EXAMINATION OF A NOVEL METHOD TO ALLOW FOR A RANGE IN THE NUMBER OF CONTRIBUTORS TO A DNA PROFILE: A KEY AREA OF SUBJECTIVITY IN DNA EVIDENCE INTERPRETATION

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Continuous probabilistic DNA profile interpretation systems have been described that model the height of allelic and stutter peaks within a DNA profile. These systems address some of the shortcomings of traditional methods of profile interpretation, not the least of which is to remove the need for subjective application of rules and thresholds. A remaining area of subjectivity when using continuous interpretation systems is assigning the number of contributors to be used in the analysis. Cooper et al 2015 explored the extent and consequences of this decision in a recent international collaborative study.

To examine the level of concordance in profile interpretation the collaborative study reviewed results from twenty different analysts across twelve different laboratories/organisations. This study included participants from groups across Australasia, USA, Canada and the United Kingdom. The three questioned profiles selected exhibited a range of template and complexity, where the true number of contributors was difficult to assign. The participants were asked to review the profiling information, assign a likely number of contributors, progress a mixture interpretation and provide a likelihood ratio to the given person of interest, as appropriate. The compiled results demonstrated that the use of probabilistic software can compel a level of concordance between different analysts. However there remain differences between the participants, particularly with the objective assignment of the number of contributors to the DNA profiles.

Following on from this study, we set out to explore the performance of the method published by Taylor et al. 2014, which allows a range in the number of contributors to be incorporated into a continuous method of profile interpretation. We examine a variety of GlobalFiler™ mixtures where the ground truth number of contributors was known. Single source, two and three person profiles were created by computer simulation or *in vitro* and analysed proposing a range in the likely number of contributors, where the ground truth (*N)* plus or minus one contributor were considered. We discuss the preliminary findings drawn from these results and comment on how this method may help address this key area of subjectivity in DNA profile interpretation.