

Table 1 Comparisons of imputation methods

Software	Model	Uses reference?	Optimization method
IMPUTE ³	Hidden Markov Model	Yes	Markov Chain Monte Carlo
MACH ⁷	Hidden Markov Model	Yes	Iteratively assigns haplotypes to the genotypes based on the converging model
BIMBAM ¹³ (FastPHASE ⁵)	Hidden Markov Model	Yes	Uses a small number of states (haplotype clustering)
TUNA ²	Weighted haplotype proxies	Yes	Greedily searching for the proxies
SNPStat ⁶	Likelihood-based diplo-type proxies	Yes	Maximizes likelihood based on the possible diplotypes explaining the genotype
CAMP ¹⁰	Coalescent	No	Builds an approximate perfect-phylogeny tree