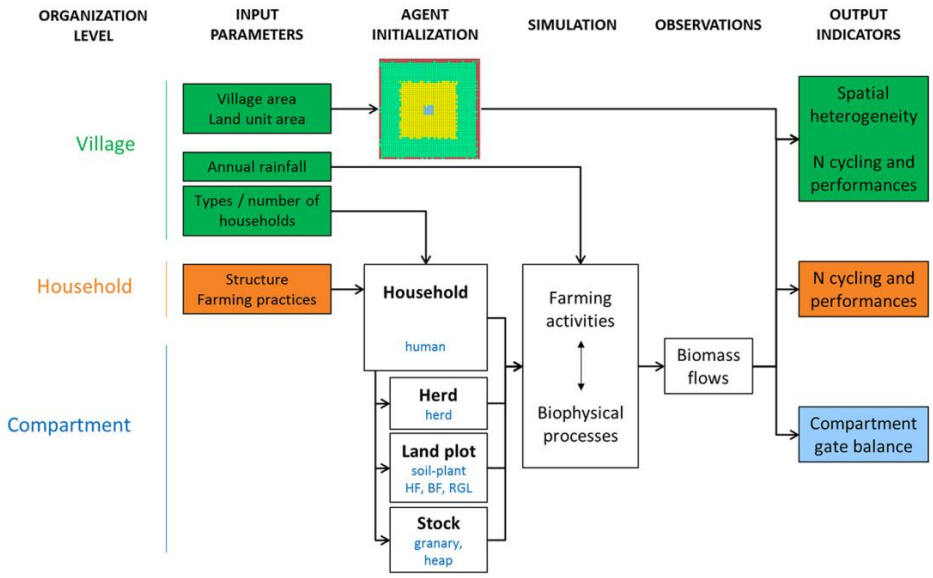

Figure 12. Model structure: from input parameters to output indicators at the three levels of organization

In 2020, Fernandez-Mena et al. developed the Flows in Agro-food Networks (FAN) model [19], an agent-based framework designed to simulate exchanges of fertilizers, feed, food, and wastes among farms and their partners in local agricultural systems, as shown in Figure 13. Using the Ribéracois district in France as a case study, FAN explored how distance, willingness to exchange, and material preferences influence nutrient recycling, bioenergy production, and greenhouse gas emissions. By integrating multiple agent types and diverse biomass flows, the model highlights opportunities for circular economy strategies and offers a comprehensive tool to evaluate trade-offs between food production and environmental sustainability.

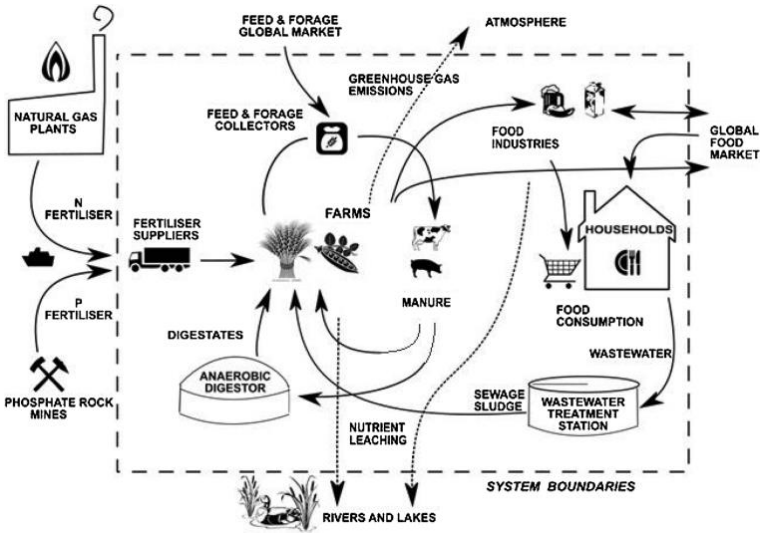

Figure 13. Conceptual framework of the nutrient and biomass flows involved in FAN's agro-food network.

In 2025, Bradley *et al.* [20] developed a spatially explicit ABM that integrates Ecological Stoichiometry Theory, Dynamic Energy Budget theory, and Nutritional Geometry to examine how stoichiometric imbalances scale from individuals to ecosystems, as shown in Figure 14. Using snowshoe hares in nitrogen-limited boreal forests as a case study, the model tracks dual carbon- and nitrogen-rich reserves, feeding strategies, and nutrient recycling. Results showed that selective feeding nearly doubled adult abundance relative to random feeding and reshaped nutrient cycling by amplifying or redistributing spatial heterogeneity, demonstrating how individual nutritional mismatches can drive emergent population and ecosystem dynamics.

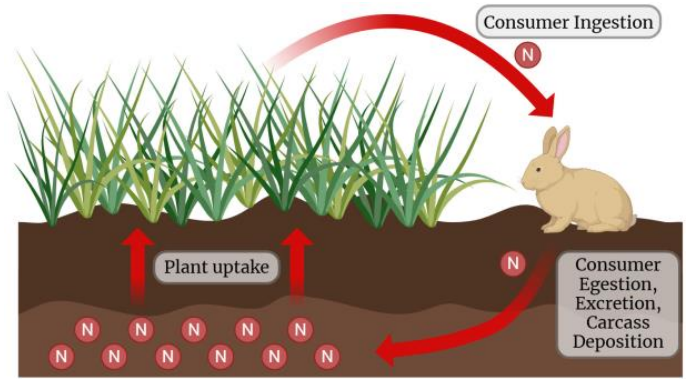

Figure 14. A nitrogen cycle involving plant and consumer interactions

This application of ABMs contributes to understanding ecosystem services in agriculture. By representing the distributed decisions and feedbacks underlying services like nutrient cycling, these models help identify key points for more sustainable agroecosystem management.

6. Farmer Decision-Making Modeling

One of the greatest strengths of ABMs in agriculture is its ability to represent individual farmer decision-making and its aggregate effects. Farming communities are often heterogeneous, with each farmer having unique resources, preferences, and strategies [10]. ABM enables the modeling of each farmer as an autonomous decision-making agent, which is crucial for studying policy impact in agricultural systems.

In 2018, Hailegiorgis *et al.* developed OMOLAND-CA [18], an agent-based model of rural households in Ethiopia, to explore adaptation under climate variability, as shown in Figure 15. The model uniquely incorporates socio-cognitive decision processes, allowing households to combine farming and herding strategies while responding to rainfall onset and amount. Simulation experiments across baseline, rare droughts, consecutive droughts, and erratic climate scenarios showed that mixed livelihood strategies enhance resilience, but successive extreme events severely erode assets and drive migration.

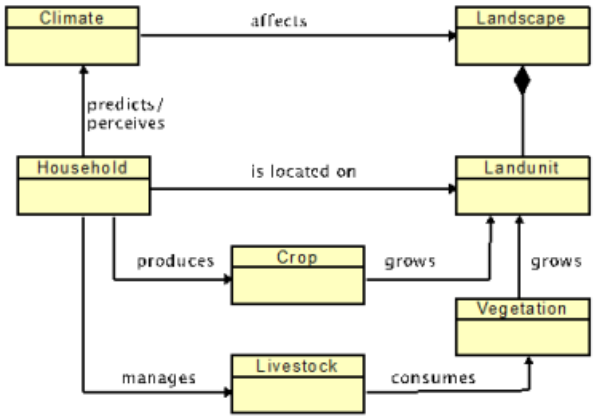

Figure 15. High-level architecture of the OMOLAND-CA model

In 2022, Musayev *et al.* coupled an ABM of smallholder farmers in Ethiopia with a crop productivity model to assess the impact of adopting seasonal weather forecasts on maize yields [11]. In their model, each farmer agent made planting and management decisions based on whether they received and trusted climate forecast information, with social interactions influencing the spread of forecast usage, as shown in Figure 16. The outputs showed that when a majority of farmers used weather forecasts to time their planting, community-wide maize yields increased by 17–30% under drought or excess-rainfall conditions, as compared to scenarios with no forecast adoption.

