

An extended likelihood ratio framework for interpreting evidence

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This paper reviews some current methods, the likelihood ratio-based approach and the full Bayesian approach for the interpretation of evidence and discusses previously identified shortcomings in them. It suggests an approach based on a compromise-based on an extended likelihood ratio – that may combine the merits of logic without overstepping acceptable bounds for the forensic scientist in the presentation of evidence. The approach is exposed formally and takes advantage of inferential networks called Bayesian networks.

Este trabajo revisa algunos de los métodos actuales, el enfoque basado en el cociente de verosimilitud y el enfoque Bayesiano completo, para la interpretación de la evidencia y discute desventajas previamente identificadas. Se sugiere un enfoque basado en un compromiso-basado en un extendido enfoque del cociente de verosimilitud- que pueda combinar los méritos de la lógica sin invadir los límites aceptables del científico forense para aceptar la evidencia. Se expone formalmente el enfoque y se aprovechan las redes de inferencia denominadas redes bayesianas.

In dieser Arbeit werden einige aktuell angewandte Verfahren zur Interpretation von Beweismaterial, deren Ansätze auf dem Verhältnis von Wahrscheinlichkeiten bzw. dem Bayes' Theorem basieren, besprochen und bereits früher festgestellte Mängel in diesen diskutiert. Es wird ein Ansatz basierend auf einem Kompromiss – einem erweiterten Wahrscheinlichkeitsverhältnis – vorgeschlagen, der die Vorzüge der Logik einsetzen kann ohne die zulässigen Schranken für den kriminaltechnischen Sachverständigen in der Beweisaufnahme zu überschreiten. Dieser Ansatz wird formell dargelegt und nutzt folgernde Netzwerke, sog. Bayes' Netzwerke, aus.

Cet article passe en revue quelques méthodes utilisées à l'heure actuelle, l'approche basée sur un rapport de vraisemblance et l'approche bayésienne complète pour l'interprétation des indices, et discute certaines faiblesses identifiées précédemment dans ces méthodes. Il suggère une approche basée sur un compromis - fondé sur un rapport de vraisemblance étendu – qui combine les mérites de la logique sans dépasser les limites acceptables dans la présentation de moyens de preuve pour le scientifique. Cette approche est présentée formellement et tire profit des réseaux d'inférence appelés les réseaux bayésiens.

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Key words Interpretation of evidence, Bayesian framework, likelihood ratio, Bayesian networks

1. Introduction

This paper reviews some current methods for the interpretation of evidence and discusses previously identified shortcomings in them. It suggests a novel approach that may combine the merits of logic without overstepping acceptable bounds for the forensic scientist in the presentation of evidence. Some may argue that the presentation of scientific evidence should bend to conform to the courts' requirements and indeed a court can almost compel this. An instance could be the Doheny and Adams ruling in the UK [1]. However we believe that the claims of logic should be considered first and that only as a second stage should it be considered how this logic may be presented in court. This, therefore, will be the philosophical basis of this paper.

We discuss here three alternatives to the presentation of evidence: the likelihood ratio (with only two propositions), the full Bayesian approach, and a novel method suggested here that is in effect a hybrid of the logical approach and the full Bayesian approach. This last will be termed the 'extended likelihood ratio approach'.

2. The LR-based approach involving only two propositions

The idea of assessing the weight of the evidence using a relative measure (known as the likelihood ratio), explored at the beginning of the 20th Century [2], has been implemented routinely in paternity cases since 1930 [3]. It is however only in the latter stages of the 20th century that it made inroads into many other fields of forensic science [4, 5]. It now dominates the literature as the method of choice for interpreting forensic evidence across evidence types [6–10].

Let:

- H_p : be a hypothesis or proposition advanced by the prosecution
- H_d : be a hypothesis or alternative put forward by the defence
- E : signify the findings (referred to here as the evidence)
- I : refer to all the framework of circumstances relevant to the case

The laws of probability lead to

$$\frac{\Pr(H_p | E, I)}{\Pr(H_d | E, I)} = \frac{\Pr(E | H_p, I)}{\Pr(E | H_d, I)} \times \frac{\Pr(H_p | I)}{\Pr(H_d | I)} \quad (\text{equation 1})$$

that is known as the odds form of Bayes' theorem [11]. Because it follows from the laws of probability, it is accepted as a logical framework for interpreting evidence probabilistically. Equation 1 is often given verbally as

$$\text{posterior odds} = \text{likelihood ratio} \times \text{prior odds} \quad (\text{equation 2})$$

The question of the agreement on a set of appropriate and fit-for-purpose prosecution and defence hypotheses is vital to all methods of interpretation. It is only discussed briefly here. This is the subject of a large-scale project in the UK Forensic Science Service, the Case Assessment and Interpretation (CAI) project [12–14]. Propositions are classified into three levels:

offence, activity or source. The further down (towards the source level) in the hierarchy that the scientist operates the more the responsibility for interpreting the evidence is transferred to the court. Typically a forensic scientist would avoid dealing with offence level hypotheses since these operate at the level that would require him to assess issues around the relevancy of the forensic evidence to the offence under examination. However the decision as to whether to operate at the activity or source level needs careful consideration.

