

Genealogical network visualization and recent positive selection in humans

Positive natural selection has widespread effects on human populations during the last 20,000 years. The positive selection of a new allele leaves a strong signature of linkage disequilibrium across a segment of the genome, the length of which depends on the time of origin of the allele. Selection on standing variants has a more subtle effect, elevating frequencies of selected alleles without strong linkage, which can be examined by correlated effects across interacting gene networks. Selection influences the genealogical structure of the population, but because these effects are dispersed across many parts of the genome, they have posed a challenge for visualization and study. Network visualization methods provide ways to understand the relation of selected and neutral gene networks, as well as the effect of selection on the genealogical structure of a population. Applied to recent human populations, network animations help to illustrate how selection has recently changed the pattern of human population structure. These methods also help to clarify the pattern of archaic human contribution to recent populations.