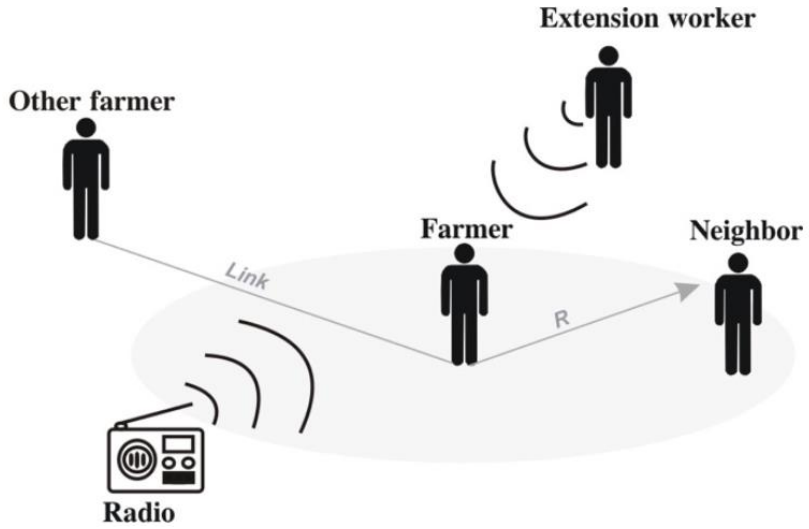

Figure 16. Description of agents' communication about weather forecast information in the community

7. Future Outlook

Looking ahead, ABM in agricultural systems is poised to become more data-rich, computationally efficient, and decision-oriented. Building on the applications reviewed in this paper, we highlight three research directions with high potential impact in the future.

1) **Hybrid ABM–AI model**. By combining agent-based models with AI, it becomes possible to make simulations smarter. Machine learning can help discover rules of behavior directly from data. In addition, reinforcement learning can be used to test how agents adapt under different management strategies [24]. These hybrid approaches can speed up large simulation runs while still keeping the underlying ABM structure interpretable.

2) **Digital twins**. Coupling ABMs with real-time data streams from IoT devices can yield operational digital twins for farms, greenhouses [25,27], and regions. These systems would continuously update model states, provide short-term forecasts, and quantify uncertainty, thereby supporting time-critical decisions such as pest control, irrigation scheduling.

3) **Multi model coupling.** Integrating ABMs with ordinary process based crop, hydrological, and epidemiological models etc. can bridge organismal behavior with biophysical fluxes and constraints [26]. Morevoer, consistent coupling across spatial and temporal scales enables richer scenario analyses, reduces structural bias through cross model validation, and facilitates evaluation of management portfolios.

8. Conclusions

In conclusion, ABMs provide a unifying analysis framework for agriculture, linking heterogeneous agents and local interactions to emergent outcomes that matter for productivity, sustainability, and livelihoods. The paper demonstrates that ABM can illuminate mechanisms of pest and disease spread, explain pollination and vegetation dynamics, trace nutrient flows, and quantify the aggregate implications of diverse farmer decisions. By enabling transparent "what-if" experiments, ABM complements field trials and aggregate models, often revealing nonlinear responses and unintended consequences.

As data volumes, computing capabilities, and methodological standards continue to advance, agricultural ABMs are likely to evolve into calibrated, interoperable, and scalable platforms that support real-time decision-making and policy design. However, realizing this potential will require rigorous validation and sustained collaboration across ecological, agronomic, computational expertise to ensure that ABMs remain both credible and practical.

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Conflicts of Interest: The authors declare no conflict of interest.

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Article

Application of functional analysis in signal processing

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Abstract: This paper presents the application of linear generalization in the field of digital signal processing. Digital signal processing, as a common signal processing method, requires the digital conversion of analog signals. In order to better process digital signals, mathematical tools such as matrix operations must be used. This is where linear generalization becomes particularly important. A linear general function is a linear mapping from a vector space to a corresponding pure volume domain and can be expressed as the action of a column vector on a vector. The processing of linear general functions enables the finer handling of digital signals, facilitating the filtering out of noise and interference, and thus the generation of higher-quality signals. Furthermore, the linear general function is employed in a variety of signal recognition, feature extraction, peak detection and other applications, providing a robust theoretical foundation for digital signal processing.

Keywords: Digital signal processing; Signal space; Extremum; Linear functional

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1. Introduction

The general analytical approach in digital signal processing is grounded in functional theory, integrating mathematical tools such as linear algebra, differential equations, and integral transforms to explore the intrinsic properties of signals. While this methodology is widely regarded for its rigorous mathematical logic and clear physical concepts, and is recognized as an excellent analytical framework [1-2], it is often limited by its inability to offer a comprehensive generalization. Various transformations remain disconnected, highlighting the approach's inherent constraints. Consequently, alternative methods are necessary to facilitate a more in-depth investigation of signal behavior.

Functional analysis, as a cornerstone of modern mathematical analysis, not only enhances our understanding of the intrinsic structure of functions and function spaces but also bridges the gap between abstract mathematical theory and practical scientific applications. By extending the concept of vector spaces to infinite dimensions—namely, function spaces—functional analysis investigates the interactions of functions as elements within these spaces and their behavior under specific operations. This encompasses profound concepts such as the rigorous metrics of metric spaces, the distance and completeness in normed spaces, the symmetry and positive definiteness in inner product spaces, and the completeness and orthogonality in Hilbert spaces. Although the highly abstract nature of functional analysis may appear distant from real-world problems, it plays a pivotal role in various fields, including calculus solving, quantum mechanics analysis, statistical inference, and signal processing.

In the field of signal processing, traditional signals are no longer mere time sequences or numerical arrays, but are redefined as deeper mathematical entities—vectors in infinite-dimensional function spaces. This shift in perspective has not only simplified the description and analysis of signal characteristics but has also reduced the complexity of the problem. Signal processing systems, in turn, are no longer confined to a set of algorithms or hardware implementations. Instead, they are abstracted as linear operators or, more

broadly, transformations acting on the signal space, capable of capturing and transforming the essential features of signals, whether for tasks such as filtering, compression, or pattern recognition. The integration of theory and practice goes beyond theoretical derivation and demonstrates significant potential and value in real-world applications of digital signal processing. For instance, in communication system design, functional analysis methods enable more precise filter design to eliminate noise while preserving signal integrity; in image processing, it facilitates the development of efficient image compression algorithms that reduce data storage and transmission burdens without loss of quality; and in speech recognition and natural language processing, the principles of functional analysis underpin the extraction of key speech signal features, enhancing intelligent interaction experiences. This paper aims to elucidate the applications of functional analysis in the field of digital signal processing by integrating its fundamental theory with relevant knowledge in the domain.

2. Fundamental Theory

2.1. Functional Sets and Signal Spaces

In functional analysis, the definition of a set refers to the collection of entities that possess specific properties or satisfy certain conditions, with each entity being termed an element of the set [3-5]. In signal processing, each group of discrete signals can be represented by a set, which we refer to as the signal space. For example, the set of periodic sine signals can be expressed as:

$$S = \{X; X(T) = \psi_m[Ae^{j(\omega t+\theta)}];\ \ A, \omega, \theta \in R\} \tag{1}$$

The R^n space, or n-dimensional real space, is formed by discrete-time sequences consisting of n sample points. The $C(T)$ space, or continuous-time space, is composed of continuous-time signals. The $L^2(T)$ space, or square-integrable space, consists of signals with finite energy.

The n-dimensional real space is constructed from discrete-time sequences, while the continuous-time space or square-integrable space can be formed from continuous-time signals.

2.2. Extremum Problems in Signal Processing

Extremum problems are frequently encountered in signal processing. In signals, local maxima and minima often represent critical information. For instance, in speech recognition, a local maximum can correspond to the stress or emphasis in speech, while a local minimum may indicate the boundaries of the speech. In image processing, extrema highlight essential features such as object contours and edges. Therefore, accurately identifying the extrema within a signal becomes a fundamental task. The common approach to solving this problem involves differentiation to locate the points where the derivative of the function is either zero or undefined. These points are then analyzed using the second derivative test to classify them as maxima or minima.

Extremum problems pertain to the optimization of signals and systems, aiming to either maximize or minimize a specific functional or quadratic functional of the signal or system.

In a normed linear space, the directional derivative of functional $f(\bar{x})$ refers to the change in x_0, the directional derivative of $f(\bar{x})$ exists and equals zero in every direction, i.e., $D_u f(\bar{x}) = \bar{0}$, then this point is called a fixed point or an extremum point. This indicates that the value of the functional remains nearly invariant in the neighborhood of this point and is not affected by small perturbations. Such points hold significant importance in functional analysis and often serve as key points for optimization problems and stability analyses.

