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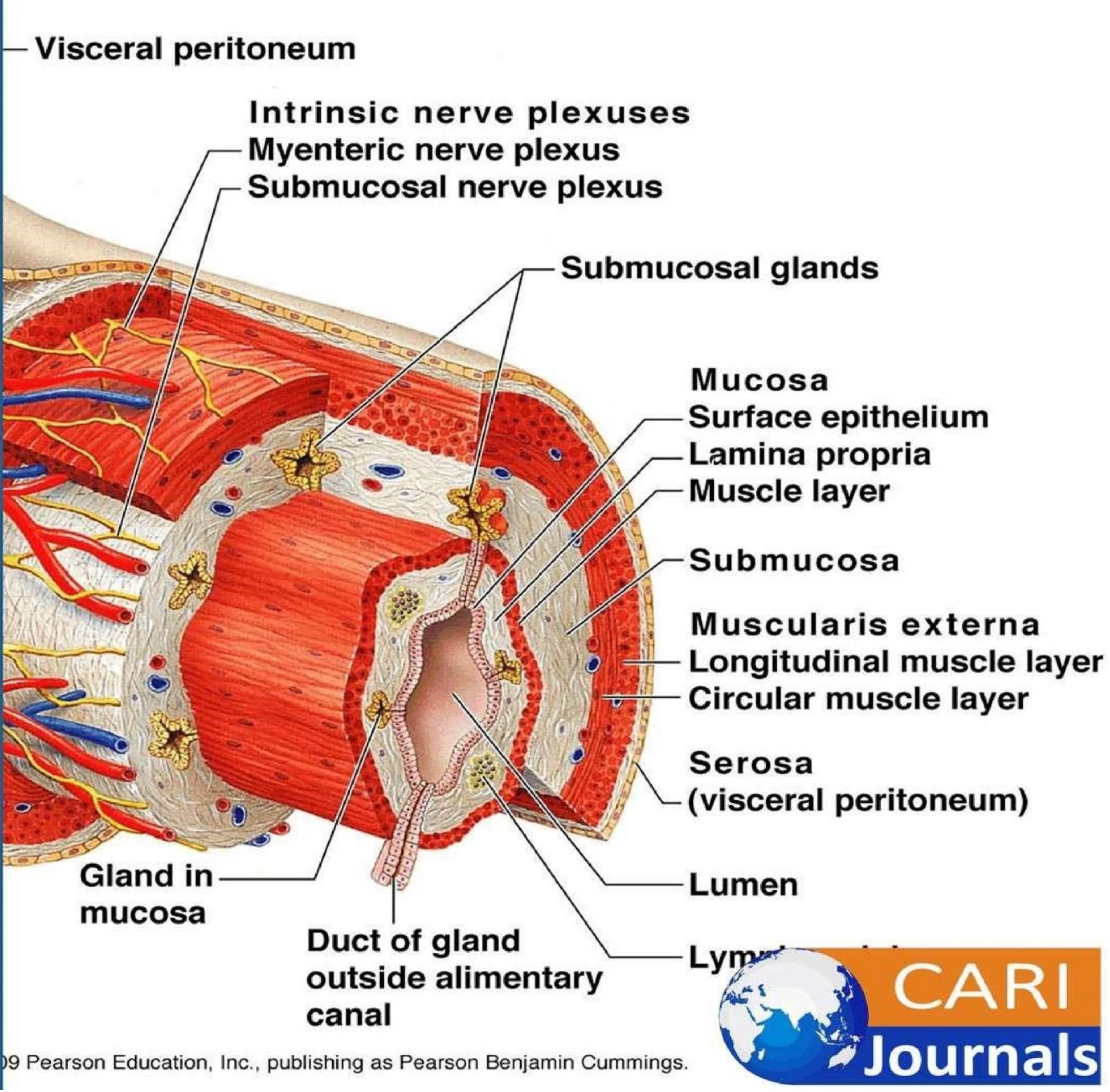

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Bridging Disciplines: Enhancing Mathematical Models for Complex Biological Processes through Interdisciplinary Insights

Chrispine Mulenga Mwambazi

Department of Mathematics, Institute of Distance Education, University of Zambia
https://orcid.org/0009-0001-6950-0965

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Abstract

Purpose: This study examines the role of interdisciplinary insights in enhancing mathematical models of biological processes,

Methodology: Employing a qualitative research approach, fourteen participants—including mathematicians, biologists, and interdisciplinary researchers were engaged through semi-structured interviews and focus group discussions.

