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Extended Abstract

Archives of Physics Research, 2017, 08 (3)
(https://www.scholarsresearchlibrary.com/journals/archives-of-physics-research/)

ISSN 0976-0970
CODEN (USA): APRRC7

Mathematical models versus physical mechanisms

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In physics, mathematical models verify observed phenomena with high accuracy but do not explain the underlying principles. Furthermore, are these mathematical models physically sound? Is it reasonable that mass can increase just by a transformation of coordinates? How can a particle behave like a wave? Remember, the mathematically correct epicycle model also led to incorrect conclusions in Physics in ancient times. Now is the time to study physical mechanisms e.g. in the Yokto range (10-24 m), which have the potential to explain observations in the quantum world, rather than continuously extending mathematical models. Unfortunately, current theories are taken for granted and scientists are too averse to challenge accepted norms. Disproving the Theories of Relativity offers an opportunity to address this impasse and could motivate scientists to open their mind to other ideas. In this talk I propose an experiment, which could substantiate that the expected symmetry of observations for the Relativistic Doppler effect does not exist because the effect can also be interpreted as a geometric mean of classical Doppler effects. In this case the principle of relativity would not be valid, which demonstrates that the mathematical basis of the Theories of Relativity is incorrect. I will also present some ideas to explain these mechanisms. An increasing number of publications include modeling. Often, such studies help us to gain a deeper insight into the phenomena studied and break down barriers between experimental and theoretical communities. However, combining experimental and theoretical work is challenging for authors, reviewers, and readers. To help maximize the usefulness and impact of combined theoretical and experimental research, this Primer describes the purpose, usefulness, and different types of models and addresses the practical aspect of integrated publications by outlining characteristics of good modeling, presentation, and fruitful collaborations. The complex world of biology is governed by physical and chemical laws: molecules diffuse due to Brownian motion, molecular motors transport cargo by turning over ATP, cell walls counteract turgor pressure, plants grow toward light sources, fish regulate their buoyancy, and flows of nutrient determine the growth of a population. In all of these cases, fundamental laws of physics and chemistry are key to understanding processes of life. In addition, mathematics governs the dynamics of populations: regularly dividing cells lead to an exponentially increasing population size, and random birth and death events in a population determine the fate of new alleles in a population. A quantitative and, where applicable, physical description of these phenomena is the domain of models.

With the aim of providing some guidance for good modeling, we focus on physical and mathematical models in experimental papers that investigate phenomena similar to those listed above. We thereby touch upon rather than discuss the overarching question of the role and utility of mathematical models in the life sciences. When designing an experiment or interpreting data, is it advisable to aim for a physical or mathematical model? Despite the title of this article, the answer might often be no. Overwhelming progress has been made in the biological sciences without explicit quantitative modeling. A series of knockout strains informs us about the structure of pathways in cells. A co-localization experiment or co-immunoprecipitation study can directly tell us about the interaction between proteins. A field study can characterize an ecosystem and inform us about the interaction between species—again, without the need for a physical or mathematical model. In all of these cases, quantitative models often would not help to understand the data. Nevertheless, a quantitative description can in the future increase or challenge our current understanding of these biological questions. For example, while not long ago ChIP was used to test a hypothesis between binding of protein and DNA qualitatively, the data from genome-wide analyses obtained via ChIP-seq now call for quantitative models. A model might be needed, however, to interpret data or to confirm or reject a hypothesis via generating predictions. Naturally, that is often the case when the data are quantitative in nature. A great example is the seminal work of Luria and Delbrück (1943) (see Box 1). The two opposing hypotheses for the emergence of resistance to phage in a bacterial population—acquired immunity or random mutations—could only be addressed using the apparently indirect comparison with the two corresponding models. As the authors write, “Repeated tests on a bacterium at different times, or on a bacterium and on its offspring, could therefore give no information of help in deciding the present issue. Thus, one has to resort to less direct methods. Mutations of Bacteria from Virus Sensitivity to Virus Resistance “When a pure bacterial culture is attacked by a bacterial virus the culture will clear after a few hours due to destruction of the sensitive cells by the virus. However after further incubation for a few hours, or sometimes days, the culture will often become turbid again, due to the growth of a bacterial variant which is resistant to the action of the virus.”

Bottom Note: *This work is partly presented at 2nd International Conference on Physics August 28-30, 2017, Brussels, Belgium*