It would be reasonable to leave the interpretation of higher-level hypotheses (at say the activity level) to the court if it is the best body to undertake this interpretation. However if the matter requires expert knowledge regarding phenomenon such as transfer and persistence it would seem wise for the scientist to attempt interpretation at a higher level in the hierarchy or at least, to warn and equip the court to make such an attempt. It must be accepted that the evidence must eventually be interpreted by the court at the offence level. If the evidence cannot be put in the context of the offence then it runs the risk of being, in itself, irrelevant to the court. In this paper, we will leave this fundamental issue aside to concentrate on the principles running across the levels.

The prior odds are the odds on the hypothesis H_p versus H_d before the scientific evidence is produced. The posterior odds are these odds after the scientific evidence. The likelihood ratio informs us how to relate these two and how to update our opinion in a logical manner having heard the evidence. The prior odds represent the view on the prosecution and defence hypothesis before the scientific evidence, E , is presented. This is something that is formed in the minds of the judge and jury. It is very unlikely that it will be numerically expressed and indeed there is no need that it should be numerical.

Strictly it is not the remit of the scientist to form a view as to the value of the prior odds and most scientists would strictly avoid this. These odds are based on the non-scientific evidence and their assessment is the duty of judge and jury (for a dissenting view see Meester and Sjerps and the associated commentary [15, 16]).

The practical use of this philosophy typically leads forensic scientists to report the weight of the evidence through a likelihood ratio. By doing this the scientist reports the weight of the evidence without transgressing on those areas reserved for the judge and jury. This is the reason why we have chosen the term 'logical' or 'likelihood ratio' to describe this approach. We felt the need to avoid referring here to 'the Bayesian approach' which is the term used in most papers on this subject including our own. Strictly speaking, presenting a ratio of likelihoods does not necessarily imply the use of the Bayesian method. Most authors have intended the presentation of the likelihood ratio alone without necessarily implying that a discussion of Bayes' theorem and prior odds would follow in court. The intent was to present the scientific evidence in the context of a logical framework without necessarily presenting that framework.

However the advantage of the logical approach is that the likelihood ratio can be put in a context of the entire case in a consistent and logical framework. This advantage is somewhat lost if judge, jury and scientist are reticent to use or even discuss Bayes' theorem in full.

A critique of the likelihood ratio approach typically includes reasonable arguments regarding the difficulty of implementation and less reasonable criticisms arising largely from a lack of understanding of the underlying logic.

If we start with difficulty of implementation, one reasonable criticism of the logical approach when compared with a frequentist alternative is the ponderous nature of statements involving a likelihood ratio. Contrast:

A: The frequency of this profile amongst unrelated males in the population is less than 1 in a billion.

With:

B: This evidence is more than a billion times more likely if the DNA came from the suspect than if it came from an unrelated male.

Many people would prefer statement A over B and in fact studies have demonstrated [17, 18] that there are serious problems with uptake of statements like B. It is fair to say that the likelihood ratio wording is more ponderous and will take more explanation and skill to present. But logical correctness should take precedence over ease of presentation. Frequentist measures of uncertainty and evidential value can be equally misleading as exemplified by recent cases in the UK (e.g. the Sally Clark Case [19]). The very advantage of the logical approach is that the likelihood ratio can be placed in the context of a logical framework. This logical framework requires application of Bayes' rule and hence some assessment of priors. However the legal system of many countries relies on the 'common sense' of jurors and would hesitate to instruct jurors how to think in Bayesian terms. Forcing jurors to consider Bayes' theorem would be unacceptable in most legal systems [20]. It is likely that application of common sense will lead to logical errors and it has been shown that jurors do not handle probabilistic evidence well. However there is no reason to believe that these logical errors would be removed by application of a partially understood logical system, which is the most likely outcome of trying to introduce Bayes' theorem into court. If we recoil from introducing Bayes' theorem in court then the likelihood ratio approach forfeits one of its principal advantages although it certainly retains many others in assisting the thinking of the scientist.

This is not a fatal limitation as likelihood ratios have been presented in paternity evidence since the mid 1900s [3]. In this context they are typically termed paternity indices and are the method of choice in paternity work.

