Using Networks in Evolutionary Genetics and Genomics

Networks consist of nodes interconnected by edges. In evolutionary biology, the nodes can be alleles, individuals, populations, species, etc. The edges reflect relationships or associations between the nodes, such as linkage disequilibrium, social interactions, genetic similarity, etc. Three examples will be given of how networks can be used to gain powerful new insights in evolutionary genetics and genomics: the role of landscape structure on social, dispersal, and gene flow networks; coadapted genetic complexes in a spatially varying environment, and population structure.

Dr. Alan R. Templeton

Alan Templeton received his Master’s in Statistics and Ph.D. in Human Genetics in 1972 from the University of Michigan, Ann Arbor. He is currently the Charles Rebstock Emeritus Professor of Biology and Statistical Genomics at Washington University in St. Louis, Missouri, and a visiting professor at the Institute of Evolution and the Department of Evolutionary and Environmental Biology at the University of Haifa, Israel. He applies genomics and statistical population genetics to a variety of basic and applied problems on the genetics of complex diseases, evolutionary biology, human evolution, bioinformatics, and conservation biology.