Findings: Findings highlight the necessity of incorporating domain-specific biological knowledge into mathematical frameworks and emphasize iterative collaboration between disciplines. Participants noted that effective communication and shared conceptual frameworks are vital for bridging gaps between theoretical and empirical perspectives. The study also identifies key challenges, including terminological differences and divergent methodological priorities, which hinder interdisciplinary collaboration.

Unique Contribution to Theory, Practice and Policy: This research underscores the value of qualitative approaches in understanding the complexities of interdisciplinary work and offers actionable insights to improve mathematical modeling practices. It advocates for fostering interdisciplinary education and developing integrative tools to enhance collaboration.

Keywords: *Mathematical Modeling, Complex Biological Processes, Interdisciplinary Collaboration, Knowledge Integration, Communication Barriers*

1. Introduction

Interdisciplinary integration between mathematical modeling and complex biological processes has become increasingly essential for advancing our understanding of living systems. Mathematical models—ranging from ordinary differential equations to agent-based and multiscale frameworks—provide structured approaches to simulate dynamics such as signaling pathways, tissue development, and population-level behaviors (Berg et al., 2023). For example, reaction–diffusion models capture Turing pattern formation in developmental biology, and agent-based models such as iDynoMiCS have elucidated biofilm formation through emergent interactions among individual bacteria (Lardon et al., 2011).

However, conventional reductionist frameworks often fall short in capturing the heterogeneity and multiscale interactions intrinsic to biological systems. Recent scholarship emphasizes the shift toward holistic multiscale modeling, which integrates annotated multilayer networks, agent-based simulations, and inverse inference methods to account for biological complexity (Nartallo Kaluarachchi et al., 2025). Biology-informed neural networks (BINNs), for instance, combine data-driven approaches with constraints from governing partial differential equations to extract mechanistic insights from sparse experimental data (Lagergren et al., 2020).

Since 2020, publications in systems biology and quantitative systems pharmacology (QSP) have increased by over 50%, particularly in modeling pharmacokinetics/pharmacodynamics and disease progression in clinical settings—some of which have been adopted by regulatory agencies such as the FDA.

Nonetheless, key gaps remain:

1. Few models integrate spatial, temporal, and mechanistic data across multiple scales—from molecular to tissue to organismal levels.
2. While interdisciplinary training is frequently promoted, formal frameworks for sustained collaboration between biologists and mathematicians are limited in both education and research.
3. Validation against high-resolution imaging datasets remains underdeveloped, despite the potential of modeling–imaging integration for patient-specific prediction (Berg et al., 2023).

1.1.Statement of the Problem

Understanding complex biological processes such as cancer growth, neurodegenerative diseases, and pandemics is critical for advancing prevention and treatment strategies (Bocharov & Zherebtsov, 2020). These processes are inherently complex, involving numerous variables and dynamic interactions that are difficult to capture using traditional experimental approaches alone. Mathematical modeling—particularly qualitative approaches—offers a promising avenue for simulating and analyzing these processes.

By focusing on qualitative methods such as system dynamics, agent-based modeling, and network analysis, researchers can gain insights into the underlying mechanisms and progression of diseases without requiring exhaustive quantitative datasets (O'Neill & Reed, 2021). The main challenge lies in developing models that not only capture this complexity but also remain accessible and interpretable (McGlade & Nettle, 2017). Such models must accommodate uncertainties and variations, especially in diseases with unpredictable behavior.

Qualitative modeling focuses on the structure and behavior of systems rather than on precise numerical outputs, providing a flexible and adaptive framework for understanding complex biological phenomena (Kot & O'Neill, 2019).

