

## Introduction to the conference

Biology dates back to more than 300 years before Christ. For example, Aristotle (384-322 B.C.) was the first to classify living things. In his “Origin of Species”, Charles Darwin (1809-1882) presented the theory of evolution by natural selection, which provided a unifying and organizing framework for the field of biology. One of the most important events in the history of biology is the “discoveries concerning the molecular structure of nucleic acids and its significance for information transfer in living material”, for which Francis Crick and James Watson were awarded the Nobel Prize in Physiology or Medicine in 1962. Such discoveries ushered a new era of biology, namely molecular-based biological sciences or molecular bioscience. The advances in biological technology in the past few decades have fueled the exponential growth of biological data, which in turn, had led to the burgeoning of the omics era around the dawn of the millennium. The advent of massive biological data, the availability of high performance computers, the advance of computational algorithms, and the development of mathematical models have paved the way for biological sciences to undertake another historic transition from being qualitative, phenomenological, and descriptive to being quantitative, analytical, and predictive, like quantum mechanics did a century ago.

Mathematical Molecular Bioscience and Biophysics (MMBB) concerns the development of mathematical theories, models, methods, schemes, and algorithms for understanding molecular mechanisms and for addressing challenges at the forefront of molecular bioscience and biophysics, such as those associated with drug design and discovery. Almost all areas of mathematics including algebra, geometry, topology, analysis, group theory, graph theory, combinatorics, differential equations, and numerical analysis play distinguished roles in addressing fundamental challenges in molecular bioscience and biophysics. Mathematical approaches, such as multiscale modeling, calculus variation, algebraic topology, differential geometry, and graph theory, are becoming increasingly popular in molecular bioscience due to their ability to significantly simplify the structural complexity of biomolecules or effectively reduce the number of degrees of freedom while still maintaining an essential and adequate description of biomolecular interactions.

This conference is unique in bringing together experts from mathematics, biology, biophysics, and pharmaceutical industry to tackle challenging problems in molecular bioscience and biophysics. It will act as a catalyst to fully exploit the synergy between mathematicians and other scientists, and to create a network of collaborations that will sustain future activities in MMBB. This conference will foster the training of the next generation of mathematicians or mathematical biologists to command modern mathematics and to have a molecular-level understanding of bioscience. Therefore, it will have a lasting impact on both mathematics and biology.

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