B96 Threshold to Probabilistic DNA Profile Interpretation: Why Change?

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After attending this presentation, attendees will have expanded their knowledge base in relation to advances in DNA profile interpretation, particularly in the area of probabilistic interpretation methods. This presentation is intended to address the question: Why change from a binary/threshold-based method?

This presentation will impact the forensic science community by providing an overview of the changing science behind DNA profile interpretation and re-addressing the known shortcomings of current interpretation methods. The use of actual casework examples will help facilitate the transfer of knowledge.

There have been a number of recent reviews of laboratory practice that have resulted in negative media reports. These have led to some laboratories questioning their interpretation protocols and whether these are still fit for the purpose. One such review occurred in Australia in 2009 and resulted in the implementation of an Australasian consensus approach to profile interpretation. Since then, uptake of probabilistic software in casework has increased significantly around the world with many more laboratories currently investigating the move away from traditional threshold/binary based or combined probability of inclusion models.

A number of fully continuous probabilistic methods have been described that model allelic and stutter peak heights within a DNA profile. Such models can help address the known shortcomings of traditional methods of profile interpretation, such as those within a binary model.[1-3]

So, why change? This presentation will look back at traditional DNA profile interpretation methods and highlight known shortcomings. The use of probabilistic models and software will be shown to address these issues. This will demonstrate the power of such models and their ability to decrease rates of false inclusion and false exclusion for a range of profile types. In addition, results of previous studies demonstrating how the use of probabilistic software can, under certain circumstances, help facilitate a consistent approach to the interpretation and reporting of statistical findings in a given case will be provided.[4]

Actual casework examples will be provided, demonstrating the benefits which would not have been realized without the use of probabilistic software. These examples will hopefully allow attendees to visualize the advantages for actual casework samples and put the use of such models into context within the criminal justice system.

This presentation will conclude with a discussion of possible future directions for probabilistic software and the further benefits which this may yield.[5]

Reference(s):

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2. Taylor D., Bright J.A., Buckleton J.S. The interpretation of single source and mixed DNA profiles. *Forensic Science International: Genetics*. 2013; 7(5):516 – 528.
3. Bright J.A., Taylor D., Curran J.M., Buckleton J.S. Developing allelic and stutter peak height models for a continuous method of DNA interpretations. *Forensic Science International: Genetics*. 2013; 7(2):296 – 304.
4. Cooper S.J., McGovern C.E., Bright J.A., Taylor D., Buckleton J.S. Investigating a common approach to DNA profile interpretation using probabilistic software. *Forensic Science International: Genetics*. 2015; 16:121 – 131.
5. Taylor D., Bright J.A., Buckleton J.S. Interpreting forensic DNA profiling evidence without specifying the number of contributors. *Forensic Science International: Genetics*. 2014; 13: 269 – 280.

Probabilstic Interpretation, Continuous Models, Casework Examples