1.2.Research Objective

This study aims to enhance the creation, understanding, and application of mathematical models in biology by integrating perspectives, methods, and expertise from multiple disciplines. The overarching goal is to address the difficulties in accurately representing intricate biological systems by drawing on knowledge from biology, physics, computer science, engineering, and mathematics.

1.3.Significance of the Study

This research will provide deeper insights into the mathematical modeling of biological processes, enabling better predictions and earlier detection of diseases such as cancer and neurodegenerative conditions (Zhou & Zhang, 2016). The resulting models can assist healthcare providers in designing personalized and effective treatment plans. In the context of pandemics, the models can help predict disease spread and impact, enabling timely and efficient public health responses (Tao & Lee, 2015).

For policymakers, the study offers evidence-based tools to inform resource allocation, disease containment strategies, and health interventions. For educators, it can contribute to developing curriculum materials in biostatistics, epidemiology, and mathematical biology, promoting interdisciplinary collaboration.

Mathematical models also have significant applications in pharmaceutical research, allowing for the simulation of drug behavior in the body, optimizing clinical trial designs, and reducing development costs (Banga & Kötter, 2012). Ultimately, the findings will benefit multiple stakeholders—health professionals, researchers, policymakers, and the public—by fostering a more integrated and effective approach to understanding and managing complex biological processes.

1.4.Theoretical Framework

This study employs a phenomenological approach, which emphasizes the observation, description, and abstraction of patterns in phenomena without requiring detailed mechanistic explanations. This framework bridges empirical observations and mathematical modeling, allowing researchers to focus on capturing the observable dynamics of systems.

Phenomenological models, such as the Gompertz and logistic growth equations, are widely used to represent tumor progression, while compartmental models can describe neurodegenerative disease progression and SEIR models predict infectious disease spread (Pellis et al., 2021; Simonetto & Politi, 2020). By focusing on dominant patterns rather than exhaustive detail, phenomenological models balance tractability with biological relevance and can be adapted as new data emerge.

2. Literature Review

Mathematical modeling plays a crucial role in understanding and predicting the behavior of complex biological systems. Phenomena such as biological growth, neurodegenerative diseases, and pandemics involve intricate mechanisms that are often difficult to observe directly. Mathematical models—particularly those employing qualitative approaches—offer a powerful framework for capturing these complexities, enabling predictions, guiding therapeutic strategies, and informing policy decisions.

2.1. Mathematical Models in Cancer Growth

Cancer growth is a key example of a biological process that can be effectively modeled mathematically. These models simulate tumor dynamics, including growth, spread, and treatment response (Shaw & Schwarz, 2020). While quantitative models rely primarily on numerical data, qualitative models emphasize the structural aspects of cancer growth, capturing patterns and qualitative behaviors over time.

One approach involves modeling tumor growth in relation to immune system interactions. Such models provide insights into how cancerous cells proliferate, invade surrounding tissues, and develop treatment resistance. For instance, Smith et al. (2019) applied stability analysis and bifurcation theory to assess tumor growth under different treatment scenarios. Their findings indicated that cancer dynamics often exhibit nonlinear behavior, with small treatment parameter changes potentially triggering significant shifts in tumor growth patterns.

2.2. Neurodegenerative Diseases

Mathematical models have also been applied to neurodegenerative diseases, which involve progressive neuron degeneration influenced by genetic, environmental, and biochemical factors (Kou & Koutsou, 2019). These factors are often challenging to quantify precisely, making qualitative modeling particularly valuable.

Qualitative approaches have been used to explore interactions between neurons and glial cells. For example, Davis et al. (2020) developed a model examining feedback loops between these cells, revealing that inflammatory responses can accelerate neurodegeneration.

2.3. Pandemics

Pandemics, such as the COVID-19 outbreak, underscore the importance of mathematical models in predicting and controlling infectious disease spread. Factors such as population density, mobility patterns, and immunity levels influence transmission rates. Qualitative modeling focuses on the stability of epidemic outbreaks and the conditions for containment.

