



The highest posterior density for the Monte Carlo effect in STRmix™

We have tested the highest posterior density (HPD) method for applying a lower bound to the variation induced by the Monte Carlo effect in the probabilistic genotyping system, STRmix™ (not including allele frequency uncertainty or uncertainty in theta). Tests show that the approach is not giving the desired 99% coverage for some profiles. Observed coverage ranged from 76% to 100%. We do not consider this to be a miscode within STRmix™ - the published method is being applied as intended. Rather, the method itself is occasionally underperforming when used to account for uncertainty in the genotype weights. Notably, the method performs as expected when used to account for uncertainty in allele frequencies and/or theta.

Although less effective than desired in some instances, this method does provide a layer of conservatism that is additional to the other layers within the *LR* assignment including the population genetic model and values of theta. We expect that *LRs* assigned within STRmix™ are strongly conservative once all layers of conservatism have been applied.