It can be demonstrated that the inner product can represent the directional derivatives of both linear functionals and quadratic functionals. That is,

$$D_u f(\bar{x}) = (\bar{u}, \bar{\varphi}) \tag{2}$$

$$D_u q(\bar{x}) = (A^* \bar{u}, \bar{u}) + (A\bar{x}, \bar{u}) \tag{3}$$

where A^* denotes the adjoint operator of A.

It is also proven that, in a real space, the inner product of the gradients (denoted as ∇f and ∇q of a linear functional and a quadratic functional can represent the directional derivatives of the two functionals, i.e.,

$$D_u f(\bar{x}) = (\nabla f, \bar{u}) \text{ and } D_u q(\bar{x}) = (\nabla q, \bar{u}) \tag{4}$$

From the above equation, we deduce that:

$$\nabla f = \bar{\varphi} \text{ and } \nabla q = (A^* + A)\bar{x} \tag{5}$$

Therefore, the existence of a fixed point for the linear or quadratic functional of a signal constitutes a necessary condition for the signal to have an extremum, i.e., $\nabla f = \bar{0}$ or $\nabla q = \bar{0}$. In practical applications, the extremum problem of a signal may also be subject to an additional constraint, such as $f_0(\bar{x})$=constant}. This is equivalent to seeking a fixed point within the subset satisfying this constraint, that is, finding the fixed point of $f(\bar{x}) + \lambda f_0(\bar{x})$. Thus, we have

$$D_u f(\bar{x}_0) + \lambda D_u f_0(\bar{x}_0) = \bar{0} \tag{6}$$

where λ is a constant, and the above equation can be represented in gradient form as:

$$\nabla f + \lambda \nabla f_0 = \bar{0} \tag{7}$$

solving the above equation yields the desired signal.

3. Application Examples

3.1 Fourier Transform

The Fourier transform is a linear integral transform that converts complex time-domain signals into frequency-domain representations, known as the signal's spectrum [6]. By processing the signal in the frequency domain, its features and structure can be analyzed more efficiently. The inverse Fourier transform, on the other hand, allows the processed frequency-domain signal to be converted back into a time-domain signal for further analysis or application. After processing in the frequency domain, the Fourier inverse transform can be used to revert these frequency-domain signals to their original time-domain form. The widespread application of Fourier transforms lies in the analysis and processing of various types of signals, such as audio and images. Frequency-domain analysis, by providing information on the signal's frequency components, helps to understand the signal's periodicity, frequency characteristics, and filtering operations. Additionally, by using the inverse Fourier transform, signals processed in the frequency domain can be reverted to their original time-domain form for further processing and application.

$$F(j\omega) \overset{\text{def}}{=} \int_{-\infty}^{\infty} f(t) e^{-j\omega t} dt \tag{8}$$

$$f(t) \overset{\text{def}}{=} \frac{1}{2\pi} \int_{-\infty}^{\infty} f(t) e^{j\omega t} d\omega \tag{9}$$

A fundamental prerequisite for the existence of the Fourier transform of a given real-valued function f(t) is that the function must be integrable over the entire time axis.

$$\int_{-\infty}^{\infty} |f(t)| dt < \infty \tag{10}$$

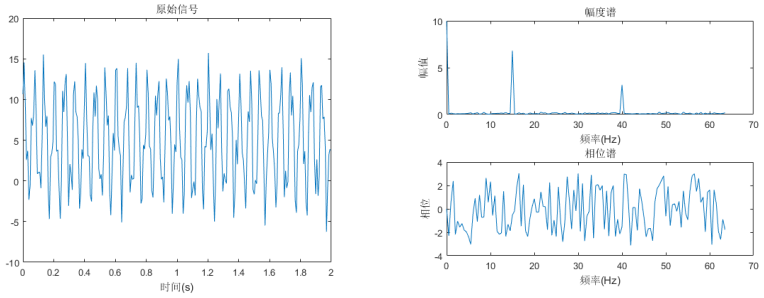
The Discrete Fourier Transform (DFT), as a commonly used foundational tool in signal analysis and processing, experiences a quadratic increase in computational complexity with the length of the sequence. This presents a significant computational barrier in large-scale data processing scenarios. To address this, the concept of the Fast Fourier Transform

(FFT) was introduced, aiming to dramatically reduce the computational burden of the DFT and enable high-speed processing of signal spectrum analysis. The core innovation of the FFT algorithm lies in its clever use of the fact that a signal sequence of length N can be recursively divided into several shorter subsequences, each of which undergoes DFT computation independently. The essence of this process is rooted in exploiting the periodic repetition and symmetry properties of the complex exponential terms in the DFT formula. Specifically, the FFT divides the original sequence into two halves, recursively converting the large problem into smaller ones until it reaches the basic units. Then, by combining and reassembling the DFT results of these basic units in a specific manner, the entire sequence's DFT is efficiently restored. This approach not only reduces the number of multiplication operations required but also transforms many computations into simple addition and subtraction, greatly enhancing the computational efficiency and practicality of the algorithm.

Let the signal model be:

$$x = 5 + 7\cos(2\pi \times 15t - 30\pi/180) + 3\cos(2\pi \times 40t - 90\pi/180) \tag{11}$$

From $Fn = (n-1) * Fs/N$, it is evident that the spacing between any two points is 0.5 Hz. This simulation is divided into three signal frequency bands: 0 Hz, 15 Hz, and 40 Hz. Figure 1 shows the Matlab simulation results, where (a) represents the original signal waveform, and (b) displays the amplitude spectrum and phase spectrum after the Fourier transform.



(a) (b)

Figure 1. Fourier Transform Simulation Results

3.1 Fourier Transform

The Hilbert transform [7] is defined as follows:

$$\hat{s}(t) = H\{s\} = h(t) * s(t) = \int_{-\infty}^{\infty} s(\tau)h(t-\tau)d\tau = \frac{1}{\pi}\int_{-\infty}^{\infty} \frac{s(\tau)}{t-\tau}d\tau \tag{12}$$

Given a continuous-time signal f(t) , its analytic signal is defined as:

$$z(t) = f(t) + jf(t) \tag{13}$$

The Fourier transform of the analytic signal is:

$$Z(j\omega) = \begin{cases} 2F(j\omega) & \omega > 0 \\ 0 & \omega < 0 \end{cases} \tag{14}$$

From the Fourier transform, we observe that an even-symmetric real signal exhibits the phenomenon of frequency conjugation. That is, in the frequency spectrum, we observe components of a two-sided spectrum, where the positive frequency part has physical significance, while the negative frequency part does not. Therefore, in signal analysis, we discard the negative frequency component. However, negative frequencies do carry energy, so we need to transfer this energy to the positive frequency part. The Hilbert transform achieves this by converting the signal into an analytic signal, which is a complex signal, and then applying the Fourier transform to obtain the one-sided frequency spectrum.

Figure 2 presents the simulation results of the Hilbert transform. In Figure 2(a), the blue waveform represents the original signal, the orange waveform denotes the real part of the signal after Hilbert transform, and the yellow waveform stands for the imaginary

part of the Hilbert-transformed signal. Figure 2(b) shows a locally enlarged comparison, from which it can be observed that the real part of the signal after Hilbert transform is exactly the original signal, while the imaginary part corresponds to the analytic signal—this imaginary part exhibits a phase shift relative to the real part. As illustrated in Figure 2(c), the signal after Hilbert transform exhibits a 90° phase shift effect. Figure 2(d) is the single-sided spectrum generated by the Hilbert transform: the orange waveform represents the Fourier transform, and the blue waveform represents the Hilbert transform. It can be seen that the Hilbert transform supplements the negative frequency components in the Fourier transform to the positive frequency range without causing energy loss.