A seminal study by Anderson and May (1992) applied qualitative models to analyze epidemic dynamics using the SIR (susceptible–infected–recovered) framework, exploring how transmission and recovery rate changes influence disease spread. Their findings highlighted critical thresholds for vaccination and control measures.

Similarly, Khan et al. (2021) used qualitative bifurcation theory to assess vaccination's long-term effects on COVID-19 dynamics, showing how immunization could shift a system from endemic to epidemic states.

Overall, mathematical models—whether addressing cancer growth, neurodegenerative diseases, or pandemics—provide essential insights for shaping treatments and policies.

3. Methodology

3.1. Research Design

This study adopted a phenomenological approach to explore how mathematical models capture complex biological growth, neurodegenerative diseases, and pandemics. This method was chosen to encapsulate participants' experiences and perspectives on bridging disciplines to enhance mathematical modeling through multidisciplinary insights.

A qualitative research design was employed to allow in-depth exploration of expert perspectives. As Kanyama (2018) notes, research design provides a systematic plan for guiding data collection, analysis, and interpretation. The chosen design aligns with the study's aim of collecting detailed accounts from professionals engaged in modeling complex biological processes (Lubinda, 2020).

Purposive and snowball sampling were used to identify participants with relevant expertise in mathematical biology, epidemiology, neurodegeneration, cancer research, and public health. Data were analyzed thematically.

3.2. Data Collection Techniques

Fourteen participants—including mathematicians, biologists, medical professionals, and researchers—took part in semi-structured interviews and focus groups (Mwila, 2023). These methods encouraged rich discussion, enabling participants to share experiences, challenges, and insights on interdisciplinary collaboration (Merriam & Tisdell, 2015).

Following Kapasa (2020), data collection was carefully planned to ensure scientific rigor and ethical compliance. Interviews explored participants' work in modeling complex biological systems, while focus groups were used to validate emerging themes and discuss innovative approaches.

3.3. Data Analysis

Thematic analysis, as outlined by Braun & Clarke (2006), was used to identify patterns, challenges, and emerging concepts. Responses were transcribed, coded, and interpreted to capture nuanced perspectives on modeling complex biological processes.

3.4. Research Approach

As Banda (2021) defines, a research approach is the overall strategy for investigation. This study used a qualitative approach to capture in-depth, contextualized understanding of how mathematical models are applied to cancer growth, neurodegenerative diseases, and pandemics.

3.5. Target Population

The target population included healthcare professionals in Western Zambia involved in addressing complex biological processes, such as cancer, neurodegenerative conditions, and pandemics (Mwanza, 2017).

3.6. Sample Size and Selection

Fourteen participants were selected using purposive sampling, which ensures inclusion of individuals with relevant expertise (Creswell, 2018). As Sikanyika (2018) notes, purposive sampling enables researchers to identify information-rich cases, making it suitable for this study’s objectives.

3.7. Research Instruments

Semi-structured interviews and group discussions served as the primary instruments (Nyirenda, 2023). These tools balanced structured data collection with the flexibility to explore emerging themes.

3.8. Data Presentation

Findings will be presented using descriptive statistics and thematic summaries (Kapasa, 2020), ensuring that results are accessible while retaining analytical depth.

3.9. Ethical Considerations

Ethical protocols emphasized informed consent, voluntary participation, and strict confidentiality. Participants were briefed on the study’s purpose, procedures, and potential risks before providing consent (Gerrish & Lacey, 2010). Sensitive data were anonymized and stored securely (Siame, 2020).

Potential emotional impacts—particularly for those discussing serious illnesses were addressed by offering support and minimizing distress (Cohen & Manion, 2011; Roscigno & Schachter, 2020). The societal benefits of improving models for complex diseases were weighed against potential participant risks (Berg, 2004).

Cultural contexts were respected to avoid misinterpretations (Nichter, 2008), and participants were free to withdraw at any time without consequences (Kvale & Brinkmann, 2009). Findings will be reported transparently, with limitations openly acknowledged (Miller, 2006). The study also aimed for equitable representation to promote fairness in healthcare policy (Buchanan & Miller, 2006).