The considerations given above are real issues when applying the logical approach. There are a few more objections that arise

largely from a misunderstanding of the underlying logic [21]. These include criticisms of conditioning on I and H_p and the arbitrariness of the verbal scale.

Forensic scientists are raised in a culture that they should avoid bias that may arise from ideas seeded into their mind by the prosecution (or anyone else). This has led to the interpretation that they should consider the evidence in isolation from the background facts or the prosecution hypothesis. This idea is a misconception or misreading of the use of the conditioning in the probability assessment. In essence all probabilities are conditional and the more relevant information that is used in the conditioning the more relevant the resulting probability assignment will be. Failure to consider relevant background information would be a serious disservice to the court. We recognise that forensic scientists might be susceptible to numerous biases that have been well described by Saks et al. and Risinger et al. [22, 23]. However there is a need, in order to provide appropriate and useful guidance to courts, to condition the assessment of the likelihood ratio on the knowledge of a framework of relevant known or transparently assumed elements of the case.

The second argument is a verbal confusion. Consider the numerator of the likelihood ratio. This is $\Pr(E | H_p, I)$ which can be read as: The probability of the evidence given that the prosecution hypothesis is correct and also given the background information. The fallacious argument would be that it is inconsistent with the presumption of innocence to 'assume that the prosecution hypothesis is true'. This is a misconception or a misreading of the conditioning. When assessing the likelihood ratio we are not assuming that the prosecution hypothesis is true, which indeed would be biased, and would be manifested by introducing a prior probability of 1 for this hypothesis. What we are doing is weighing the prosecution and defence hypotheses against each other by calculating the probability of the evidence if these hypotheses were true. This is an instance where the verbal rendering of Bayes' rule can be misconstrued to give a false impression never intended in the logical framework.

3. Hypotheses partitioning and the need for a full Bayesian approach

The analysis given under the previous section works well if there are two clear simple hypotheses aligned with the prosecution and defence positions. However it is often difficult to summarise all the issues of a real casework problem using two hypotheses.

To put this in context: consider a relatively simple DNA STR case. We have a stain at the scene of a crime. Call this stain c and the genotype of this stain G_c . A suspect comes to the attention of the Police. Call this person s and his genotype G_s . The genotype of the suspect and the crime stain are found to be the same. We will write this as $G_s = G_c$.

Let the hypotheses being considered at source level be:

H_p : The DNA came from the suspect

H_d : The DNA came from a male not related to the suspect

We then calculate the probability of the evidence under each of these hypotheses [5]. We take $\Pr(G_c \mid G_s, H_d) = f$ (the match probability). $\Pr(G_c \mid G_s, H_p) = 1$ since the crime genotype will be G_c if it came from the suspect who is G_s (assuming no laboratory error).

Hence

$$LR = \frac{1}{\Pr(G_c \mid G_s, H_d)} = \frac{1}{f} \quad (\text{equation 3})$$

that is (typically) very much larger than 1 and hence there is evidence against H_d and for H_p .

But we have to recognise that these two hypotheses are not exhaustive. What about those people who are related to the suspect who might require consideration under the defence perspective? Should they be considered? Population genetic theory would suggest that these are the most important people to consider, and should not be omitted from the analysis, because of the strong impact of relatedness on the likelihood ratio. This need to consider relatives has been also highlighted by Redmayne in his discussion of the *Doheny* decision (R v. *Doheny* [1997] 1 Cr App R 369) [24]. If, according to *Doheny*, the DNA evidence is conveyed to the jury through an illustration of its ability to whittle down a large group of possible suspects (e.g. ‘white males in the United Kingdom’ or ‘the Caucasian, sexually active, males in the Manchester area’) to a much smaller group, the issue of blood relatives should come into play. What we need is a number of hypotheses. In fact taking that line to the limit, we could envisage the situation where there is a hypothesis for every person that the court would like to consider. Each of these people will have a varying degree of relatedness to the suspect. Let:

$H_1 = H_p$: The DNA came from the suspect

H_2 : The DNA came from person 2 the brother of the suspect

H_3 : The DNA came from person 3 the father of the suspect

...

H_i : The DNA came from person i related in whatever way to the suspect

...

H_N : The DNA came from person N so distantly related that we consider him effectively unrelated to the suspect.

Hence using this nomenclature, we have the following partitioning showing a more complex defence proposition:

$H_p = H_1$

$H_d = \{H_2, H_3, \dots, H_i, \dots, H_N\}$

We need a formulation that can handle from three to many hypotheses. In the extreme formulation – involving the population of the Earth – there would be about $N = 6$ billion such hypotheses.