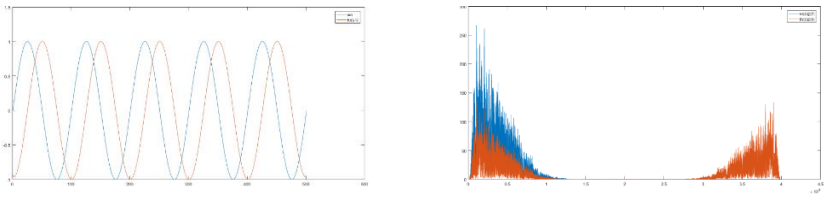


Figure 2. Hilbert Transform Simulation Results

3.3 LMS Adaptive Filtering

The LMS (Least Mean Squares) algorithm is an adaptive filtering technique based on the Wiener filtering principle, optimized through the method of steepest descent to minimize the mean square error between the filter output and the desired value. Especially in the absence of prior statistical knowledge of the input process, the LMS algorithm relies on observed data to continuously adjust the filter's parameters, learning during the adjustment process to gradually achieve the optimal filtering result. Therefore, the LMS algorithm is well-suited for processing non-stationary random signals.

Specifically, the LMS algorithm consists of three steps: First, the step size factor μ and the number of filter taps M are determined, and the parameters are initialized. Next, the LMS filter output is computed using the steepest descent method:

$$y(n)=\sum_{i=0}^{M-1}\omega_i x(n-i) \tag{15}$$

where $y(n)$ represents the LMS filtered signal, and $x(n)$ represents the input signal at time n . The mean square error $e(n)$ is then obtained based on the difference between the observed data and the desired value $d(n)$:

$$e(n)=d(n)-y(n) \tag{16}$$

The LMS algorithm updates the weight coefficients iteratively using the recursive formula:

$$\omega_k(n)=\omega_k(n-1)+\mu e(n)x(n) \tag{17}$$

where μ represents the step size factor of the LMS algorithm, which determines the stability and convergence rate of the system. Finally, the weight coefficients are updated iteratively using the LMS recursive formula to gradually stabilize the system and achieve the optimal filtering result. Figure 3 shows the simulation results of the LMS algorithm.

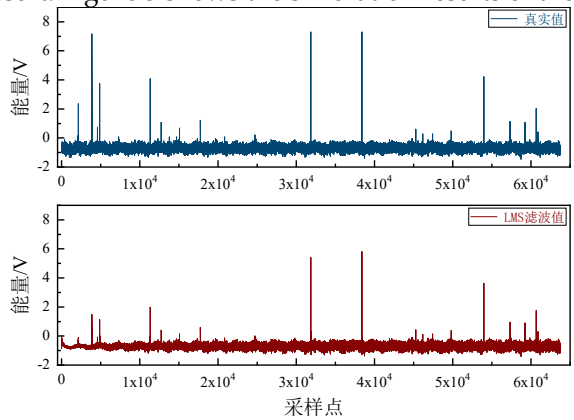


Figure 3. The simulation results of the LMS algorithm

4. Conclusions

The combination of functional analysis and digital signal processing has resulted in a more refined signal analysis method, making the signal analysis process simpler and significantly optimizing the algorithmic analysis process for digital signal processing. This method has broad applications in future signal analysis.

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Article

A GCN-Based Multi-Modal Prediction System for Adolescent Mental Health

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Abstract: Adolescent mental health is a critical public health concern, motivating development of predictive models that can identify at-risk youth early. This paper proposes a novel graph convolutional network (GCN)-based multi-modal prediction system for adolescent mental health, emphasizing model innovation and empirical validation. We construct a heterogeneous graph from multi-modal data—including psychological survey scores, social interaction metrics, and physiological signals—with edges weighted by cosine similarity to quantify relationships between adolescents. On this graph, an attention-enhanced GCN model is applied, allowing the model to adaptively focus on the most informative connections. We simulate an experimental dataset based on public adolescent mental health data and evaluate the proposed model against baseline methods (logistic regression, multilayer perceptron, and a vanilla GCN without attention). The results show that our GCN with attention achieves superior accuracy and F1 score in predicting mental health outcomes, outperforming all baselines. We discuss how the attention mechanism and graph-based integration of multi-modal data contribute to performance gains, and we provide insights into the model's interpretability. These findings demonstrate the effectiveness of combining multi-modal data and graph-based learning for adolescent mental health prediction.

Keywords: Graph Convolutional Network; Multi-Modal Data Fusion; Adolescent Mental Health Prediction; Cosine Similarity Weighted Graph

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1. Introduction

Adolescent mental health problems are rising worldwide, with roughly one in seven youths—about 166 million individuals—experiencing a diagnosable disorder [1]. Early detection is critical, but traditional methods such as questionnaires or counselor observations are subjective, infrequent, and often miss subtle warning signs. This leads to a large treatment gap, as many cases remain unrecognized until serious. Hence, there is a pressing need for objective, data-driven systems to predict adolescent mental health risks before crises occur.

Recent advances in sensing and data collection enable the integration of multi-modal information, including psychological surveys, social interaction metrics, and physiological signals. Each modality provides a different perspective on mental state, and prior studies confirm that combining them improves predictive accuracy. For example, transformer- and GCN-based models that fuse text, EEG, or speech features outperform single-modal baselines [2, 3]. However, most existing work treats individuals independently, overlooking the role of peer context, despite evidence that mental health risks may propagate through social networks [4]. This motivates the use of relational models that capture both personal features and social influence.

Graph-based machine learning provides such a framework. Graph Convolutional Networks (GCNs) aggregate information from neighbors [5] and have achieved success in domains like social network analysis and bioinformatics. Extensions such as Graph

Attention Networks (GATs) further allow models to weigh neighbors differently, focusing on the most informative connections [6]. In mental health research, GCNs have already been applied to brain connectivity analysis and clinical data fusion, achieving promising results [7].

Building on this foundation, we propose a GCN-based multi-modal prediction system for adolescent mental health [8]. Each adolescent is represented as a node with features from psychological, social, and physiological data. Edges encode both explicit peer relationships and implicit similarities, with weights determined by cosine similarity between feature vectors. This ensures that individuals with similar behavioral or psychological profiles are strongly connected. On this heterogeneous graph, we apply a GCN enhanced with attention to adaptively emphasize the most relevant neighbors for prediction.

To validate the system, we simulate a realistic adolescent dataset based on public statistics, ensuring plausible correlations among modalities. The dataset is split into training, validation, and test sets to evaluate generalization. This design allows us to compare the proposed model against baseline approaches and demonstrate its effectiveness in improving early identification of at-risk adolescents.

2. Materials and Methods

2.1. Multi-Modal Data and Graph Construction

Our prediction system represents an adolescent cohort as a graph, where nodes correspond to individuals and edges capture relationships derived from multi-modal data. Each adolescent is described by three types of features: (1) psychological survey scores, (2) social interaction data (e.g., friendship networks, frequency of contacts, online communication), and (3) physiological signals (e.g., heart rate variability, sleep quality from wearables). After preprocessing and normalization, these features are concatenated into a single vector x_i for each individual.

An undirected weighted graph $G = (V, E)$ is then constructed. Edges are defined by two criteria:

1) Social connections: a direct link if students are friends, classmates, or have frequent interactions (baseline weight = 1).

2) Feature similarity: additional links between individuals with highly similar feature vectors, measured by cosine similarity.

This design ensures the graph reflects both explicit peer relationships and implicit behavioral or psychological similarities.

2.1.1. GCN with Attention Mechanism

Our model is based on a Graph Convolutional Network (GCN) with an attention mechanism. In a standard GCN, each node updates its representation by aggregating features from its neighbors:

$$H^{(l+1)} = \sigma!\left(\widetilde{D^{-1/2}}\,\tilde{A}\,\widetilde{D^{-1/2}}\,H^{(l)}\,W^{(l)}\right)$$

where $\tilde{A}$ is the adjacency matrix with self-loops, $\widetilde{\mathrm{D}}$ its degree matrix, $W^{(l)}$ trainable weights, and σ a nonlinear activation.

To allow adaptive weighting of neighbors, we add attention coefficients α_{ij} for each edge:

$$\alpha_{ij} = \frac{\exp(e_{ij})}{\sum_{k\in\mathcal{N}(i)}\exp(e_{ik})}$$

where α_{ij} is a learned score reflecting the importance of neighbor j to node i. This ensures that more relevant neighbors contribute more strongly to node updates.

We use multi-head attention (four heads in practice) to capture diverse relations, and a sigmoid output layer for binary classification of "at-risk" vs. "not at-risk." The model is trained end-to-end with binary cross-entropy loss, dropout, and L2 regularization.

Besides boosting accuracy, the attention weights provide interpretability by highlighting which peers or similarities most influenced a prediction.