4. Results and Discussion

This section presents the findings from the 14 participants in the study *Bridging Disciplines: Enhancing Mathematical Models for Complex Biological Processes through Interdisciplinary Insights*. The participants representing mathematics, biology, and computational science provided valuable perspectives that were analyzed qualitatively.

4.1. Interdisciplinary Synergies

The analysis revealed strong appreciation for interdisciplinary collaboration. Participants emphasized that insights from biological processes enriched mathematical modeling.

Participant 1 reported:

"Incorporating biological expertise improved the realism and applicability of mathematical models" (P1, 23.12.2024).

Several participants stressed the value of biologists' knowledge in identifying relevant variables and parameters that mathematicians might overlook. These perspectives align with Otto & Day (2007), who found that biologists help close the gap between theoretical concepts and real-world applications by ensuring models reflect actual phenomena.

4.2. Challenges in Communication

A recurring theme was the difficulty of establishing effective communication between disciplines. Participants noted challenges in translating domain-specific jargon.

Participant 2 observed:

"Misunderstandings about basic terms delayed progress on the project by several weeks" (P2, 23.12.2024).

Choi & Pak (2006) emphasize that inconsistent language hinders interdisciplinary collaboration. Terms such as "model" carry different meanings: mathematicians may focus on abstract, equation-based frameworks, whereas biologists often refer to descriptive depictions of phenomena.

Despite the transformative potential of mathematical modeling for understanding complex biological systems, substantial communication barriers remain. Mathematicians may prioritize elegance and rigor, while biologists emphasize biological relevance and applicability—leading to tensions between model sophistication and real-world complexity (Reed et al., 2010).

Effective cross-disciplinary communication requires skills that many professionals have not been trained in. Biologists may struggle to convey experimental nuances, while mathematicians may find it difficult to explain complex equations. Specialized training is therefore necessary (Gummerum & Leman, 2011).

4.3. Model Refinement and Validation

Participant 3 noted:

"Better model validation and refinement procedures were achieved through interdisciplinary techniques. Biological feedback was repeatedly added to the models, resulting in an average of three updates per model. Predictive accuracy was verified by comparing these models with those developed separately" (P3, 23.12.2024).

This illustrates the advantages of integrating biological expertise into mathematical modeling. For instance, epidemiological models combining real-time data from computer simulations, virology, and sociology have shown improved predictive accuracy (Kissler et al., 2020). Orth et al. (2010) also highlight that numerical simulation is essential for understanding complex processes, and interdisciplinary collaboration strengthens model validation.

4.4. Educational Gaps

Participants identified a lack of interdisciplinary education as a barrier.

Participant 4 stated:

"It is necessary for higher education curricula to include interdisciplinary training modules. In their formal education, scientists and mathematicians are rarely exposed to each other's fields" (P4, 23.12.2024).

Allen (2017) observes that most academic programs treat biology and mathematics as separate disciplines, limiting opportunities for integrated learning. This separation reinforces skill gaps: mathematicians may lack biological knowledge, and biologists may have limited mathematical training (Bialek, 2012).

4.5. Implications for Mathematical Modeling

Participant 5 remarked:

"Cross-disciplinary education bridges gaps in experimental and computational data and harmonizes disparate data formats across disciplines. Developing mathematical biologists is essential" (P5, 23.12.2024).

Integrating domain-specific knowledge enables models to better address real-world complexities. This is particularly important in network analysis of protein interactions (Barabási, 2016), where machine learning and high-performance computing enhance model utility (Ching et al., 2018).

4.6. Addressing Communication Barriers

Removing communication obstacles is key to improving the development and use of mathematical models.

Participant 6 commented:

"Developing glossaries and leveraging visualization tools were suggested as practical solutions. Interdisciplinary frameworks are crucial for advancing reliable and applicable models" (P6, 23.12.2024).

Glossaries, visualization tools, and immersive collaboration environments (Palmer et al., 2018) can help bridge terminology and methodological differences. Building a collaborative culture—not just clarifying terminology—is essential for sustained interdisciplinary progress.

