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Mathematics in medical and life sciences: a multidisciplinary journal championing accessible, complete and transparent communication of mathematics applied to medical, biological and ecological systems

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INTRODUCTION

Mathematics in medical and life sciences: a multidisciplinary journal championing accessible, complete and transparent communication of mathematics applied to medical, biological and ecological systems

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The application of Mathematics – broadly interpreted to include computational and statistical modelling – to Medicine, Biology and the Life Sciences, has a long-established history. Several enduring journals were established between the 1960s and 1980s, and as the intensity and scope of activity has grown internationally, research at the interface of these disciplines increasingly appears in the relevant "domain" (e.g. physiology, cell biology, cancer, infectious disease, botany, ecology and evolution) literature as well as multidisciplinary journals. Indeed several journals have appeared in the last 20 years which explicitly target the intersection between mathematics and biology. Against this context, the question arises as to why another journal is needed in this space.

In developing the journal proposal and assembling the founding editorial board, discussions with experts across the areas mentioned above, and more, a common theme emerged. While both theoretically-and domain-focused mathematical biology have clear homes, a great proportion of activity occupies a space which is – or at least is perceived to be – less well-served by existing journals. The mathematical literature is certainly ideal for presenting detailed mathematical modelling, theory, methodology and calculations, but often has limited impact on the domains of application. Domain and multidisciplinary journals by contrast are ideal to make an impact upon the field of application, however the latter venues are often believed to – or in some cases explicitly require – relegating mathematical detail to appendices and even (un-edited) online supplementary files. Moving the mathematical core of the work out of the main body of the article was felt to undervalue its contribution, as well as compromising peer review, communication and reproducibility. These observations chime with warnings in the wider context of how science values its methodological backbone [1]. A related theme that emerged in discussions was that it can be challenging to publish research that utilizes extensive mathematical methodology, perhaps more than can be elaborated in a domain journal, but also that does not develop new mathematical theory per se. On a more positive note, the recently-established journal *Quantitative Plant Biology* was highlighted through its ethos of championing the integral role of statistics and mathematics at every stage of the scientific process, from hypothesis generation through in silico modelling, experimental design and analysis [2].

Taken together, these observations present a challenge: can we build a better venue to communicate "maths-heavy" science across the broad scope of medicine, biology and the broader life sciences, without compromising either methodological detail or accessibility to the communities which stand to benefit from the work? The vision of Mathematics in Medical and Life Sciences (MMLS) is to provide such a vehicle.

In brief, our strategy to meet this challenge involves four levels of the academic publishing pathway:

(1) Article and special issue commissioning
(2) Article structure and drafting
(3) Peer review
(4) Engagement with domain scientists

Alongside unsolicited submissions, MMLS will, from its launch, commission articles and special issues on topics which showcase the cutting edge of mathematics in medical and life sciences. While we expect to publish many articles on long-established tools, especially systems of ordinary and partial differential equations, MMLS will particularly encourage original research and reviews in emerging areas such as topological data analysis [3], geometry [4], discrete models [5], causal inference [6], networks [7], information theory [8] and

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evolutionary game theory [9]. As Vittadello and Stumpf argue, it is clear that ever more mathematical tools and theory will be necessary to *understand life at the fundamental level* [10], and MMLS aims to promote the development and communication of this new mathematics as it emerges.

In respect of article structure, sections such as lay summaries, graphical abstracts and significance statements are becoming increasingly popular and represent excellent practice. To augment this approach further, MMLS will request that authors explicitly provide guidance to non-mathematical readers as to how to navigate their articles. Model assumptions, structure and approximations are required to be explained and illustrated as clearly as possible before delving into mathematical detail. Alongside this information, MMLS will require that findings, any uncertainties, and testable predictions, are explained in a similarly accessible way. The precise structure and form are left to the authors; an example approach is to present a plain-English model synopsis prior to the mathematical methodology section. The journal will strongly discourage the use of online supplemental information to contain any important information, especially the mathematical methodology that underpins the main findings.