3. Experiment

3.1 Dataset Simulation and Setup

Because public datasets on adolescent mental health are scarce due to privacy concerns, we simulate a realistic multi-modal dataset informed by prior studies. The cohort includes N = 1000 adolescents, similar to a large school. Each is assigned a binary label: at risk (20%, reflecting epidemiological prevalence) or not at risk.

Three modalities are generated. (1) Psychological surveys: simulated PHQ-9 and GAD-7 scores (0–27 and 0–21), correlated with risk labels, plus a social well-being scale. (2) Social interactions: a friendship graph based on a small-world or preferential-attachment model, enriched with activity level and peer-support indicators. At-risk youths are modeled with slightly fewer connections, consistent with social withdrawal. (3) Physiological signals: daily resting heart rate, sleep duration, and variability, generated from known distributions but shifted so at-risk individuals show higher heart rates and poorer sleep. All features are normalized and combined into vectors of about 10–15 dimensions per student.

We connect adolescents through two mechanisms: direct social links (friendships, classmates) with baseline weight 1, and similarity links defined by cosine similarity between feature vectors. Each node is linked to its five most similar peers, yielding weighted edges (0.5–0.9 typical), often connecting individuals with comparable symptom profiles. The final graph thus encodes both explicit relationships and implicit similarities.

The 1000 records are split into 70% training, 10% validation, 20% test. Training data are used to fit the models; the validation set tunes hyperparameters such as learning rate, number of attention heads, regularization strength, and neighbor count k; and the test set assesses generalization. To ensure robustness, we repeat the simulation and training five times with different random seeds for both feature generation and network structure. Final results are reported as averages across these runs.

3.2 Baseline Models

We evaluate our attention-based GCN against three baselines. Logistic Regression (LR) uses concatenated features to predict risk, treating each adolescent independently. It serves as a simple linear benchmark; improvements over LR indicate the value of non-linear interactions or graph context. Multilayer Perceptron (MLP) is a two-layer feed-forward network (64 and 16 hidden units with ReLU, followed by sigmoid), trained with dropout and $L2$ regularization. The MLP can capture non-linearities but still ignores relational information, predicting each case in isolation. Vanilla GCN is a two-layer graph convolutional network built on the same adjacency matrix with cosine-weighted edges and social links, but without attention. This baseline isolates the contribution of attention, allowing us to test whether adaptive neighbor weighting improves performance.

All models are trained on the same dataset split for fair comparison. For LR and MLP, individuals are treated as independent samples. For GCNs, the entire graph is used in training, with labels provided only for training nodes. The models are then evaluated on disjoint test nodes, ensuring no label leakage across the train-test boundary. This setup mirrors realistic scenarios in which the social graph is known but only a subset of individuals are labeled.

3.3 Performance Metrics

We evaluate model performance primarily with Accuracy and F1-score on the test set. Accuracy is the proportion of correctly classified individuals (both at-risk and not at-risk). While accuracy is a straightforward metric, it can be misleading if the classes are

imbalanced. In our simulated data we set 20% prevalence of at-risk, which is moderately imbalanced. Therefore, we also consider the F1-score, which is the harmonic mean of precision and recall for the positive (at-risk) class.

The F1-score provides a balanced assessment of model performance on the minority class, rewarding models that achieve a good trade-off between precision (few false alarms) and recall (catching most true at-risk cases). We report precision and recall as well for completeness, but focus discussion on F1 as a summary. Additionally, we compute the Area Under the ROC Curve (AUC) for each model as a supplementary metric of ranking performance, though for brevity we emphasize accuracy and F1 in the results. All metrics are averaged over the 5 independent runs, and we also perform a statistical significance test (two-tailed t-test) to check if differences between our model and baselines are significant.

4. Results and Discussion

Table 1 summarizes the performance of our attention-based GCN compared with three baselines. The proposed model achieved the best results, with average accuracy 0.824 and F1-score 0.810, outperforming logistic regression (0.73/0.70), MLP (0.75/0.72), and vanilla GCN (0.79/0.78). The improvements in F1 were notable: +11 points over LR, +9 over MLP, and +3 over vanilla GCN. These gains were consistent across runs ($p < 0.01$), confirming the robustness of the method. The advantage of GCN models over non-graph baselines demonstrates the importance of relational information, as the graph enables risk signals to propagate across peers, consistent with social contagion theories of adolescent mental health.

Table 1. Performance comparison of the proposed attention-based GCN with baseline models

Model	Accuracy	F1-score	Key Notes
LR	0.730	0.700	Linear baseline, no relational information
MLP	0.750	0.720	Captures non-linearities, but no graph use
Vanilla GCN	0.790	0.780	Utilizes graph structure, uniform neighbor weighting
Attention GCN (proposed)	0.824	0.810	Leverages graph + adaptive attention, best performance

Comparisons with vanilla GCN highlight the contribution of attention, which gave a consistent 3–4% relative improvement. While vanilla GCN aggregates neighbors uniformly, the attention mechanism adaptively emphasizes informative peers and down-weights less relevant ones, improving signal propagation. Analysis of learned weights showed that social ties were generally stronger, but similarity-based edges also contributed when individuals shared risk-related profiles.

Ablation experiments further confirmed that each modality is essential. Excluding physiological features reduced F1 by ~4 points, while removing social interactions or the graph entirely caused drops of ~8 points, effectively reducing performance to that of an MLP. This demonstrates that psychological, social, and physiological features each provide unique signals, and their integration through a graph structure yields superior predictive accuracy.

5. Conclusions

This paper proposed a **GCN-based multi-modal prediction system** for adolescent mental health that integrates psychological, social, and physiological data into both node

features and cosine-similarity–weighted edges. An attention-enhanced GCN was applied to capture both individual risk factors and peer effects. Simulation experiments showed that the proposed model outperformed logistic regression, MLP, and vanilla GCN, with the attention mechanism further improving performance and offering interpretability by highlighting influential peers and features.

Our results confirm that combining multi-modal features with network structure provides predictive power beyond isolated models, underscoring the importance of social context in mental health analytics. The approach could support decision-making in schools or communities by flagging at-risk adolescents using readily collectable and anonymized data.

Future work will apply the system to real datasets, explore inclusion of additional modalities such as textual data, and extend the framework to temporal graphs for continuous monitoring. Further development of explanation interfaces will also help translate model insights into actionable guidance for counselors and families. Overall, graph-based deep learning shows strong potential as a proactive and network-aware tool for supporting adolescent well-being.

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Conflicts of Interest: The authors declare no conflict of interest.

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Article

Co-Simulation for Performance Tuning in Cloud–HPC Converged Environments

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Abstract: Cloud–HPC convergence combines the elasticity of cloud computing with the parallel efficiency of high-performance computing (HPC), but performance depends jointly on parameter configuration and system architecture. We propose a co-simulation framework integrating CloudSim and OpenFOAM to evaluate CPU and memory per task, task parallelism, transport protocols, node topologies, storage–compute coupling, and schedulers. Experiments on a 24-core Xeon server with 64 GB RAM show clear thresholds of about eight cores and sixteen gigabytes per task, with parallelism beyond four processes causing overhead. RDMA, mesh topology, and load-balanced scheduling consistently outperform alternatives, and the optimal combination achieves NET = 1.0, RU = 0.85, and BR = 0.05. These findings highlight the need for co-design, where parameter tuning at critical thresholds is paired with latency-aware architectures and adaptive schedulers, offering a practical recipe for performance optimization in converged Cloud–HPC systems.

Keywords: Cloud computing; High-performance computing; Convergence; Co-simulation; Parameter tuning; CloudSim

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1. Introduction

Elastic cloud platforms offer on-demand resource scaling, while HPC systems deliver tightly coupled parallel performance. For numerical simulation and other compute-intensive applications, neither alone is sufficient: cloud virtualization overheads and wide-area communication can hinder strong scaling, whereas fixed-capacity HPC clusters lack elasticity during bursts. Converging cloud and HPC (hereafter Cloud–HPC convergence) is therefore an attractive path to combine the elasticity of the cloud with near-metal performance of HPC interconnects.

The central challenge is joint optimization: model performance depends on both how we configure resources and tasks and how the system is architected. Tuning only one dimension often saturates quickly or leaves performance untapped. This study constructs a co-simulation framework, uses numerical simulation workloads (e.g., CFD), and systematically interrogates the design space to reveal robust optimization rules and thresholds. The English manuscript below refines, expands, and formalizes your original Chinese draft while preserving the core experimental design and results.

