

#11: Fast and robust detection of ancestral positive selection from genomic data
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Natural selections leave unique genetic signatures on a population, and are greatly informative of their past biology and environment. Advances in whole-genome sequencing has dramatically increased the size and complexity of available genomic data, while powerful tool for detecting ancestral positive selections are still lacking. We therefore developed the Ancestral Branch Statistic (ABS) based on genetic distances among 4 sub-populations to detect sweeps on the internal branch. We prove ABS to have comparable power with the newly-published likelihood-based method 3P-CLR, with a much faster computing speed. Scanning genomic data of East Asians, Europeans and Africans reveal both expected and new candidate genes.