


复旦大学数学科学学院

数学综合报告会

报告题目：**Achieving Diverse and Monoallelic Olfactory Receptor Selection Through Dual-Objective Optimization Design**

报告人： Jianhua Xing

（University of Pittsburgh）

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摘要： Olfaction, or the sense of smell, can be essential for the proliferation and survival of an organism. Thus most species have evolved highly sensitive olfactory system. A large number of olfactory receptor (OR) neurons, 40 millions for humans, located on the nose epithelium, sense odor molecules through the transmembrane ORs, then transmit electric signals to the brain. OR genes are the largest gene superfamily in vertebrates, ~ 1,300 (including ~20% pseudogenes, i.e., dysfunctional genes that have lost protein-coding ability) found in mouse and ~ 900 (including ~63% pseudogenes) in humans. In their Nobel-Prize winning studies, Axel, Buck and coworkers showed that each OR neuron stochastically expresses one and only one type of the ORs. Actually each cell only expresses one of the two alleles, which means two copies of a gene from the two parents, of an OR gene. The studies of Axel and Buck raise an intriguing question that has been puzzling the field since then: how can a cell activate the expression of one and only one allele of a single OR gene out of a large number of different types of ORs, and maintain its stable expression through the life of the cell, which is about 90 days in mice? Decades of studies have accumulated extensive information, but many observations seemingly make the problem even more complex for understanding.In the talk I will show how olfactory receptor neurons may use simple physics and engineering design principles to achieve single allele activation, and several other functional requirements, such as maximizing OR expression diversity, at the same time. Our model has every of its components correspondingly directly to an experimentally measurable quantity. The model makes a large number of predictions, many of which have been experimentally confirmed. I suggest that the study is an example that very simple physical principles often lie behind seemingly complex biological phenomena.At the end of the talk, I will also briefly introduce our efforts on using integrated experimental and computational systems biology approaches to study cell fate transitions.