

# **VALIDATION OF BULLETPROOF PROBABILISTIC GENOTYPING SOFTWARE FOR THE INTERPRETATION OF COMPLEX DNA MIXTURES**

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Mixtures of DNAs from evidence and their subsequent DNA STR profiles have posed a formidable challenge when trying to determine the guilt or innocence of a suspect. The general acceptance of likelihood ratios for the statistical interpretation of contributors to evidence from a crime scene has opened the way to a new type of analysis. The BulletProof probabilistic genotyping program employs a method for interpreting autosomal mixed DNA profiles based on continuous modelling of peak heights where MCMC is applied with a model for allelic and stutter heights to produce a probability for the data given a specified genotype combination. The program's underlying mathematical algorithms are those developed for EuroForMix; an open source software (Belka, Storvik, and Gill, Forensic Sci. Int. Genet. 21, 35-44, 2016). BulletProof is also designed to take into account allele drop-in, degradation and sub-population structure. The theory used in the program extends to handle any number of contributors and replicates, although practical implementation limits analyses to four contributors. The program employs a graphical user interface (GUI) that is browser based for ease of use and broad compatibility. STR DNA profile data from known contributors at varying ratios have been generated using the PowerPlex Fusion and Globalfiler STR kits and analyzed to validate the BulletProof program. Simple excel data tables are exported from your analysis software and uploaded into Bulletproof. DNA mixtures obtained from evidence samples from CTS proficiency tests and sexual assault cases were also evaluated. Parameters such as peak heights, DNA degradation, and number of possible contributors have been evaluated for their effect on the outcome of the analysis. The program's statistical analysis is presented in straightforward tables and graphs. The final analysis is displayed as the overall likelihood ratios based on the Maximum Likelihood, Bayesian MCMC, Sensitivity Base Conservative and Bayesian Integral methods in scientific notation and in Log<sub>10</sub> formats. All information can then be printed out for inclusion in the final case file. BulletProof has proved to be a highly effective tool for the rapid analysis of complex DNA mixtures providing a strong statistical conclusion as to the guilt or innocence of a suspect.