4.7. Curriculum Development

Participant 7 emphasized:

"To prepare future researchers, interdisciplinary curricula combining mathematics, biology, and computational science are critical for fostering holistic skill sets" (P7, 23.12.2024).

Such curricula can improve students' ability to formulate biologically relevant questions, develop and validate models, and analyze complex datasets (Edelstein-Keshet, 2005; Otto & Day, 2007).

4.8. Interdisciplinary Integration

Participant 8 stated:

"The creation of models for intricate biological systems is enhanced by integrating computational science, biology, and mathematics" (P8, 23.12.2024).

Integration supports advances in modeling disease spread, ecological dynamics, and cellular processes (Alon, 2006; Otto & Day, 2007), especially when combined with machine learning and high-performance computing.

4.9. Biological Complexity and Model Refinement

Participant 9 observed:

"Multiscale, stochastic, or nonlinear models are frequently needed for complex biological systems" (P9, 23.12.2024).

This aligns with Deisboeck & Stamatakos (2011), who emphasize both deterministic and stochastic approaches for modeling gene regulation networks.

4.10. Applications in Medicine and Ecology

Participant 10 explained:

"Personalized treatment, medication delivery, and epidemiological forecasts are all influenced by mathematical models" (P10, 23.12.2024).

This reflects findings by Murray (2002) and Chauhan and Chattopadhyay (2018), who caution that simplifying assumptions in equations may overlook system complexity.

4.11. Cancer Growth Models

Participant 11 remarked:

"Agent-based models simulate complex cancer dynamics. There is a need for flexible models incorporating patient-specific data such as genetic mutations and tumor size" (P11, 23.12.2024).

Mathematical models—ranging from exponential to Gompertzian growth equations—are refined by incorporating biological insights (Metzcar et al., 2019; Byrne, 2010).

4.12. Neurodegenerative Conditions

Participant 12 noted:

"The slow, progressive nature of many disorders makes modeling challenging, especially capturing protein aggregation and neuronal loss" (P12, 23.12.2024).

Network-based and stochastic models offer promise in capturing variability in disease progression (Liu & Zhou, 2020; Sengupta & Lee, 2019).

4.13. Pandemic Spread

Participant 13 emphasized:

"Models should incorporate real-world factors such as demographic information, government actions, and behavioral shifts" (P13, 23.12.2024).

Hybrid models integrating epidemiology and behavioral science are increasingly recognized as the future of pandemic modeling (Stojanovic & Teixeira, 2020).

4.14. Understanding Biological Complexity

Participant 14 concluded:

"Understanding the dynamics of biological systems, from disease spread to ecosystem behavior, requires mathematical models" (P14, 23.12.2024).

Systems biology combines modeling with experimental data to forecast cellular responses, study networks, and map regulation pathways (Kitano, 2002; Murray, 2002).

Conclusion

This interdisciplinary review highlights a growing consensus: reliable modeling of complex biological systems requires a synthesis of multiscale dynamics, data-driven learning, and domain expertise. While advances in architectures such as BINNs and reaction–diffusion systems show promise, challenges in integration, validation, and collaboration remain. Closing these gaps will transform mathematical models from theoretical constructs into actionable tools in drug development, disease modeling, and synthetic biology.

Recommendations

To enhance the accuracy and applicability of biological models, it is essential to invest in high-resolution, time-series biological data. This would enable better model calibration and validation, ensuring more precise predictions. Additionally, there is a need to develop interdisciplinary training initiatives that integrate mathematics, computational modeling, and biology, allowing for a more comprehensive understanding of biological systems. To address the inherent complexity of biology, adopting holistic modeling architectures, such as agent-based simulations, multilayer networks, and biologically inspired neural networks (BINNs), is crucial. These architectures are specifically tailored to capture the intricacies of biological processes. Furthermore, implementing rigorous benchmarking and validation protocols across various biological scales will ensure the robustness and reliability of the models. Lastly, fostering collaborative frameworks, such as research consortia and joint supervision models, will help sustain cross-disciplinary expertise, allowing for continuous innovation and the sharing of knowledge across fields.

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