

PROFILE

Liaofu Luo: A pure scientist of theoretical biophysics

Lirong Zhang, Junjie Liu*

School of Physical Science and Technology, Inner Mongolia University, Hohhot 010021, China

* Correspondence: pyljj@imu.edu.cn

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Liaofu Luo is a senior Professor of Physics at the Inner Mongolia University, China. He was born in Shanghai in September 1935. Following his graduation with honors from the Department of Physics of Peking University, in 1958, Professor Luo developed his career at the Inner Mongolia University, where he has been working in theoretical physics and interdisciplinary sciences for more than 60 years. Prof. Luo has been the author of more than 400 scientific articles in particle physics and biophysics and initiated a research group focused on bioinformatics research. Today, at the age of 85, Luo is still active at the forefront of the scientific research of his country. He says that there is nothing he would rather do.

Liaofu Luo is a morally pure scientist. He is indifferent to fame and fortune, just simply working hard and living unpretentiously. Prof. Luo's character has also been seen in significant actions: together with his wife, he has made a very generous donation of 100,000 CNY, accumulated

for years, to the Inner Mongolia Charity Federation aiming to help the children at the Hope Primary School.

In his youth, Luo worked in particle physics and published several papers that were highly acclaimed by colleagues from home and abroad. Altogether, these publications have made him to win the National Science Congress Award in 1978. In 1982 and while as a forerunner in his field, Prof. Luo has focused his research on theoretical biology, to become a national pioneer in that field. After decades of puzzling efforts, Prof. Luo and his team have achieved a lot of significant results [1–3]. Most particularly, he made great contributions in the field of the genetic code and genome evolution, genome sequence information analysis, and the development of quantum biology theory. Because of his outstanding achievements and contributions on the study of bioinformatics, Prof. Luo was awarded the China Bioinformatics Lifetime Achievement Award, in September 2020.



Professor Liaofu Luo

EVOLUTION OF GENETIC CODE

Prof. Luo proposed the concept of mutational deterioration (MD) in 1988, demonstrating that the degeneracy rule of codons and the arrangement of amino acids on the code table followed the rule of minimum MD, therefore elucidating the logic behind the genetic code. He proved that the standard amino acid code is the optimal code under constraints during the initial fixation of early amino acids and assumed the consequent precursor-product relations in biosynthetic pathways [4,5]. This has provided a better solution for the problem of evolutionary stability of the standard code and inspired the enlargement and changing of the genetic code in genetic engineering. The success of his study on the genetic code showed that, in biology, the integration of the traditional experimental approaches with rational quantitative methods could reveal and understand the laws of life.

GENETIC LANGUAGE AND GENOME EVOLUTION

Considering the tremendous amount of information that can be obtained from gene sequences and its important scientific value, Prof. Luo led his group to firstly study nucleic acid sequences as a type of genetic language, back in 1986. Synthetically employing information theory, statistical methods, oligo-nucleotide (k-mer) searching, spectrum representation, Markovian chain, and DNA diagrammatic representation they found strong background noises in the genetic language and a universal short-range dominance of base correlation. The averaged information-theoretic parameter (mutual information), describing neighboring base correlation, grew during evolution in the coarse-grained meaning. Additionally, gene expression was studied by searching the express-enhancing-network sites and a di-peptide correlation was found to be an essential factor for protein secondary structure determination. Furthermore, Prof. Luo's groups were able to calculate the fractal dimension of DNA walk for different species and proposed the evolutionary equations of DNA sequences under mutation selection and segmental repetition. A mathematical theory on the evolutionary mechanism of gene sequences using maximum information principle was proposed, in order to unify mutations and selection in evolution. These results were published originally between 1988–1997 [3,6]. After, the framework structure of protein [3], the RNA information contributing to protein structure [7], and the problem of DNA curvature and flexibility were focused on his research [3]. Based on the study of sequence feature and evolution Prof. Luo's research group have developed an algorithm – increment of diversity with quadratic determinant analysis – to identify gene sequences and their related functional segments [8]. Accompanying other proposed algorithms, such as the inhomogeneous

index, they have successfully predicted gene splicing sites, promoters and transcription starts, secondary structures of proteins, and other classification problems of bioinformatics with higher accuracy.

PROTEIN FOLDING IS A QUANTUM FOLDING

Based on the analysis of the conformation of biological macromolecules and their frontier electrons being the main variables in life processes, Prof. Luo proposed the conformation dynamics of macromolecules in 1987. The conformational change of biological macromolecules was investigated from the point of quantum transition. He said, “compared with other dynamical variables such as mobile electrons, chemical bonds, and stretching-bending vibrations, the molecular torsion has the lowest energy and can be looked as the slow variable of the system; simultaneously, from the multi-minima property of torsion potential, the local conformational states can well be defined.” Following the idea that the slow variables slave the fast ones and by using the non-adiabaticity operator method, he deduced the Hamiltonian describing conformational change and indicated that the influence of fast variables on the macromolecule could fully be taken into account, through a phase transformation of slow variable wave function. Starting from the conformation-transition Hamiltonian, the non-radiative matrix element was calculated and general formulas for the protein folding rate were deduced. He first explained the time scale of millisecond of the elementary folding process. The correct temperature dependence of the protein folding rate was obtained and the curious non-Arrhenius temperature relation was interpreted by his team [9,10]. The proposed folding rate formula provided a unifying approach for the study of large class problems of biological conformational change. He and his coworker's review paper was collected in “Advances in Quantum Chemistry Vol 82: Quantum Boundaries of Life” [10].

Apart from the aforementioned three fields, Prof. Luo and his team have also studied the relationship between structures and functions for some specific genes and proteins, introduced the thermodynamics approach into the study of cancer to calculate the generation of cell entropy, proposed the theory of the origin of chirality according to the solution of biomolecular chirality induced by weak interaction of parity non-conservation, and more recently proposed the quantum theory of genome evolution.

SCIENTIFIC IDEALS AND BELIEFS

In the 21st century, the development of modern sciences presents more challenging for the mindset of a scientific researcher. Aristotle once said that surprise, leisure, and

freedom are three necessary conditions for the emergence of science. This point is consistent with Einstein's view that scientific progress requires two freedoms, namely external freedom and inner freedom. Prof. Luo pointed out that the three Aristotelian conditions have an enlightening and critical impact on Chinese academic society. From his own experience, he believes that the inner and pertinacious enthusiasm for science is the most important factor for the development of the pure science. He emphasizes that the strong and perpetual internal motivation rooted in each scientist is the fundamental guarantee for developing basic science research in our country.

He said, "life is random, diverse, and sudden, but it is rational in nature. We should not be puzzled in big data's accumulation, as what we should do is to control the data and reveal the inherent and logical beauty of life information." Moreover, he believes this logic is "code – sequence – structure – function." "This is how information is transmitted from a primary mRNA to a protein. This is also how information is transmitted from nucleosome and nucleosome-deleted region to mRNA and non-coding RNA." He wrote the following formula for his students:

"Selection of Research Topic + Exploration of Mechanism + Quantitative Study = Success."

Firstly, a biological topic with essentially innovative significance should be chosen. Then, the exploration of mechanism means that the intrinsic mechanism should be researched, instead of focus at phenomena only. This mechanism is often based on certain laws of biology and also consistent with basic laws of physics. Finally, calculation based on quantitative data should be performed in order to obtain new results that could be tested in experiments. The three major factors pointed out by Prof. Luo in this formula have provided guidance and assistance for his students and contributed to the success of innumerable studies.

COMPLIANCE WITH ETHICS GUIDELINES

The authors Lirong Zhang and Junjie Liu declare that they have no conflict of interests.

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