The general form of Bayes’ theorem provides such a formulation. Indeed situations involving many hypotheses cannot be handled easily using a LR approach because it is not possible to separate the likelihoods from the respective priors. It is necessary to implement the full form of Bayes’ theorem to compute the posterior probability of H_p .

This was first brought to the attention of forensic scientists in the DNA area by Balding, Donnelly, Nichols, Evett and Weir [8, 25-28]. They state

$$\Pr(H_p \mid E) = \frac{\Pr(E \mid H_p) \Pr(H_p)}{\sum_{i=2}^N \Pr(E \mid H_i) \Pr(H_i)} \quad (\text{equation 4})$$

This equation is very instructive for our thinking but it is difficult to see how to apply it directly in the current court environment because the terms $\Pr(H_i)$ relate to the prior probability for the i^{th} hypothesis. The introduction of such considerations by a forensic scientist is unlikely to be allowed or welcomed in court. However such an approach of computing the posterior probability of the prosecution view may be possible if the court were to supply its view of the priors. The terms ‘forensically relevant populations’ [29] and ‘relevant subgroup’ [20] contain an implicit reference to such priors, and we can envisage the situation where a court instructs the witness to only consider the sub-group ‘Caucasian sexually active males in the Manchester area’ which includes the defendant. However, we are tempted to think that these cases will remain the exception and not the rule.

At this time this approach must be consigned to the best and most useful tool for the scientist to use, but currently difficult if not impossible to present in court. The unanswered question is whether the compromise approach to be given below is an acceptable solution to the courts.

4. A Possible Solution: an extended likelihood ratio

There is a ‘halfway house’ between the likelihood ratio approach and the unifying full Bayesian equation that may have some merit. Adopting the same nomenclature as above we consider an exclusive and exhaustive partition of $H_d = \{H_2, \dots, H_N\}$. Using this partition and the law of total probability we expand $\Pr(E \mid H_d)$ and rewrite the likelihood ratio as

$$LR = \frac{\Pr(E \mid H_p)}{\Pr(E \mid H_d)} = \frac{\Pr(E \mid H_p)}{\sum_{i=2}^N \Pr(E \mid H_i, H_d) \Pr(H_i \mid H_d)} \quad (\text{equation 5})$$

This proposal gives identical results compared with the proposal by Aitken and Taroni [30, p.248 ss] or Taroni and Biederman [31]. However their formula requires an assessment of the prior probabilities on all hypotheses (including the prosecution’s proposition). The advantage of this approach is that it only

requires the values of the prior probabilities, $\Pr(H_i \mid H_d)$, of the partition under H_d . There is hence no requirement for the relative priors on H_p and H_d . Thus we circumvent the need for assigning $\Pr(H_p)$ and focus the analysis on the defence hypotheses. It may be possible for all parties to agree that whatever the value of $\Pr(H_d)$, that H_2 will contribute (say) 99% of it ($\Pr(H_2 \mid H_d) = 0.99$), H_3 0.5%, and $H_4 \dots H_N$ together the remaining 0.5%. More likely is the possibility that each side in the adversarial process will argue for priors that optimize the evidence from their perspective. Such a debate may actually be a scientifically credible way to argue the case. Another possible benefit is that it may be simpler to evaluate the probabilities of the evidence, E , conditioned on the elements of the partition, $\Pr(E \mid H_i, H_d)$, than $\Pr(E \mid H_d)$ itself. Although our motivating discussion has used presentation of DNA evidence it is important to stress that this approach is completely general, and could be used to present the findings from consideration of many different types of forensic evidence.

5. Example

We consider here a simple case treated in each of the three ways. Consider the situation where we have a stain at the scene that matches a single suspect. The findings (E) are the two reported matching profiles. The chance that an unknown, unrelated person would match is assigned as 1 in a billion. We add that the probability that an untyped full brother would match is 1 in 10,000. In the region where the crime was committed there are 100,000 alternative suspects ($N-1$), one of whom is the brother of the suspect. Hence in total, we have $N = 100,001$ potential donors including the suspect. There are no other relations of the suspect in this region.

Likelihood ratio approach with two propositions:

Assuming the numerator of the likelihood ratio to be 1, the approach would lead to different reporting depending on the pair of propositions considered. Indeed, a likelihood ratio of 10^9 would be reported for the propositions:

H_p : The suspect is the donor of the DNA

H_d : An **unrelated** person is the donor of the stain

Whereas a likelihood ratio of 10^4 would be stated for the following pair of propositions:

H_p : The suspect is the donor of the DNA

H_d : A **full brother** of the suspect is the donor of the stain.

