

What Kind of Information Can We Extract from Evolutionary Genome Sequence Analysis?

Saitou Naruya

*Division of Population Genetics and DNA Data Bank of Japan
National Institute of Genetics, Mishima, Japan*



Massive amount of genome sequences made us possible to conduct various kinds of evolutionary or comparative genomic analyses. They include (1) construction of gene trees for all orthologs so as to reconstruct the species phylogeny, (2) comparison of paralogs to elucidate evolutionary dynamics of gene duplications, (3) synonymous and nonsynonymous substitution estimation for protein coding genes to detect positive or negative selection, (4) detection of evolutionary conserved DNA regions for extracting protein coding and non-protein coding gene regions, (5) inferring nucleotide changes within species (SNP data) or between species to estimate nucleotide substitution patterns, (6) comparison of closely related multi-species sequences to detect lineage specific changes and estimation of ancestral sequences, and (7) examination of correlations between sequence changes and any postgenomic data such as gene expression patterns. I would like to give brief review of each aspect.