

MATH Mathematics Colloquium Series The Chinese University of Hong Kong

This Colloquium Series in Pure Mathematics is organized by the Department of Mathematics at The Chinese University of Hong Kong. The series focuses on all areas of pure mathematics together with theoretical developments and applications.

Date: April 16, 2024 (Tuesday)

Time: 14:30-15:30 (Hong Kong Time)

Venue: LPN LT

Grand Biological Universe: The geometric construction of genome space and its applications

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Abstract: Imitating Hilbert who proposed 23 problems in mathematics in 1900, Defense Advanced Research Projects Agency (DARPA) proposed 23 problems in pure and applied mathematics in 2008. These problems will prove to be very influential for the development of mathematics in the 21st century. In the DARPA problems, we are asked to understand “The Geometry of Genome Space” (the number 15) and “What are the Fundamental Laws of Biology” (the number 23). Our convex hull principle for molecular biology states that the convex hull formed from Natural Vectors of one biological group does not intersect with the convex hull formed from any other biological group. This can be viewed as one of the Fundamental Laws of Biology for which DARPA has been looking for since 2008. On the basis of the convex hull principle, we can construct the geometry of the genome space. A genome space consists of all known genomes of living beings and provides insights into their relationships. The genome space can be considered as the moduli space in mathematics, and genome sequences can be canonically embedded in a high-dimensional Euclidean space by means of Natural Vectors. In this space, a sequence is uniquely represented as a point by the nucleotide distribution information of the sequence. Similar sequences lie closely, and convex hulls of different groups are disjoint according to the convex hull principle. The geometry of space is reflected in the similarity of sequences. The

similarity of sequences can be measured by the Natural Metric, which is different from the induced metric from the ambient Euclidean space. Like our physical world, dark matter and dark energy play a crucial role in the construction of the correct Natural Metric in genome space. Our goal is to construct the genome spaces of seven kingdoms with Natural Metrics. These metrics are quite different in each genome space because different dark matter and dark energy may bend space-time as predicted by Einstein's theory. As applications, we provide the first mathematical method to find undiscovered genome sequence. Our theory allows us to explore the phylogenetic relationships of biological sequences and where SARS-CoV-2 originated from. It provides a novel geometric perspective to study molecular biology. It also gives an accurate way for large-scale sequences comparison in real-time manner.

Bio: Professor Stephen S.-T. Yau obtained his B.S. from the Chinese University of Hong Kong in 1973 and earned his Ph.D. from State University of New York at Stony Brook in 1976. Professor Stephen S.-T. Yau is a Distinguished Professor Emeritus at the University of Illinois at Chicago, and currently a full Professor at Tsinghua University and Beijing Institute of Mathematical Sciences and Applications. Professor Stephen S.-T. Yau has a very board interest in research and has made tremendous contributions to area such as bioinformatics, complex algebraic geometry, singularities theory, and nonlinear filtering. Professor Stephen S.-T. Yau was awarded the Sloan Research Fellowship in 1980 and the Guggenheim Fellowship in 2000. He was elected an IEEE Fellow in 2003 and a fellow of the American Mathematical Society in 2013.
