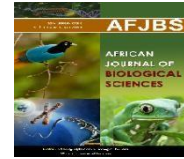**African Journal of Biological Sciences**

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Geometric Principles in Biological Systems

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Abstract: The purpose of this paper is to provide a concise overview of the role of geometry in biological systems.

Keywords: Differential geometry, Finsler geometry, Biological structure

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According to P. L. Antonelli, R. S. Ingarden, and M. Matsumoto [1], P.L. de Maupertuis introduced the "Principle of Least Action" in a precise mathematical form in 1746. This principle was further developed by Euler, Hamilton, and Lagrange, who established the fundamental principles of classical mechanics as we know them today. Maupertuis believed that this principle could be applied not only to physical systems but also to biological systems. He envisioned its potential in studying the movement of animals, the growth of plants, and physiological processes. Maupertuis was not just a theoretical biologist; as historian Bently Glass suggests, he conducted both experimental and theoretical research in evolutionary biology, placing him well ahead of his 18th-century contemporaries. Glass even proposes that Maupertuis was exploring evolutionary biology a century before Darwin (Glass, 1959).

The authors' [1] main goal is to present the principles and methods of sprays (path spaces) and Finsler spaces, as well as examples of their applications in physical and life sciences. They aim to create an introductory book on Finsler geometry and its advanced applications. The authors plan to highlight the significant applications of this field in thermodynamics, optics, ecology, evolution, and developmental biology. The authors discuss a nonlinear extension of Huxley and Needham's allometric theory. They utilize Maupertuis' principle of least action to develop a framework suitable for studying colonial organisms, which exhibit characteristics of both individuals and colonies. The focus is on analyzing natural events within a local environment and the interconnected processes that govern them. This approach adopts a

phenomenological perspective, which inherently determines the appropriate level of description for these phenomena.

Based on the study of "The Theory of Finslerian Laplacians and Applications" [2], Finslerian Laplacians have emerged as a result of the need to model the complexities of the modern world. However, the origins of the Laplacian concept can be traced back to the sixteenth century. The Prologue of this volume provides a comprehensive account of its phylogeny and history. The main text commences with a concise introduction to stochastically derived Finslerian Laplacians, which have found applications in fields such as ecology, epidemiology, and evolutionary biology. The mathematical concepts are then thoroughly presented, followed by generalizations to Lagrange geometry, the focus abruptly shifts to the local mean-value approach to Finslerian Laplacians, and a Hodge-de Rham theory is developed to represent real cohomology classes through harmonic forms on the base manifold. The paper also covers modern topics, including nonlinear Laplacians, Bochner and Lichnerowicz vanishing theorems, Weitzenböck formulas, as well as Finslerian spinors and Dirac operators. The genealogy and historical background are detailed in the Prologue of this publication. The main text commences with a concise overview of stochastically derived Finslerian Laplacians, with applications in ecology, epidemiology, and evolutionary biology.

Jacques Demongeot, Jean-Pierre Françoise, Mathieu Richard, Franck Senegas, Thierry-Pascal Baum [3] demonstrate how basic analysis of bio-arrays images can result in peak segmentation for analyzing gene activity. The unique structure of bio-arrays images is the focus of their work, aiming to introduce a mathematical method for automated processing. The differential geometry approach utilized in this study can be applied to various image types with grey level peaks indicating functional activity or chemical concentration. The mathematical method relies on fundamental techniques of differential geometry and dynamical systems theory, offering a straightforward and effective algorithm for isolating peaks during segmentation.

Cells exhibit intricate and organized structures, displaying a wide array of shapes and internal arrangements. The complexity of cellular geometry is evident in both single-celled organisms and cells found in multicellular organisms. The origin of a cell's geometry remains a mystery, as questions similar to those in developmental biology arise when studying cells. The extent to which global cell polarity cues influence cellular organization compared to local interactions between cellular components is still uncertain. Moreover, it is unclear whether cellular structure remains consistent across cell generations or how cell geometry relates to tissue organization. Additionally, the scaling of intracellular structures in relation to the overall size of the cell raises further questions. The field of cell biology is currently grappling with these complex inquiries [4].

Change detection plays a crucial role in medical imaging as it provides a non-invasive and measurable tool for diagnosing and evaluating the effectiveness of tumor treatments. The authors [5] introduce a novel quantitative approach to identify changes in volumetric medical data and cluster anatomical structures. This method involves assessing volumetric distortions

necessary to deform a test three-dimensional medical dataset segment onto a previously-acquired reference or a given prototype in the case of clustering. Unlike traditional voxel-based techniques, our algorithm operates on tetrahedral meshes, allowing it to be applied to both closed, simply-connected surfaces and volumetric domains with complex boundaries.

Jürgen Jost [6] explores the existence and interaction of biological structures in space. While space is 3D, it is not Euclidean from the perspective of biological organisms due to the influence of gravity on Earth's surface. This results in the mobility and interactions of terrestrial organisms being more akin to 2D. At the cellular level, this limitation plays a lesser role. However, the DNA, one of the most crucial structures, is organized in a one-dimensional manner. This is because a 3D interior is not easily accessible for reading or copying, and a 2D structure is not as suitable for sequential, temporal processing. Linear structures are better adapted for this purpose, especially in dealing with bottlenecks like the ribosome where polypeptides are synthesized.

The central argument presented in the article [6] posits that the fundamental characteristic of biological life lies in its capacity to govern and oversee various processes, while retaining this ability over an extended period. This regulation can occur in a hierarchical or reciprocal manner, and it occurs within a three-dimensional framework. Consequently, it follows that the information required by a biological process pertains solely to the control aspect, rather than the specific content of those processes. Furthermore, these controlled processes can be considerably more intricate than the controlling process itself, and this discrepancy is indeed essential. Notably, each biological process relies on the intricacies of its surrounding environment.

The primary objective of this work [7] is to investigate the concepts and manipulations of geometry and topology, dynamic variables, and specific biological mechanisms, as well as their interconnections. Additionally, it aims to emphasize the importance of utilizing integrated models in research. Simply examining gene and protein data alone does not provide sufficient understanding of the numerous biological processes at work in living organisms. Tissues, being intricate dynamic systems, rely on the interactions of hundreds of thousands of biomolecules to carry out various organismal functions. The development of complex organisms heavily relies on several topological mechanisms, such as four-dimensional transformations, which operate across the three levels of organization, regulation, and evolution in biological systems.

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