This approach makes no assumptions about priors, but forces a clear-cut choice between two pairs of propositions. That would have been the case every time the change of the proposition (more often on the defence side) impacts on the assessment of the probability of the findings $\Pr(E \mid H_d)$.

The reporting mechanism makes no mention of the pool of $N-1$ other potential donors among which one full brother has to be accounted for.

Extended likelihood ratio approach:

These limitations are overcome by using the extended likelihood ratio. Given the endorsement of some assumptions about the priors to be considered under the defence proposition: i.e. in the example it is assumed that the brother and the unrelated people are all equally likely to be the alternative source of the stain, the extended likelihood ratio approach would report the value of likelihood ratio LR of the order of 5×10^8 for the hypotheses:

H_p : The suspect is the donor of the DNA

H_d : An **unknown** person (unrelated or a brother) is the donor of the stain

We have a total $N = 100,001$ potential donors sorted and indexed $i = 1$ for the suspect, $i = 2$ for the full brother and $i = 3$ to $N = 100,001$ for the unrelated individuals considered.

$$\begin{aligned} LR &= \frac{\Pr(E \mid H_p)}{\sum_{i=2}^N \Pr(E \mid H_i, H_d) \Pr(H_i \mid H_d)} \\ &= \frac{\Pr(E \mid H_p)}{\Pr(E \mid H_2, H_d) \Pr(H_2 \mid H_d) + \sum_{i=3}^{i=N} \Pr(E \mid H_i, H_d) \Pr(H_i \mid H_d)} \\ &= \frac{\Pr(E \mid H_p)}{\Pr(E \mid H_2, H_d) \Pr(H_2 \mid H_d) + \Pr(E \mid H_i, H_d) \sum_{i=3}^{i=N} \Pr(H_i \mid H_d)} \\ &= \frac{1}{\frac{1}{10^4} \times \frac{1}{100,000} + \frac{1}{10^9} \times \frac{99,999}{100,000}} \\ &= 500,002,500 \end{aligned}$$

The same results will also occur if the brother has the average prior of the unrelated people.

Full Bayesian approach:

Under the same set of propositions (where $H_p = H_d$), the full Bayesian approach would report a posterior probability of 0.9998 that the suspect is the donor of the stain.

$$\begin{aligned} \Pr(H_p \mid E) &= \frac{\Pr(E \mid H_p) \Pr(H_p)}{\sum_{i=1}^N \Pr(E \mid H_i) \Pr(H_i)} \\ &= \frac{\Pr(E \mid H_p) \Pr(H_p)}{\Pr(E \mid H_1) \Pr(H_1) + \Pr(E \mid H_2) \Pr(H_2) + \Pr(E \mid H_i) \sum_{i=3}^{i=N} \Pr(H_i)} \\ &= \frac{1 \times \frac{1}{100,001}}{1 \times \frac{1}{100,001} + \frac{1}{10^4} \times \frac{1}{100,001} + \frac{1}{10^9} \times \frac{99,999}{100,001}} \\ &\approx 0.9998 \end{aligned}$$

Again some assumptions have been made about the priors: in the example it is assumed that the brother, the suspect and the unrelated people are all equally likely to be the alternative source of the stain. The same results will again also occur if the brother and suspect have the average prior of the unrelated people.

6. Exploring these three options with Bayesian Networks:

A Bayesian network is a graphical model for expressing the probabilistic relationships between a set of variables. It consists of a directed graph where nodes represent variables and the directed arrows between them represent the probabilistic (often causal) dependencies. The arrows show the direction of the reasoning expressed through probabilities. A node represents an uncertain event that can take several states.

In the context of forensic science, Bayesian networks assist scientists not only in describing a complex problem but also in computing the effect of the scientific evidence on the plausibility of the relevant proposition. They are used as ‘inference networks’, as models of complex processes whose ingredients or variables can be linked together in very complex ways. Through their use, it is hoped to make all of the implications of reasoning clear to lay people, without them having to understand any of the underlying mathematics or how to perform any calculation [32].

The use of graphical models to represent legal issues is not new. Wigmore made extensive use of hierarchical representation to summarize the range of issues in legal cases [33]. Probabilistic networks have been reintroduced recently with the analysis of complex and famous cases such as the Sacco and Vanzetti case, the Omar Raddad case and the O.J. Simpson trial [34–36].

Several recent monographs [37, 38] and the availability of simple and intuitive computer packages to develop Bayesian networks have promoted a steady growth of applications of Bayesian networks including those to forensic science problems. Aitken et al., Curran et al., and Dawid and Evett developed early applications of probabilistic networks in forensic science [10, 39–42]. Recent papers deal with paternity cases, DNA mixtures interpretation, the

interpretation of small quantities of DNA at activity level and scenarios, previously solved algebraically, involving bloodstains taking account of their relevance and fibre evidence and the evaluation of cross-transfer evidence in DNA cases [43–48]. That leads to a recent monograph which is entirely devoted to the application of Bayesian Networks in forensic science [49].