Regarding peer review, MMLS will seek evaluations from both mathematicians and domain scientists, and explicitly pose the question of whether the work has been communicated in a balanced way that allows its significance to be understood; while the decision for publication will ultimately rest with the editorial board, in general the expectation will be that positive evaluations from reviewers in both communities are required for publication.

Finally, to engage domain scientists, MMLS will work with authors to identify key figures who can provide authoritative commentary articles evaluating published findings, thereby engaging the target community, and increasing impact. The journal will also seek and welcome domain scientists to pose new questions to the mathematical community, along with workshop reports exploring new areas for multidisciplinary research.

We of course do not believe that we are inventing a completely new type of journal format; there are many examples of excellent practice along the lines above in recent literature, and so we instead see the role of MMLS as providing strong encouragement and showcasing good practice in the presentation of mathematical biology. The remainder of this editorial will mention a few excellent recent examples from the theoretical and multidisciplinary literature illustrating these qualities.

Infectious disease modelling has undergone a period of extremely intensive and influential activity since the beginning of the Covid-19 pandemic. To give a pertinent example, Martcheva et al. [11] utilized both game-theoretic and behaviour-economic modelling to explore how likely social distancing is to eliminate infectious disease spread. The authors introduce the mathematical model in accessible language, before proving rigorous theorems in the main text of the article, and then frame their findings in terms of the questions that domain scientists, policy makers and the public would immediately recognize – for example *Can social distancing lead to elimination of the disease?*

Another recent example in the field of cardiac electrophysiology [12] exemplifies the role of modelling in optimizing experimental design, and specifically accounting for cell–cell variability in model parameters. This paper again provides an example of generally accessible and mathematically comprehensive communication of application-oriented computational research, with supplemental information being used only for non-essential outputs of statistical inference, rather than core methodology. Moving to the microbial subcellular level, Pang and Lercher [13] recently considered the role of the crowding of intracellular components, its effect on reactions involving small and large molecules, and the optimal crowding density for each type, thereby providing insight into observed differences in cellular densities in nutrient-rich and poor environments. The modelling scheme and equations are again set out clearly and in detail in the main article, with supporting figures and tables being used selectively for in-depth aspects of model validation and parameter inference. Both articles exemplify the style of model presentation and usage of supplemental information that we wish to encourage at MMLS.

Demonstrating excellent practice in scientific software development and its communication, in Ref. [14] Johnson and co-authors describe *ChemChaste*, an extension to the established open-source computational biology package *Chaste* which provides for modelling of an arbitrary number of spatially-diffusing biological reactants, with heterogeneous diffusion coefficients and combining bulk and intracellular reactions. This article concisely motivates the need for the extension, its structure and integration with the core Chaste package, provides several examples which illustrate its capabilities in turn, and the supplementary data appropriately takes the form of an online code repository. MMLS will strongly encourage code to be made available in this way, especially where it forms the main substance of the research.

In the field of neglected tropical diseases and parasitology, the recent work of Crellen and co-authors [15] utilizes mechanistic modelling to interpret data on the dispersion of helminth burden in different geographical regions, thereby inferring differences in parasite fecundity, revealing high false negative rates in diagnostics, and demonstrating that observed and true prevalence may differ significantly due to parasite aggregation. This work provides a striking example that modelling is not simply something to be guided or tested by observations but also that it can be a powerful tool to enable and qualify how observations are interpreted. MMLS will very much encourage this ethos.

The final example we will mention is an editorial article by C. Hui [16], which discusses the usage of Species Distribution Models (SDM) in ecology; these are statistical models which integrate occurrence records and geographic data to map species distributions. Hui writes about the application of SDM to predict and visualize biological invasions, thereby providing a tool to guide policy, and specifically cautions about the risks of overinterpretation if key assumptions of SDMs are not met. This analysis thereby illustrates the broader issue that modelling, particularly when presented in an appealing and compelling way, has the potential for overinterpretation by those who are not mathematically specialist. It should therefore be noted that there is a significant responsibility for authors, reviewers and editors to ensure that modelling assumptions have been transparently stated, and any uncertainties or caveats are made clear – especially when findings are publicized or used to guide policy decisions. MMLS recognizes that compelling and persuasive communication must also be transparent and honest.

