DOI: 10.54254/2753-8818/2025.GL25312

The Assistance of Applied Mathematics in Biomedical Sciences

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Abstract. This paper focuses on the facilitating role of applied mathematics in biomedical sciences. As an interdisciplinary field integrating biology and medicine, biomedical science faces challenges such as handling large amounts of data and integrating multiple disciplines in its development. Mathematics, statistics, and computational methods have played a significant role in this field. This paper finds that the SIR model in mathematical modeling has been instrumental in epidemic prevention and control, the NCC model has provided new ideas for cancer treatment, and the QSAR model has played a crucial role in drug development. Statistical principles such as regression analysis and variance analysis are indispensable in biomedical research. Computational methods also have extensive and critical applications in bioinformatics, medical imaging, systems biology, and other areas. These disciplines are interdependent, transforming raw biological data into actionable insights. Although there are challenges such as data integration, their continuous integration and technological advancements are expected to open up new frontiers in areas such as precision medicine and drive the future development of human healthcare.

Keywords: Applied mathematics, Biomedical sciences, Mathematical modeling, Basic statistical principles, Computational methods

1. Introduction

Biomedical science is an interdisciplinary subject that integrates knowledge from biology and medicine, focusing on the study of health and disease in living organisms. It's very important that it can help people prevent infection and the spread of sickness by understanding the theory and process of disease. At the same time, it plays an important role in the research of medicine and provides a theoretical base for medical technology. But in the sphere of biomedical science, there are also many challenges, such as the difficulty in dealing with a large amount of data, obstacles from multi-disciplinary integration and so on.

This paper will emphasize the role of mathematics, statistics and computational methods in biomedical research to help scientists to deal with these challenges. This research will specify the specific principles and functions of each discipline respectively and cite some literature and examples.

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2. The application of mathematics in biomedical science

2.1. Application of mathematical models in biomedical

The mathematical models have many applications. First of all, this paper will use a virus that occurred from 2019 to 2022 as an example. During the period when the virus spread quickly, the government used the mathematical model called SIR to divide people into three groups (Susceptible, Infectious and Recovered). According to some parameters, the model can reveal the propagation tendency of the virus clearly. The scientists will change the parameters, as the population density in different areas and provide predicted data to the government in order to help the government generate a strategy. The information that Professor Lin mentioned in "Four-tier response system and spatial propagation in China by a network model" in 2020 shows that the government has four levels that correspond to different conditions [1].

Another example is about the research on cancer. In 2022, Professor Chen's team introduced the Normalized Cross-Correlation (NCC) model, which simulates the progression of six major cancer types by integrating cell proliferation, apoptosis, and pathogenic influence. This model enables personalized treatment strategies to avoid over-treatment and enhance efficacy [2]. The NCC model combined six simulation models of six major types of cancer, which are based on the influence on the growth of cancer cells by cell proliferation, apoptosis and pathogenesis. According to the models, doctors can make individual treatment methods to avoid the harm caused to the patients by the excessive treatment and enhance the efficiency.

After presenting two examples, the paper will discuss how mathematical models can assist in understanding complex biological systems. The informations that professor Fischer and Hans Peters writed in their research paper "Mathematical modeling of complex biological systems: from parts lists to understanding systems behavior", mention that the requirments which are needed to understand the complex biology system and diseases, are not only identify and characterize the individual molecules in the system but also obtain a thorough understanding of the interaction between molecules and pathways [3]. The mathematical model can help simplify the complex system. It can transform the reaction into a mathematical equation. At the same time, it can simulate the process of evolution while the biological system is undergoing dynamic changes. The example mentioned above is the best evidence.

2.2. The role of mathematics in drug development

The paper "What Can Mathematics Do for Drug Development?", which is written by Moore, Helen, Allen, Richard, mainly discusses the role of mathematics in drug development, covering aspects such as drug design, efficacy prediction and clinical trial design [4]. For example, a model called QSAR is able to utilize mathematical methods to estimate the relationship between structural parameters of the compound and biological activity according to a period of compounds with similar structure. In the design of antihypertensive drugs, this model plays an important role in compiling a series of new types of ACE inhibitors and improving the success rate of drug design.

