LAXMI PARIDA, IBM Research

Random Graphs in Population Genomics

The modeling of the evolutionary dynamics of evolving populations as random graphs offers a new methodology for analysis. This exploration begins as a quest for understanding the reconstructability of common evolutionary history of populations. It provides new insights including a purely topological (or graph theoretic definition) of traditional population genomic entity like the GMRCA (Grand Most Common Ancestor) of individuals under mutations as well as recombinations. Apart from giving interesting characterizations of another important structure called the ARG (Ancestral Recombinations Graph), it provides the basis for identifying a mathematical minimal nonredundant structure in the ARG and for adapting the coalescence theory (a well-studied notion in population genetics) very naturally in designing ARG sampling algorithms. This connection also opens the door for many interesting questions ranging from human migration paths, to genetic diversity study in plant (cacao) cultivars.