The above articles are mentioned to illustrate the ethos of accessible, complete, and transparent communication, the crucial role of mathematics in multidisciplinary research, and the scientific breadth across medicine and life sciences that we aim to encompass. The aim of MMLS will be to recognize and disseminate sound methodological development, to enable the transfer of concepts between sub-fields within applied mathematics – in its broadest sense – as well as to promote the understanding, acceptance, critical uptake and positive impact of modelling beyond the mathematical sphere. On behalf of our founding board of biological and ecological mathematicians, I encourage you and your colleagues to submit your application-focused mathematics to MMLS, and I offer our assistance in disseminating and promoting your work.

Disclosure statement

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References

[1] Van Calster B, Wynants L, Riley RD, et al. Methodology over metrics: current scientific standards are a disservice to patients and society. J Clin Epidemiol. 2021;138:219–226. doi:10.1016/j.jclinepi.2021.05.018

[2] Autran D, Bassel GW, Chae E, et al. What is quantitative plant biology? Quant Plant Biol. 2021;2:e10. doi:10.1017/qpb.2021.8

[3] Nardini JT, Stolz BJ, Flores KB, et al. Topological data analysis distinguishes parameter regimes in the Anderson–Chaplain model of angiogenesis. PLoS Comput Biol. 2021;17(6):e1009094. doi:10.1371/journal.pcbi.1009094

[4] Twarock R, Luque A. Structural puzzles in virology solved with an overarching icosahedral design principle. Nat Commun. 2019;10:4414. doi:10.1038/s41467-019-12367-3.

[5] Jensen OE, Revell CK. Couple stresses and discrete potentials in the vertex model of cellular monolayers. Biomec Model Mechanobiol. 2023;22:1465–1486. doi:10.1007/s10237-022-01620-2

[6] Laubach ZM, Murray EJ, Hoke KL, et al. A biologist's guide to model selection and causal inference. Proc R Soc B. 2021;288:20202815. doi:10.1098/rspb.2020.2815

[7] Rodgers N, Tiňo P, Johnson S. Strong connectivity in real directed networks. Proc Natl Acad Sci USA. 2023;120(12):e2215752120. doi:10.1073/pnas.2215752120

[8] Cohen AA, Ferrucci L, Fülöp T, et al. A complex systems approach to aging biology. Nature Aging. 2022;2(7):580–591. doi:10.1038/s43587-022-00252-6

[9] Wölfl B, te Rietmole H, Salvioli M, et al. The contribution of evolutionary game theory to understanding and treating cancer. Dyn Games Appl. 2022;12:313–342. doi:10.1007/s13235-021-00397-w

[10] Vittadello ST, Stumpf MPH. Open problems in mathematical biology. Math Biosci. 2022;354:108926. doi:10.1016/j.mbs.2022.108926

[11] Martcheva M, Tuncer M, Ngonghala CN. Effects of social-distancing on infectious disease dynamics: an evolutionary game theory and economic perspective. J Biol Dyn. 2021;15(1):342–366. doi:10.1080/17513758.2021.1946177

[12] Lei CL, Clerx M, Gavaghan DJ, et al. Model-driven optimal experimental design for calibrating cardiac electrophysiology models. Comput Methods Programs Biomed. 2023;240:107690. doi:10.1016/j.cmpb.2023.107690

[13] Pang TY, Lercher MJ. Optimal density of bacterial cells. PLoS Comput Biol. 2023;19(6):e1011177. doi:10.1371/journal.pcbi.1011177

[14] Johnson CG, Fletcher AG, Soyer OS. ChemChaste: simulating spatially inhomogeneous biochemical reaction–diffusion systems for modeling cell–environment feedbacks. GigaScience. 2022;11:giac051. doi:10.1093/gigascience/giac051

[15] Crellen T, Haswell M, Sithithaworn P, et al. Diagnosis of helminths depends on worm fecundity and the distribution of parasites within hosts. Proc R Soc B. 2023;290(1991):20222204. doi:10.1098/rspb.2022.2204

[16] Hui C. The dos and don'ts for predicting invasion dynamics with species distribution models. Biol Invasions. 2023;25(4):947–953. doi:10.1007/s10530-022-02976-3