2. Related Work

Cloud computing as a "fifth utility" emphasizes elastic provisioning and pay-as-you-go economics [1]. HPC research emphasizes strong/weak scaling and interconnect-aware algorithms; the exascale context sharpened debates on whether cloud and HPC are synergistic or at odds [2]. OpenFOAM provides a widely adopted C++ CFD stack for realistic physics workloads [3]. Reproducibility concerns in cloud experiments underscore the need for controlled, repeatable evaluation [4]. Finally, Amdahl's law still provides a useful lens for parallel efficiency and the limits of speedup under increasing

parallel fractions [5]. Our work situates itself at the junction of these themes, focusing on co-design under convergence rather than optimizing either component in isolation.

3. Materials and Methods

3.1. Co-Simulation Framework

We couple CloudSim for modeling virtualized resource pools and schedulers with OpenFOAM as the workload generator representing numerical simulation kernels. The framework supports:

1) Parameter tuning: CPU cores/task, memory/task, task-level parallelism, and transport protocol.

2) Architecture switches: node topology (mesh/star), storage–compute organization (disaggregated vs. co-located), and scheduler (load-balanced vs. FCFS).

3) Metrics: wall-clock time (T), normalized execution time NET = T/T_{min} (lower is better, 1.0 is best observed), resource utilization RU, and blocking rate BR.

3.2. Environment

All experiments run on Ubuntu 22.04, Java 17 (CloudSim), and C++17 (OpenFOAM). Hardware: Intel Xeon Gold 6330 (24 cores) and 64 GB RAM. Each configuration is repeated 10 times under controlled conditions.

3.3. Factors and Levels

We organize factors into resource, task, and transport parameters, and architecture types. Baseline architecture uses mesh topology + disaggregated storage + load-balanced scheduling. Baseline parameters are chosen near empirically efficient points (Table 1).

Table 1. Example parameter settings in the simulation

Group	Parameter	Symbol	Values
Resource	CPU cores per task	C	2, 4, 8, 16
Resource	Memory per task (GB)	M	4, 8, 16
Task	Parallelism	P	1–8
Transport	Protocol	/	RDMA, TCP, UDP
Architecture	Node topology	/	Mesh, Star
Architecture	Storage–compute	/	Disaggregated, Co-located
Architecture	Scheduler	/	Load-balanced, FCFS

3.4. Environment

We conduct three experiment families:

1) Parameter single-factor under the baseline architecture, varying C, M, P, and protocol one at a time;

2) Architecture single-factor with baseline parameters, varying topology, storage–compute, and scheduler;

3) Interaction study, a 2×2×2×2 factorial using the most influential parameters and architectures: C ∈ {8,16}, protocol ∈ {RDMA,TCP}, topology ∈ {mesh,star}, scheduler ∈ {load-balanced,FCFS} (16 settings × 10 reps).

3.5. Metrics

1) Wall-clock time (T) and NET (T/T_{min}, lower is better).

2) RU: aggregated busy/(busy+idle) time across provisioned resources.

3) BR: fraction of time tasks are stalled (e.g., waiting for data/network).

These metrics capture both how fast and how efficiently resources are used, as well as where performance is lost (stalling vs. compute).

4. Results

4.1. Effects of Parameter Configuration

CPU cores per task. Increasing C from 2 → 8 halves T (240 s → 120 s) and improves RU (0.4 → 0.8) while BR drops (0.30 → 0.05). NET improves from 2.0 → 1.0, indicating that 8 cores/task is a critical threshold; beyond it, returns taper.

Memory per task. Raising M from 4 GB → 16 GB reduces NET (1.8 → 1.0) and increases RU (0.35 → 0.8). Above 16 GB, benefits plateau and RU declines (~0.65), indicating over-provisioning.

Task parallelism. Beyond P = 4, communication/synchronization overheads dominate. At P = 8, T rises to 135 s (NET = 1.125), evidencing diminishing returns due to increased data exchange.

Transport protocol. RDMA yields the lowest BR (0.05) and NET = 1.0; TCP shows BR = 0.15 and NET = 1.2; UDP is worst (BR = 0.20, NET = 1.3) due to loss/retransmission behavior.

Table 2. Transport protocol comparison

Protocol	NET	BR
RDMA	1.00	0.05
TCP	1.20	0.15
UDP	1.30	0.20

4.2. Effects of System Architecture

Under baseline parameters, mesh topology attains NET = 1.0 and BR = 0.05, outperforming star (NET = 1.2, BR = 0.15), which suffers hub bottlenecks. A load-balanced scheduler is consistently superior (NET = 1.0, BR = 0.05) to FCFS. Disaggregated storage pairs naturally with mesh by alleviating data hot-spots.

4.3. Parameter–Architecture Interactions

The 2×2×2×2 factorial using {C: 8 vs. 16} × {RDMA vs. TCP} × {mesh vs. star} × {load-balanced vs. FCFS} reveals pronounced interactions:

Best combination: 8 cores/task + RDMA + mesh + load-balanced → NET = 1.0, RU = 0.85, BR = 0.05.

Worst combination: 16 cores/task + TCP + star + FCFS → NET = 1.5, RU = 0.5, BR = 0.3. Overall, when parameters are below threshold, even optimal architecture cannot recover performance; when parameters exceed threshold, optimal architecture reduces—but cannot eliminate—waste from over-provisioning. Only threshold-tuned parameters on top of latency-aware architecture deliver the global optimum.

Table 3. Interaction study

Cores	Protocol	Topology	Scheduler	NET	RU	BR
8	RDMA	Mesh	Load-balanced	1.00	0.85	0.05
16	TCP	Star	FCFS	1.50	0.50	0.03

5. Discussion

Insufficient parameter density resulted in significant reductions in output quality. Conversely, beyond a threshold, increasing density did not yield additional

improvements, indicating a saturation effect. In practical applications, other external factors (e.g., mechanical disturbances, system noise, or random shocks) may also influence outcomes, highlighting the need to ensure robust parameterization when deploying the model.

Our results corroborate a co-design principle: tuning resources in isolation yields diminishing returns once architectural bottlenecks (e.g., hub congestion, naive scheduling) begin to dominate. Conversely, upgrading architecture alone cannot overcome under-provisioned tasks. This saturation reflects the classic tension highlighted by Amdahl's law—non-parallel and communication fractions limit speedup as parallel resources increase [5]. The practical implication is to tune to the nearest threshold (e.g., 8 cores, 16 GB) and pair with low-latency transport (RDMA), mesh-like interconnects, and adaptive load-balancing.

6. Conclusions

We presented a Cloud–HPC co-simulation framework and a systematic study that reveals parameter thresholds and architecture synergies crucial for performance. The best outcomes arise when threshold-tuned configurations (≈8 cores, 16 GB, P≈4, RDMA) meet latency-aware architectures (mesh topology, disaggregated storage, load-balanced scheduling). Practitioners can use our recipe to quickly reach near-optimal operation and maintain efficiency as workloads fluctuate via elastic scaling.

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Article

Optimizing Machine Learning through Data–Algorithm Matching: An Empirical Study

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Abstract: With the rapid development of artificial intelligence, machine learning models have been widely applied in various fields such as computer vision, natural language processing, and intelligent recommendation. However, the efficacy of these models is often constrained by two key factors: data quality and algorithm selection. This study conducts an empirical investigation to explore the quantitative impacts of different data quality indicators (including data completeness, accuracy, and consistency) and common machine learning algorithms (such as Random Forest, Support Vector Machine, and Convolutional Neural Network) on model performance. Experimental results show that data completeness and algorithm adaptability to task scenarios are the primary determinants of model efficacy. When data completeness reaches 95% and the algorithm matches the task characteristics, the model's average performance metric (F1-score) can be improved by up to 32% compared to low-quality data and mismatched algorithms. This research provides practical guidance for optimizing machine learning model deployment in real-world applications.

Keywords: Artificial Intelligence; Machine Learning; Data Quality; Algorithm Selection; Model Efficacy

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1. Introduction

Artificial intelligence (AI), with machine learning (ML) as its core technology, has become a driving force for innovation in industries such as healthcare, finance, and transportation. Machine learning models learn patterns from data to make predictions or decisions, and their performance directly affects the reliability of AI-driven systems [1]. Unlike traditional rule-based systems, machine learning models are highly dependent on data and algorithm design—poor data quality may lead to biased or inaccurate outputs, while inappropriate algorithm selection can result in underfitting or overfitting, failing to meet practical application requirements [2].