We can illustrate the three options outlined above using Bayesian Networks.

The simplest form of a Bayesian network dealing with DNA evidence applies when two source-level propositions are addressed:

H_p : The suspect is the donor of the DNA

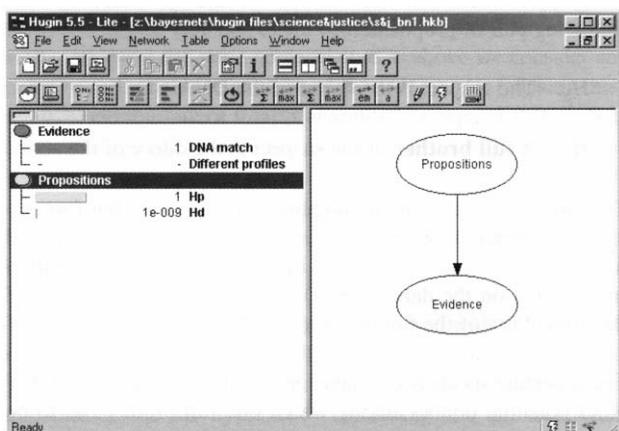
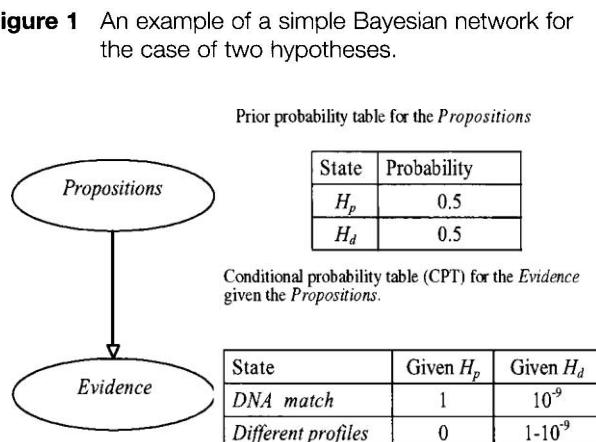
H_d : An **unrelated** person is the donor of the stain

The corresponding Bayesian network is given in Figure 1. The two nodes (*Propositions* and *Evidence*) represent uncertain events. The directed arc, symbolised by the arrow, between the two nodes expresses a conditional relationship (causal in this case). In other words, the probabilities associated with the events of the *Evidence* node will be conditioned on the truth or otherwise of the events of the *Propositions* node. For this node (called a *child node*), probabilities are expressed in terms of conditional probability tables that depend on the parent node. In this case the findings represented by the suspect and stain matching DNA profiles correspond to the state *DNA match*. All other outcomes falling into the *Different profiles* category.

Such networks can be programmed very simply using software packages such as Hugin Lite (<http://www.hugin.com>).

In addition to providing a tool for expressing dependencies for a set of variables, a Bayesian network also gives a framework for

Figure 2 Example of propagation of uncertainty in the Bayesian network given the observation of a DNA match. The ratio between the two probabilities under H_p and H_d is equal to the likelihood ratio.



probabilistic inference. It represents relationships between the possibilities at each node, but does not show the impact of any evidence. In a process known as ‘entering evidence’, we can declare that the result of the examination is known and use the Bayesian network to update all probabilities in the light of this information. Here, the update on the proposition node is of interest. Hence, as soon as the evidence is observed (for example *DNA match*), this knowledge is propagated back through the network to compute its impact on the probability of H_p . This latter probability is called a posterior probability because it has been computed after entering evidence into the network. The calculation relies on a simple application of Bayes’ Theorem, directly derived from the basic laws of probability. By adopting a 0.5:0.5 ratio for the probabilities associated to the two states of the proposition node – in other words, the a priori odds are set to evens i.e. 1 then the posterior odds will be numerically equal to the likelihood ratio. This process is shown in Figure 2.

It is straightforward to extend the network to consider more than two propositions and hence to illustrate the full Bayesian approach:

Figure 3 An example of a Bayesian network for three hypotheses.

