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Does an English appeal court ruling increase the risks of miscarriages of justice when complex DNA profiles are searched against the national DNA database?

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ABSTRACT

Likelihood ratio (LR) methods to interpret multi-contributor, low template, *complex DNA* mixtures are becoming standard practice. The next major development will be to introduce search engines based on the new methods to interrogate very large national DNA databases, such as those held by China, the USA and the UK. Here we describe a rapid method that was used to assign a LR to each individual member of database of 5 million genotypes which can be ranked in order. Previous authors have only considered database trawls in the context of binary match or non-match criteria. However, the concept of match/non-match no longer applies within the new paradigm introduced, since the distribution of resultant LRs is continuous for practical purposes. An English appeal court decision allows scientists to routinely report *complex DNA* profiles using nothing more than their subjective personal 'experience of casework' and 'observations' in order to apply an expression of the rarity of an evidential sample. This ruling must be considered in context of a recent high profile English case, where an individual was extracted from a database and wrongly accused of a serious crime. In this case the DNA evidence was used to negate the overwhelming exculpatory (non-DNA) evidence. Demonstrable confirmation bias, also known as the 'CSI-effect, seriously affected the investigation. The case demonstrated that in practice, databases could be used to select and prosecute an individual, simply because he ranked high in the list of possible matches. We have identified this phenomenon as a cognitive error which we term: 'the naïve investigator effect'. We take the opportunity to test the performance of database extraction strategies either by using a simple matching allele count (MAC) method or LR. The example heard by the appeal court is used as the exemplar case. It is demonstrated that the LR search-method offers substantial benefits compared to searches based on simple matching allele count (MAC) methods.

1. Introduction

The forensic community is moving towards the implementation of new methods to interpret complex DNA mixture profiles. The ISFG DNA commission [1,2] recommends likelihood ratio methods and provides guidance to interpret complex DNA mixture profiles. These are defined as comprising two or more contributors that are partial [3–9]. The ISFG DNA commission [1,2] guidelines has assisted in this respect. Recently, three exemplar cases were subject to challenge and heard by an English appeal court [10]. In all three cases DNA evidence had been presented where the DNA profiles were mixtures of two or more people, and were low-template so that allele drop-out was possible. The basis for the appeal was as follows – transcribed from [10]:

> 'In each case, 19 or 20 of the components of the appellant's DNA had been present in the mixture but the experts were unable to give a random match probability. The judge's decision to admit the evidence was the main issue in each of these appeals.'

All of the cases described had used the second generation multiplex (SGM plus™), which is the multiplex still employed within the UK [11,12]. In each case examined by the court, the

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prosecution relied upon evidence of 19 or 20 allelic matches. This is called the 'matching allele count (MAC) method. Alleles for a homozygote 'match' are counted twice (hence a complete match has 20 alleles). In one case (which is called 'MDS' in order to protect the anonymity of the individual) it was notable that the condition was relaxed to include an observation of only 14 alleles that were positively matched to the crime stain (*there were 6 possible 'unconfirmed' matches)*. Note that MDS was not identified as a result of a database search. However, it is quite easy to see that the statement that describes an expert's *belief* of the rarity of a match, based on personal observation, could easily be misconstrued by a court as a proxy-statistic of one in several thousands.[1] It is this unqualified 'belief', which may cause miscarriages of justice. The risks are greatly increased if the matching DNA profile was discovered as the result of a DNA database search for two reasons:

(a) In UK courts the jury is not informed that the 'match' was discovered by database search – they simply hear evidence to suggest that a profile is extremely rare in a population.[2] However, mathematically a chance match is expected to occur in a database of 5 million individuals (where the match probability of a partial profile is one in several million). However, this is effectively hidden from the court proceedings. The jury cannot place the DNA evidence into context, without this crucial information.
(b) During the evaluation of the total evidence in the case, the forensic scientist may (inadvertently) use the apparent strength of the DNA evidence to mitigate the exculpatory (non-DNA) evidence, and this is termed 'the naïve investigator effect' [13]. For a deep analysis of the effect of confirmation bias and the naïve investigator effect, with reference to real casework examples where this has occurred, the reader is referred to Gill [13].

