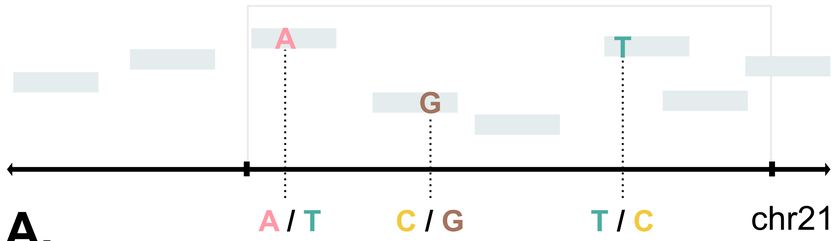
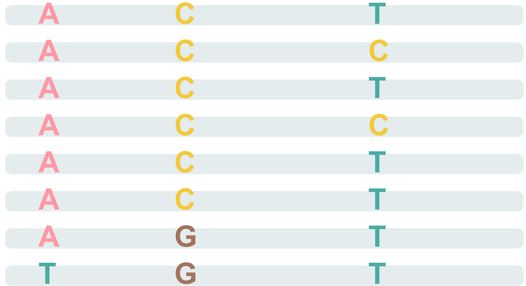
Within a defined genomic window, prioritize potentially informative reads that overlap with common SNPs



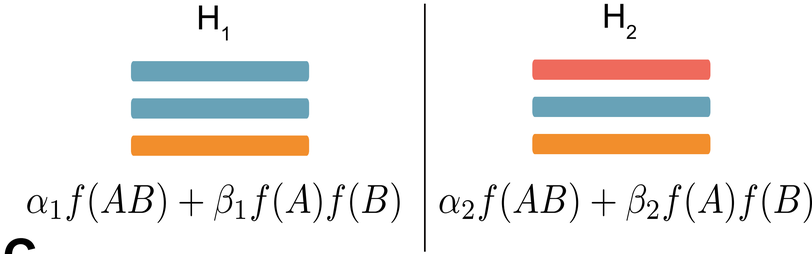
A.

Quantify corresponding haplotype frequencies within a reference panel



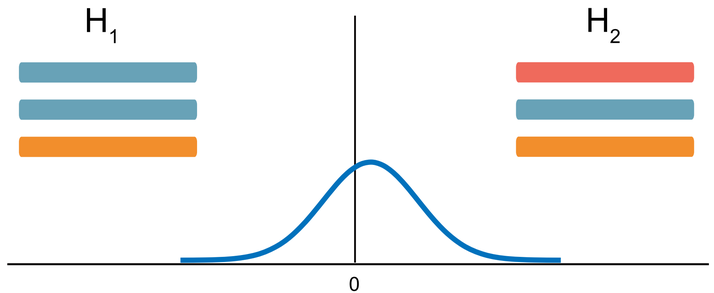
B.

Randomly resample reads and compute likelihoods of observed alleles under competing ploidy hypotheses



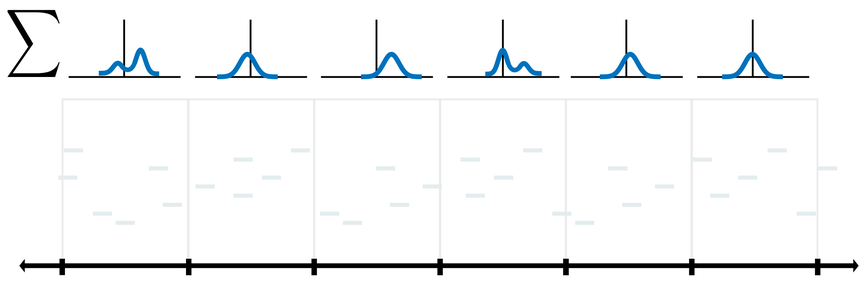
C.

Compare with likelihood ratio and repeat step **C** multiple times to form a bootstrap distribution



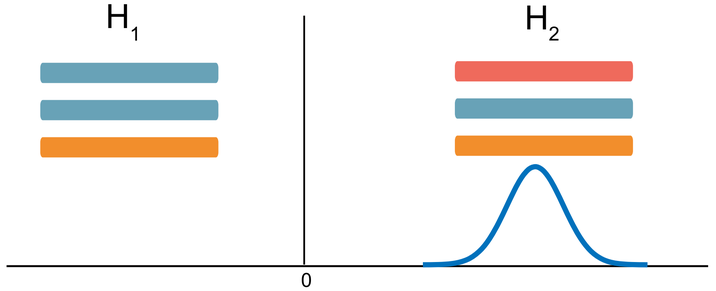
D.

Repeat steps **A** - **D** in consecutive genomic windows and sum log likelihood ratios over larger genomic intervals



E.

Classify ploidy state of the genomic interval



F.