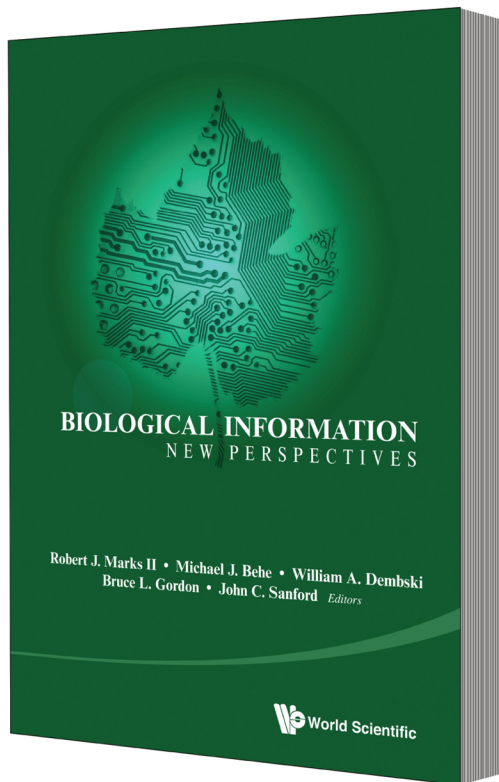


BIOLOGICAL INFORMATION

NEW PERSPECTIVES



Proceedings of the Symposium

Cornell University, USA, 31 May – 3 June 2011

edited by **Robert J Marks II** (*Baylor University, USA*), **Michael J Behe** (*Lehigh University, USA*), **William A Dembski** (*Discovery Institute, USA*), **Bruce L Gordon** (*Houston Baptist University, USA*) & **John C Sanford** (*Cornell University, USA*)

"This is by far the most rigorous and in-depth re-examination of the sufficiency of neo-Darwinian theory. Never have so many well-credentialed scientists, representing so many disciplines, united so effectively to look beyond the standard mutation-selection paradigm." -The Editors

In the spring of 2011, a diverse group of scientists gathered at Cornell University to discuss their research into the nature and origin of biological information. This symposium brought together experts in information theory, computer science, numerical simulation, thermodynamics, evolutionary theory, whole organism biology, developmental biology, molecular biology, genetics, physics, biophysics, mathematics, and linguistics. This volume presents new research by those invited to speak at the conference.

The contributors to this volume use their wide-ranging expertise in the area of biological information to bring fresh insights into the many explanatory difficulties associated with biological information. These authors raise major challenges to the conventional scientific wisdom, which attempts to explain all biological information exclusively in terms of the standard mutation/selection paradigm.

Several clear themes emerged from these research papers: 1) Information is indispensable to our understanding of what life is; 2) Biological information is more than the material structures that embody it; 3) Conventional chemical and evolutionary mechanisms seem insufficient to fully explain the labyrinth of information that is life. By exploring new perspectives on biological information, this volume seeks to expand, encourage, and enrich research into the nature and origin of biological information.

Key Features:

- Very significantly advances our understanding of the nature of biological information, and elucidates the profound difficulties inherent in explaining the origin and maintenance of biological information
- Is highly unique due to its non-traditional approach to these issues, and it contains various landmark papers

Readership:

Academics, researchers, postgraduates and advanced undergraduates in bioinformatics. Biologists, mathematicians/statisticians, physicists and computer scientists.

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