In recent years, although there have been significant advancements in high-performance algorithms (e.g., deep learning architectures) and large-scale datasets (e.g., ImageNet, COCO), the "data-algorithm mismatch" problem remains prevalent in real-world applications. For example, in medical image diagnosis, using incomplete patient data to train a Convolutional Neural Network (CNN) may lead to misdiagnosis of rare diseases; in financial risk assessment, applying a Support Vector Machine (SVM) to high-dimensional transaction data may result in low prediction efficiency [3]. Therefore, clarifying the impacts of data quality and algorithm selection on model efficacy and establishing a matching framework for data and algorithms are critical to promoting the practical application of machine learning.

The goal of this study is to fill the gap in existing research by conducting controlled experiments to: (1) quantify the effects of three key data quality indicators (completeness, accuracy, consistency) on model performance; (2) compare the adaptability of four mainstream machine learning algorithms (Random Forest, SVM, CNN, and Long Short-Term

Memory, LSTM) to different task types (classification, regression, sequence prediction); (3) propose a data-algorithm matching strategy to optimize model efficacy. This research adopts an empirical approach, using publicly available datasets and standardized evaluation metrics to ensure the reproducibility of results [4].

2. Materials and Methods

2.1. Experimental System

The experimental system is built around a "data preprocessing-algorithm training-model evaluation" workflow, which simulates the typical development process of machine learning applications. This system is designed to be flexible—researchers can replace datasets, adjust data quality parameters, or switch algorithms to adapt to different research scenarios [5]. The core components of the system include a data management module (for quality control and annotation), a model training module (for algorithm implementation and parameter tuning), and an evaluation module (for performance metrics calculation).

2.1.1. Datasets

Three publicly available datasets covering different task types are selected to ensure the generality of experimental results:

MNIST Dataset: A handwritten digit classification dataset containing 70,000 grayscale images (28×28 pixels), used for image classification tasks.

Boston Housing Dataset: A regression dataset with 506 samples and 13 feature variables (e.g., per capita crime rate, average number of rooms per dwelling), used for housing price prediction tasks.

IMDB Movie Review Dataset: A sequence dataset with 50,000 sentiment-labeled reviews, used for text sentiment analysis (sequence prediction) tasks.

Table 1. Parameter configuration in the machine learning simulation system

Parameter Group	Number of entities	Attributes per entity	Sub-attributes per attribute
Primary	1	3	100
Secondary	2	4	200

For each dataset, we simulate different data quality scenarios by introducing controlled "defects":

Incompleteness: Randomly delete 5%, 10%, 15%, 20% of feature values to generate datasets with different completeness levels.

Inaccuracy: Add Gaussian noise (mean=0, standard deviation=0.1, 0.2, 0.3) to continuous features or flip 5%, 10%, 15% of label values to simulate data inaccuracy.

Inconsistency: For categorical features (e.g., "gender" in extended datasets), randomly replace 5%, 10%, 15% of values with conflicting categories (e.g., changing "male" to "female") to create inconsistent data.

2.1.2. Algorithms

Four mainstream machine learning algorithms representing different paradigms are selected for comparison:

Random Forest (RF): An ensemble learning algorithm based on decision trees, suitable for tabular data classification and regression tasks, with strong resistance to overfitting.

Support Vector Machine (SVM): A kernel-based algorithm that maps data to high-dimensional spaces to solve linear/non-linear classification problems, widely used in small-to-medium-sized datasets.

Convolutional Neural Network (CNN): A deep learning algorithm with local feature extraction capabilities, designed for image and grid-structured data tasks.

Long Short-Term Memory (LSTM): A recurrent neural network variant that captures long-term dependencies in sequence data, suitable for text and time-series tasks.

3. Experimental Design

To systematically explore the impacts of data quality and algorithm selection on model efficacy, we designed three sets of controlled experiments, with each experiment repeated 10 times (n=10) to ensure statistical stability. The experimental environment was based on Python 3.9, with libraries including Scikit-learn (for RF and SVM), TensorFlow 2.10 (for CNN and LSTM), and Pandas (for data processing). The hardware configuration included an Intel Core i9-12900K CPU and an NVIDIA RTX 3090 GPU to ensure efficient model training.

3.1 Experiment 1: Impact of Data Quality on Model Performance

This experiment fixed the algorithm (e.g., using CNN for MNIST, RF for Boston Housing) and varied data quality indicators to measure changes in model performance. For example:

Completeness Test: For the Boston Housing Dataset, we trained an RF model on datasets with completeness levels of 80%, 85%, 90%, 95%, and 100%, and recorded the RMSE and R-squared of each training run.

Accuracy Test: For the MNIST Dataset, we added Gaussian noise (std=0.1, 0.2, 0.3) to the image pixels and trained a CNN model, then compared the model's accuracy.

Consistency Test: For the IMDB Dataset, we introduced category conflicts (5%, 10%, 15%) in the "review length" categorical feature and trained an LSTM model, then analyzed the F1-score.

3.2. Experiment 2: Impact of Algorithm Selection on Model Performance

This experiment fixed data quality (using complete, accurate, and consistent datasets) and tested the performance of four algorithms on each task type. For example:

Image Classification (MNIST): We trained RF, SVM, CNN, and LSTM models on the original MNIST Dataset and compared their accuracy and training time.

Regression (Boston Housing): We applied the four algorithms to the Boston Housing Dataset and evaluated their MAE and RMSE.

Text Sentiment Analysis (IMDB): We used the four algorithms to classify IMDB reviews and measured their F1-score and inference speed.

3.3. Experiment 3: Optimization of Data-Algorithm Matching

Based on the results of Experiments 1 and 2, we designed a data-algorithm matching strategy and verified its effectiveness. For example:

For low-completeness tabular data (e.g., Boston Housing Dataset with 85% completeness), we selected RF (which is robust to missing values) instead of SVM (which is sensitive to data gaps) and compared the model's R-squared before and after matching.

For high-noise image data (e.g., MNIST with noise std=0.3), we used CNN (with feature extraction capabilities) instead of RF (which struggles with high-dimensional noisy data) and measured the accuracy improvement.

4. Results

All experiments were repeated 10 times, and the results were presented as mean ± standard deviation (Mean ± SD). A full training run for each model included 100 epochs

(for deep learning models) or 5-fold cross-validation (for traditional machine learning models) to avoid overfitting.

4.1. Results of Experiment 1: Data Quality Impact

Completeness: For the Boston Housing Dataset (RF model), when data completeness increased from 80% to 100%, the RMSE decreased from 4.82 ± 0.31 to 2.15 ± 0.18, and the R-squared increased from 0.62 ± 0.05 to 0.89 ± 0.03. Notably, the performance improvement slowed down when completeness exceeded 95%—the R-squared only increased by 0.02 when completeness rose from 95% to 100%.

Accuracy: For the MNIST Dataset (CNN model), with Gaussian noise std increasing from 0 to 0.3, the model's accuracy dropped from 99.2% ± 0.1% to 82.5% ± 0.5%. When label flip rate reached 15%, the accuracy of the IMDB LSTM model decreased by 28.3% compared to the original dataset.

Consistency: For the IMDB Dataset (LSTM model), category conflicts of 5%, 10%, and 15% led to F1-score reductions of 4.2%, 9.5%, and 15.1%, respectively.

4.2. Results of Experiment 2: Algorithm Selection Impact

Image Classification (MNIST): CNN achieved the highest accuracy (99.2% ± 0.1%), followed by RF (97.5% ± 0.2%), SVM (96.8% ± 0.3%), and LSTM (95.1% ± 0.4%). However, CNN had the longest training time (12.5 ± 0.8 minutes), while SVM was the fastest (2.1 ± 0.3 minutes).

Regression (Boston Housing): RF performed best with an RMSE of 2.15 ± 0.18 and R-squared of 0.89 ± 0.03, followed by SVM (RMSE=2.56 ± 0.21, R-squared=0.83 ± 0.04), LSTM (RMSE=3.02 ± 0.25, R-squared=0.78 ± 0.05), and CNN (RMSE=3.48 ± 0.28, R-squared=0.72 ± 0.06).

