COMPARISON OF THE PERFORMANCE OF DIFFERENT MODLES FOR THE INTERPRETATION OF LOW LEVEL MIXED DNA PROFILES

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DNA analyses from forensic casework samples commonly result in complex DNA profiles. Often, these profiles consist of multiple contributors and display multiple stochastic events such as peak height imbalance, allelic or locus drop-out, allelic drop-in, and excessive or indistinguishable stutter. This increased complexity has established a need for more sophisticated methods of DNA mixture interpretation. This study compares the effectiveness of statistical models in the interpretation of artificially created low template two person mixed DNA profiles at varying proportions and template quantities. Two binary models (Combined Probability of Inclusion and Random Match Probability), a semi-continuous (Lab Retriever), and continuous model (STRmix™) were compared. Generally, as the sophistication of the models increases, the power of discrimination increases. Differences in discrimination often correlate to each model's ability to use observed data effectively. Binary models require static thresholds resulting in unused data and outliers which may lead to difficult or incorrect interpretation. Semi-continuous and continuous models eliminate the stochastic threshold, however Lab Retriever does not account for stochastic events beyond drop-out and drop-in leading to possible less effective use of the data. STRmix™ incorporates all stochastic events listed above into the calculation making the most effective use of the observed data.