3. Statistical principles in biomedical science

In the research of biomedical science, the researchers will involve many statistical principles. For example, according to the sampling principle, when researchers need some volunteers for an experiment, they will randomly select volunteers as a sample from people who meet the criterion.

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Because the random selection will make the sample more representative and the result of the research will be more accurate. Principles such as regression analysis, analysis of variance, statistical inference and so on will also be used in biomedical science. In the next part, this paper will give a detailed introduction to these principles.

First of all, the regression analysis is used to predict the association between 2 different variables. This principle mainly involves using data points on the graph to find the best-fit line and compares the difference between the predicted values and observed values, so the principle of regression line can explore the dependency patterns among variables. The second one is the principle of analysis of variance. By analyzing the sources of variation in the data, the total variation is decomposed into between-group variation and within-group variation, thereby determining whether there are significant differences among different groups.

In 2024, Chinese doctors Zhang Jianting and Yang Wenjian mentioned the exploration the feasibility and long-run effects of double-plane micro-droplet injection of botulinum toxin type A compared with two traditional treatment methods (triamcinolone acetonide injection and fractional CO_2 laser) in the treatment of hypertrophic scars. “A Comparison of the Efficacy of Botulinum Toxin Type A, Triamcinolone Acetonide, and Fractional CO_2Laser in the Treatment of Hypertrophic Scars: A Randomized Controlled Trial”[5].

Patients were randomly divided into three groups and received corresponding interventions monthly for three consecutive months. The Patient and Observer Scar Assessment Scale (POSAS) was used for evaluation during the 2-year follow-up period. One-way ANOVA was used to compare the POSAS indicators before and after treatment, and two-way ANOVA was used to compare the effects of the three different treatment drugs on the scar scores. The results showed that the treatment of the three groups was effective, and the botulinum toxin group had the lowest scores in some aspects, indicating better efficacy.

Finally, this paper is going to describe a principle called“Hypothesis Testing,” which is able to determine whether the hypothesis is correct. If the researchers need to make sure about the data, they will first make a null hypothesis and an alternative hypothesis, and then they will use the data from the experiment to calculate the P-value using by calculator and compare it with the significance level. The result of the comparison can help researchers decide whether it is necessary to reject the null hypothesis. For example, when $p < \alpha$, we should reject Ho.

4. Computational methods in biomedical science

In the realm of biomedical research, computational methods have emerged as indispensable tools for addressing the complexity of biological systems, analyzing large-scale data, and accelerating scientific discovery. By integrating algorithms, machine learning, and simulation technologies, these methods enable researchers to decode genetic information, predict disease progression, and design innovative therapeutic strategies. This section explores the multifaceted applications of computational approaches in biomedicine, spanning bioinformatics, medical imaging, drug discovery, and systems biology.

4.1. Bioinformatics and big data analysis

Bioinformatics lies at the intersection of computer science and molecular biology, focusing on the development of algorithms to interpret biological data.

Genomic Analysis: During the virus pandemic, computational tools like BLAST (Basic Local Alignment Search Tool) were pivotal in tracking viral mutations by comparing millions of SARS-

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CoV-2 genome sequences. For instance, the identification of the Delta variant's Spike protein mutations through sequence alignment helped prioritize vaccine updates.

Protein Structure Prediction: The breakthrough AlphaFold2 algorithm, developed by DeepMind, revolutionized structural biology by predicting protein 3D structures with >90% accuracy from amino acid sequences alone. In 2021, this technology predicted over 200 million protein structures, including key cancer-related proteins, accelerating drug target identification [6].

Drug Discovery: Computational methods also play a pivotal role in drug design. For example, Sliwoski et al. highlighted how algorithms simulate molecular interactions to optimize compound efficacy, reducing the need for extensive experimental trials [7].