1.1. The naïve investigator effect

The naïve investigator effect is inspired by the case of 'wrongful arrest of Adam Scott' [14] where a man was arrested, accused of rape and incarcerated on the basis of a DNA-profile match. The DNA profile was eventually traced to a contamination incident, but the case is notable because the match was adventitiously obtained from a search of the national DNA database. The exculpatory evidence was initially ignored. To summarise the definition: the naïve investigator finds the closest match to a crime-stain in a national DNA database; he ignores exculpatory evidence and seeks to incriminate the matching individual. Although Scott was conveniently dismissed by the official report as a 'one-off' event – examination of the case revealed an unfortunate way of evaluating evidence that was prosecution biased, and potentially widespread – there are much wider implications to case-work in general that are discussed by Gill [13].

It is not necessary for an individual to be discovered via a database search. The suspect might be identified by other means and the DNA profile used as confirmatory evidence. The use of DNA profiling as an *investigative* tool is not disputed – but its utility to express strength of evidence requires quantitative evaluation using the likelihood ratio methods described. The DNA evidence needs to be placed into context of the non-DNA evidence.

1.2. The matching allele count (MAC) and the random man not excluded (RMNE) statistic

The question of 'matching alleles' in multi-contributor DNA profiles has been previously characterised for complete profiles [15,16]. It was previously shown [17] that the (common) practice of calculating an RMNE from loci where the suspect's alleles were fully included, whilst omitting those loci where alleles were not fully represented, was bad practice, and anti-conservative. As the number of alleles present in a profile increases with the number of contributors, it becomes more likely that a match with a random man will occur.

1.3. Use of likelihood ratio models to search databases

The appeal court [10] examined three different cases, at least one of these (*Regina v. Dlugosz*) involved matches identified as the result of a search of the national DNA database, using a matching allele algorithm. Therefore, questions are raised about the robustness of the method employed and the chance of adventitious matches. Sorting a database according to LR is routinely carried out for familial searching [18,19]. It is already known that the person of interest does not need not to rank very high. The purpose of the search is primarily for intelligence purposes – the 'evaluation' of the DNA evidence in context of the non-DNA evidence is the second step. The idea to use a likelihood ratio model to interrogate large national DNA databases with LT-DNA mixtures was originally described by Gill et al. [20]. Recently, Bleka et al. [21] compared the MAC method with a likelihood ratio search method for low template mixture evidence, demonstrating the latter to be more efficient. Here we extend the work further to characterise an exemplar case considered by an English court of appeal. The open-source software *LRmix* [5,6], was programmed to rapidly evaluate 5 *million* reference samples (using the UK national DNA database as a model) [21]. Other methods could be used if peak height information was available [22]. We show the matching allele count method to be highly inefficient. On the other hand, calculating LRs for every person in the database is shown to be much more efficient.

2. The matching allele count (MAC) method

We define the method approved by the English court of appeal as the matching allele count (MAC) method. If MAC = x, then x-alleles match between the reference profile and the crime-stain. It may be a complex partial mixture composed of multiple individuals. For the SGM plus system $x_{max} = 20$ and we describe this as a high stringency match. If relaxed to a lower figure (e.g., 14 alleles in the case of MDS) then this is described as a low-stringency match. As a much-preferred alternative [2,23], we show how likelihood ratios can be calculated [3–6] for each of the 5 *million* individuals in a database conditioned on any crime-stain profile.

3. The evidence in *Regina v. Dlugosz*

Since the necessary data (including the genotype information) were published by the court of appeal, this presents an unusual opportunity for peer review of an actual case where the defendant has been convicted of a crime and the conviction upheld after challenge. The defendant was accused of burglary and assault. The only forensic evidence in this exemplar case [10] was described as:

[1] The court has been told by an expert that he has examined thousands of cases and never observed an event. This is not a statistic and has no scientific meaning without qualification. The problem is that the scientist has made a non-scientific statement without providing any guidance about how it should be interpreted by the jury.
[2] This practice seems to be a peculiarity of adversarial systems. It does not apply to the majority of EU jurisdictions where the fact of the database search is not withheld.