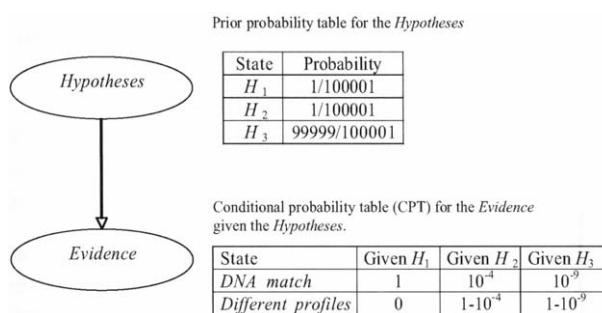
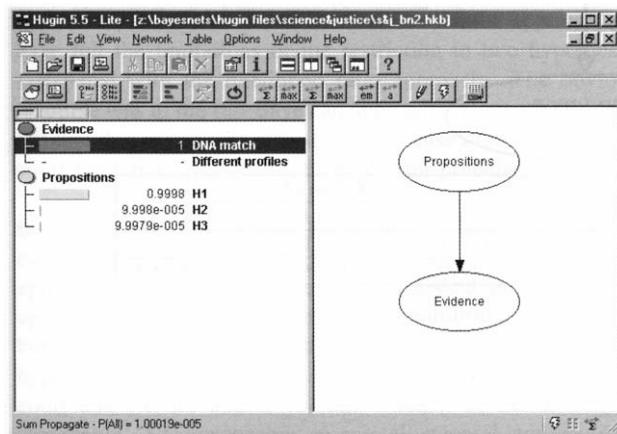


Figure 4 Computation of the posterior probabilities on H_1 to H_3 given the evidence (*DNA match*)



- H_1 : The suspect is the donor of the DNA
- H_2 : A brother of the suspect is the donor of the stain
- H_3 : An unrelated person is the donor of the stain

which results in the Bayesian network shown in Figure 3.

Note that we have limited our hypotheses to three. Although we could have assigned one hypothesis per individual considered (as implied in the formulae), we have chosen to merge all the unrelated members into one category (H_3). This approach can, of course, be extended to any number of hypotheses. Propagating evidence in this network will not allow the computation of likelihood ratios directly as before, but posterior probabilities for each hypothesis will be computed using Bayes’ theorem and the assigned prior probabilities as shown in Figure 4.

The extended likelihood ratio approach can be presented as shown in the network given in Figure 5.

The difference here is the willingness to keep two overall propositions (H_p and H_d respectively for the prosecution and defence) that will condition a set of partitioning hypotheses (H_1 to H_3). Again the analysis can be extended to any number of hypotheses.

When the evidence is declared (e.g. *DNA match*) and propagated back in the network, the ratio of the posterior probabilities on H_p and H_d respectively is the LR according to the extended likelihood ratio approach. The approach amounts to a computation of a likelihood ratio under two general perspectives (the prosecution view and the defence view) that could be formed by a family of mutually exclusive sub-hypotheses. The final LR is analogous to a weighted average

Figure 5 A Bayesian network to demonstrate the extended likelihood ratio approach

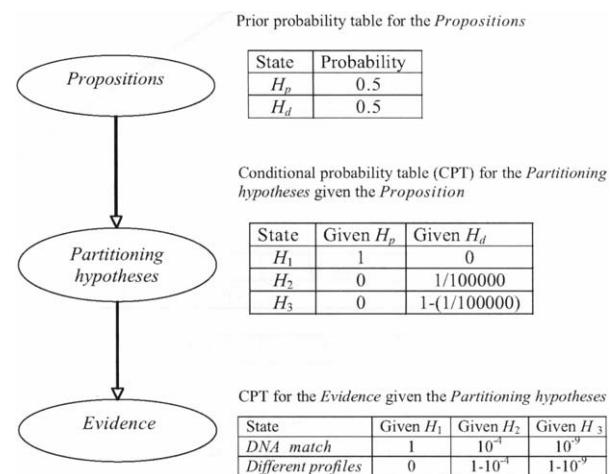
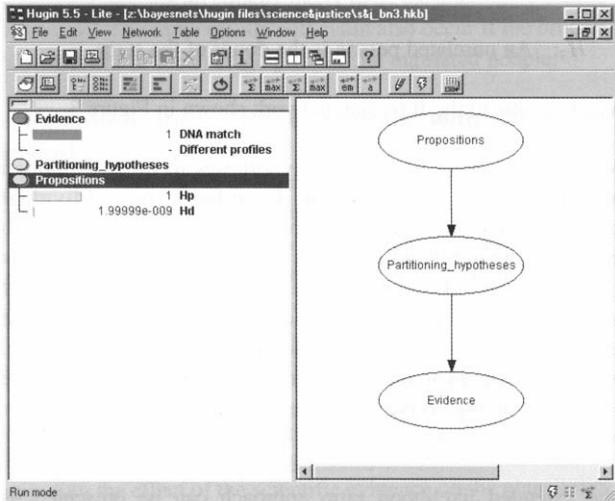


Figure 6 Computation of the extended likelihood ratio for the evidence given the propositions



conditioned on the prior distributions assigned to the sub-hypotheses given both H_p and H_d . Obviously, the approach can be generalised to any set of sub-hypotheses considered respectively by prosecution and defence. The extended likelihood ratio is obtained by entering the evidence in the system as shown in Figure 6.

