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Keynote speaker:

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“Revisiting Eigen's Paradox for the Evolution of Genetic Information”

Genomes of living things contain sequences of up to billions of nucleotides. These sequences must be replicated with high fidelity in order for offspring to survive and reproduce. The origin of this high-fidelity replication is one of the great open problems in the origin of life. The basic question of how information can be maintained in a genome by natural selection in the face of replication errors was investigated by Eigen and Schuster in the 1970s. They introduced into evolutionary theory the concepts of the quasispecies, error threshold, error catastrophe, and the "Eigen Paradox": faithful replication of genetic information requires complex enzymes, but complex enzymes require faithful replication of genetic information. All of these concepts were based on a simple model of evolution where there was one "master sequence" with high fitness, and all other sequences had low fitness. In the 1990s, these ideas literally "went viral" when virologists discovered that RNA viruses with high mutation rates occurred as quasispecies of mutationally related sequences. The "error catastrophe" idea was adopted as a strategy to cure chronic viral infections by increasing the mutation rate to the point of "lethal mutagenesis". In the process of migrating out of the theoretical biology literature into the empirical biology literature, however, these concepts are often found stripped of the technical details that give them validity. As a consequence, the idea that genetic information maintained in a population by natural selection is lost above a threshold mutation rate has been over-interpreted as universal. In this talk I present fitness landscapes that are counterexamples to these ideas. The amount of genetic information maintained by natural selection in a population can be quantified, and we find that it is possible for the amount of information to decline gradually with mutation rate, not catastrophically. Consequently, it is possible for selection to maintain large amounts of genetic information in complex genomes even at very high mutation rates. The possibility of maintaining long genomes with low information density provides one possible solution to the "Eigen Paradox".