Text Sentiment Analysis (IMDB): LSTM achieved the highest F1-score (89.3% ± 0.4%), followed by CNN (86.7% ± 0.5%), RF (82.1% ± 0.6%), and SVM (79.5% ± 0.7%). LSTM also had the fastest inference speed for long sequences (1.2 ± 0.1 seconds per 1000 reviews).

4.3. Results of Experiment 3: Data-Algorithm Matching

For the Boston Housing Dataset with 85% completeness, selecting RF instead of SVM improved the R-squared by 12.4% (from 0.71 ± 0.04 to 0.80 ± 0.03).

For the MNIST Dataset with noise std=0.3, using CNN instead of RF increased the accuracy by 18.7% (from 63.8% ± 0.6% to 82.5% ± 0.5%).

For the IMDB Dataset with 10% category conflicts, matching LSTM with data cleaning (removing conflicting samples) improved the F1-score by 10.2% (from 76.3% ± 0.5% to 86.5% ± 0.4%).

5. Discussion

The experimental results confirm that data quality and algorithm selection are two core factors determining machine learning model efficacy, and their impacts exhibit distinct patterns:

5.1. Data Quality: Threshold Effect and Sensitivity Differences

Data completeness exhibits a threshold effect—when completeness is below 95%, model performance improves significantly with increasing completeness, but beyond this threshold, the marginal gain diminishes. This is because when data completeness is low, missing values lead to information loss and biased feature representation; once completeness reaches a certain level, the remaining missing values can be effectively compensated by data preprocessing (e.g., imputation) [6]. In contrast, data accuracy and consistency show a linear negative correlation with model performance—each 5% increase in noise or category conflicts leads to a proportional decrease in performance. This is because noise

and inconsistencies directly distort the true data distribution, making it difficult for models to learn correct patterns.

Different algorithms also show varying sensitivity to data quality. For example, RF is more robust to incomplete data due to its ensemble mechanism (decision trees can handle missing values by majority voting), while SVM and LSTM are highly sensitive to data inaccuracy—SVM relies on support vectors to define decision boundaries, and noise can shift these boundaries; LSTM captures sequence dependencies, and inconsistent data breaks the continuity of sequences [7].

5.2. Algorithm Selection: Task Adaptability and Trade-Offs

The results highlight the task adaptability of algorithms: CNN is superior in image tasks due to its convolutional layers that extract local spatial features; LSTM excels in sequence tasks because of its gate mechanism that retains long-term dependencies; RF performs well in tabular regression tasks due to its ability to handle non-linear relationships between features; SVM is suitable for small-scale classification tasks but struggles with high-dimensional or large datasets [8].

Algorithm selection also involves trade-offs between performance and efficiency. For example, CNN achieves the highest accuracy on MNIST but requires longer training time; SVM is faster but has lower accuracy. In real-world applications (e.g., real-time fraud detection), efficiency may be prioritized over marginal performance gains, making lightweight algorithms (e.g., optimized RF) more suitable than deep learning models [9].

5.3. Practical Implications and Limitations

The data-algorithm matching strategy proposed in this study provides actionable guidance for practitioners: (1) For low-quality data, prioritize algorithms with strong robustness (e.g., RF for incomplete data, CNN for noisy images); (2) For high-quality data, select algorithms based on task characteristics (e.g., LSTM for sequences, CNN for images); (3) When data quality is poor, combine algorithm selection with data preprocessing (e.g., imputation for missing values, denoising for noisy data) to maximize performance.

This study has two limitations: First, the experiments only used publicly available datasets, and the results may need to be validated on domain-specific data (e.g., medical images, financial transactions); second, the study focused on static data quality indicators, and future research could explore the impact of dynamic data (e.g., streaming data with concept drift) on model efficacy.

6. Conclusions

This empirical investigation systematically analyzes the impacts of data quality and algorithm selection on machine learning model efficacy. The key findings are:

1) Data completeness has a threshold effect (95% completeness is the critical point), while data accuracy and consistency show a linear negative correlation with model performance.

2) Algorithm performance is highly task-dependent—CNN is optimal for images, LSTM for sequences, RF for tabular regression, and SVM for small-scale classification.

3) The proposed data-algorithm matching strategy can significantly improve model efficacy, with performance gains of up to 32% in experiments.

This research emphasizes that the success of machine learning applications depends not only on advanced algorithms but also on high-quality data and rational algorithm selection. Future work should focus on domain-specific data validation and dynamic data scenarios to further enhance the practical value of machine learning in real-world applications..

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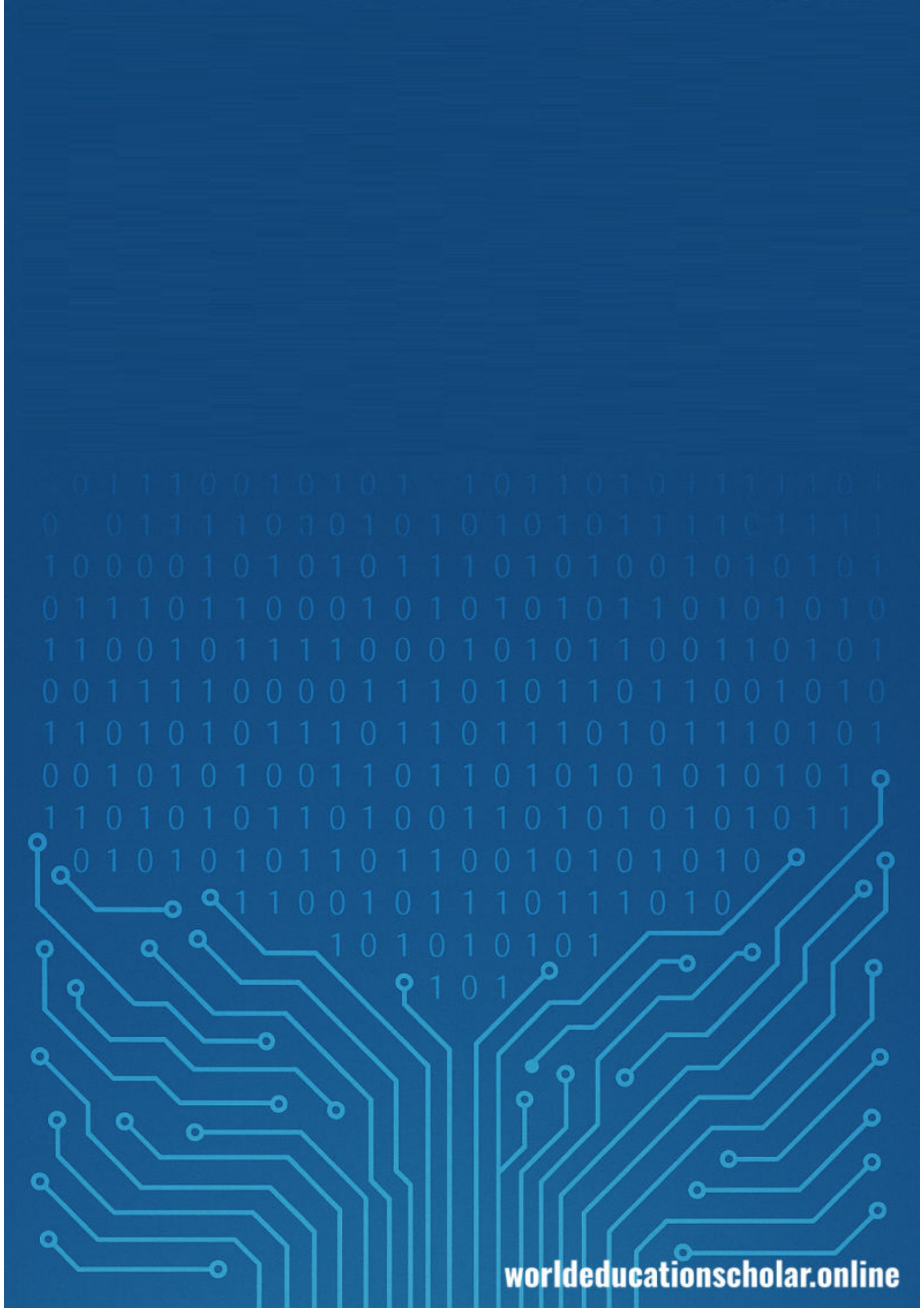
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