The real power of Bayesian networks lies in their ability to deal with increasing degrees of complexity, where a full algebraic solution may be more difficult to obtain. For example, the previous example may be taken further by taking into consideration that uncertainty may remain on the ethnicity of the donor of the stain. To give our analysis more relevance (without losing generality), we will assume that the DNA profile obtained from the stain is partial, results have been obtained from the loci D3 (12,16), D18 (12,16) and TH01 (6,9). We will consider three generic classes for ethnic appearance: RC1 for Caucasian, RC3 for Afro-Caribbean and RC4 for Asian Indian. We will assume that the suspect is of Caucasian appearance and so would be his brother. The Bayesian Network given in Figure 7 has been designed:

Figure 7 A Bayesian network for a more complex case

Conditional probability table (CPT) for the *ethnicity* given the *Propositions* and *Partitioning hypotheses*.

State	Given H_p		Given H_d	
	Given H_1	Given H_2	Given H_3	Given H_4
RC1	1	1	0.1	
RC3	0	0	0.1	
RC4	0	0	0.8	

Prior probability table for the *Propositions*

State	Probability
H_p	0.5
H_d	0.5

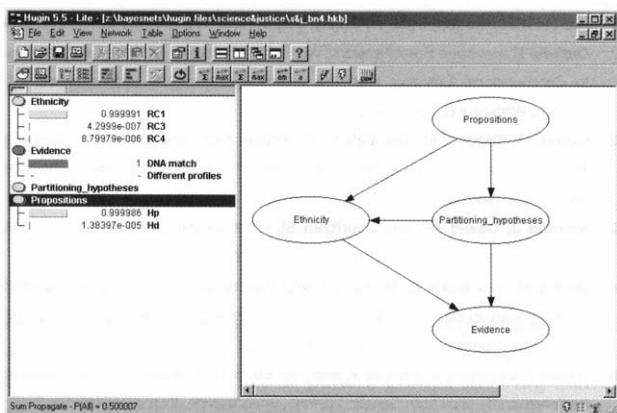
CPT for the *Partitioning hypotheses* given the *Propositions*.

State	Given H_p	Given H_d
H_1	1	0
H_2	0	$1/100000$
H_3	0	$1-(1/100000)$

CPT for the *Evidence* given the *Ethnicity* and the *Partitioning hypotheses*.

State	Given H_1		Given H_2			Given H_3		
			Given $RC1$	Given $RC3$	Given $RC3$	Given $RC1$	Given $RC3$	Given $RC3$
Full DNA match	1	0	0.041	0.039	0.047	$4.2 \cdot 10^{-5}$	$4.3 \cdot 10^{-6}$	$1.1 \cdot 10^{-5}$
Other outcomes	0	1	0.959	0.961	0.953	0.999958	0.999996	0.999989

Figure 8 Computation of the extended likelihood ratio for the evidence *DNA match* in a Bayesian network combining ethnicity and partitioning hypotheses



For this Bayesian network we had to specify two ‘prior’ distributions:

- as before, we specified the prior distribution for the two sub-propositions (H_2 and H_3) under the defence perspective (H_d);
- and we specified the prior distribution for the ethnicity assuming that an unrelated person is the donor of the stain (H_3).

The approach used to handle ethnicity amounts to the stratified approach proposed by Buckleton *et al.* [50] on blood groups.

In this case as shown in Figure 8, the extended likelihood ratio, given the *DNA match* and assuming that the ethnicity of the donor is unknown, is equal to about 72,255.

Conclusion

In this paper we have discussed two previously published interpretation frameworks: The likelihood ratio-based approach considering only two propositions and the full Bayesian approach. As we have attempted to tackle more and more complex cases utilising a formal structured approach we have felt the limitations of the restriction to two hypotheses associated with the likelihood ratio approach. The obvious recourse was to the full Bayesian approach. However we have felt that this option was closed to us because of understandable court limitation over assumptions of prior probabilities.

In our search for useable methods we have suggested a compromise, presented here as the extended likelihood ratio approach. Compared to previous published proposals, this approach does not require the prior probabilities of H_d and H_p but rather only a relative partitioning of the prior on the hypotheses covered by H_d . As yet the method is untried in court and we are unable to state whether or not it will be acceptable. The approach is completely general, and could be

used to present the findings from many types of forensic evidence.

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