Single-Cell RNA Sequencing: Tools like Seurat leverage dimensionality reduction techniques (e.g., t-SNE) to analyze gene expression data from thousands of individual cells. This has enabled the discovery of rare immune cell subtypes in tumor microenvironments, such as exhausted T cells, guiding personalized immunotherapy strategies.

4.2. Medical imaging and artificial intelligence

Computational models have transformed medical imaging from qualitative observation to quantitative diagnosis, enhancing accuracy and efficiency in disease detection.

Cancer Detection: Deep learning models have significantly improved diagnostic accuracy. For instance, Poplin et al. demonstrated that deep learning on histopathology images can predict breast cancer metastasis with high sensitivity, outperforming traditional manual analysis [8]. Similarly, Google's DeepMind achieves 94.4% sensitivity in detecting lung cancer nodules from CT scans, reducing false positives by 45% compared to traditional methods.

Neurological Disorders: Functional MRI (FMRI) combined with convolutional neural networks (CNNs) can predict Alzheimer's disease up to five years before symptom onset by analyzing brain activity patterns. The Alzheimer's Disease Neuroimaging Initiative (ADNI) uses such models to track cognitive decline and evaluate therapeutic efficacy.

Surgical Guidance: Robotic systems like the da Vinci Surgical System integrate 3D reconstruction algorithms to overlay real-time imaging onto surgical fields, enabling sub-millimeter precision in tumor resection.

4.3. Systems biology and simulation

Computational simulations offer insights into the dynamic interactions of biological systems, from gene regulatory networks to population-level disease spread.

Gene Regulatory Networks: Boolean network models simulate how transcription factors regulate gene expression during embryonic development. For example, Wolpert's "French Flag model" computationally explained positional information in cell differentiation, providing a foundation for regenerative medicine.

Multi-Scale Modeling: The Virtual Heart project by Cardiome combines ion channel dynamics and myocardial cell mechanics to simulate cardiac electrophysiology, aiding the development of anti-arrhythmic drugs by modeling abnormal heart rhythms.

Epidemiological Modeling: During the pandemic, Vabalas et al. used mobility data and machine learning to forecast infection trajectories, showing that behavioral interventions could effectively reduce transmission rates [9]. This complements models like Epifor, which integrates social contact patterns to inform public health strategies.

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5. Conclusion

In conclusion, biomedical science thrives at the intersection of mathematics, statistics, and computational methods, which collectively serve as powerful tools to surmount its inherent challenges.

As emphasized in this article, these disciplines do not exist independently but are interdependent: mathematical formulas lay the foundation for statistical models, while statistical models provide the basis for computational algorithms. Together, they transform raw biological data into feasible insights, bridging the gap between basic research and translational medicine. Although challenges such as data integration and model interpretability still exist, the continuous integration of these fields, coupled with technological advancements, is expected to open new frontiers in precision medicine, disease prediction, and personalized treatment. By embracing this interdisciplinary synergy, biomedical science is expected to solve the unsolved mysteries in health and disease, drive innovation, and shape the future of human healthcare.

This paper still has many places to improve. In terms of research methods, when discussing the cross-application of biomedicine and multiple disciplines, it mainly relies on case studies and principle explanations, without using meta-analysis to integrate previous research for quantitative analysis. Incorporating this method can precisely summarize the differences in application effects in different subfields and enhance the persuasiveness of the conclusion. In the integration of data dimensions, when discussing the application of computational methods, it fails to fully integrate clinical phenotypes, omics, and imaging data for multimodal analysis, and lacks discussion on the data synergy in the integration process.

Future research can focus on multiple directions, such as innovating cross-modal models, leveraging advanced technologies to integrate multi-omics and clinical data to facilitate precise disease diagnosis and treatment; conducting dynamic evolution modeling of biomedical systems, simulating changes in tumor microenvironments and disease courses of neurological disorders to provide support for intervention; exploring the ethical and regulatory adaptation for multi-disciplinary applications, establishing a supporting system to promote the clinical transformation of research outcomes.

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