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## Genetic Variability within and between Populations

Guest Editor:

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### **Message from the Guest Editor**

The difference in the genetic variation within and between populations is an important measure that is routinely used in population genetics, ecology, and evolutionary biology. A number of methods have been developed to capture this difference, which is called the fixation index or FST. This reveals the level of genetic structure and gene flow between populations. With the advent of DNA sequencing technologies, population structure or differentiation was estimated using microsatellites and single nucleotide variations (SNVs). Recent developments in sequencing technologies have resulted in a drastic reduction in the cost of sequencing whole genomes, which has enabled researchers to decipher the sequences of whole genomes of populations. Importantly, whole genome- or SNP array-based estimates are able to detect the fine-scale population structure in many species that were not recognized before. These results have provided detailed insights and revised our understanding of the demography of populations and the signatures of natural selection that shaped the evolution of various species.



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