Forensic Science International: Genetics 50 (2021) 102406

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen

Research paper

When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?

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ARTICLE INFO

Keywords:
Forensic DNA
likelihood ratio
propositions
exhaustive

ABSTRACT

We seek to develop a rational approach to forming propositions when little information is available from the outset, as this often happens in casework. If propositions used when evaluating evidence are not exhaustive (in the context of the case), then there is a theoretical risk that an *LR* greater than one may be associated with a proposition in the numerator that - if all meaningful propositions had been considered - would in fact have a lower posterior probability after consideration of the evidence.

Ideally, all propositions should be considered. However, with multiple propositions, some terms will be larger than others and for simplification very small terms can be neglected without changing the order of magnitude of the value of the evidence (i.e. *LR*). Our analysis shows that mathematically a contributor's DNA can be assumed to be present under both prosecution and alternative propositions (H_p and H_a) if there is a reasonable prior probability of their DNA being present and their inclusion is supported by the profile. This is because the terms associated to these sub-propositions will dominate our *LR*. For example, in the absence of specific information, when considering two persons of interest (POI) as potential contributors to a mixed DNA profile we suggest the assumption of one when examining the presence of the other, after checking that both collectively explain the profile well. This represents more meaningful propositions and allows better discrimination.

Slooten and Caliebe have shown that the overall *LR* is the weighted average of *LR*s with the same number of contributors (NoC) under both propositions. The weights involve both an assessment of the probability of the crime scene DNA profile and the probability of this NoC given the background information.

1. Introduction

The best known and most used form of Bayes' rule in forensic science is the odds form. This is because the notion of likelihood ratio (*LR*) is central to the evaluation of evidence – as outlined for example by Royall[1] ([1] @ pg 8 cited in [2]) or more specifically by Evett et al. [3]. The formulation of this rule in odds form requires at least two propositions which are usually chosen to align with the prosecution position and a sensible alternative. The alternative will be based on the case circumstances, ideally on information given by the defence (thus, the alternative is often referred to in the literature as the defence proposition, but we advocate a change from this terminology). As well as nicely representing the concept of exhaustivity that we later discuss, the use of 'alternative', also considers the fact that an evaluation may be carried out in an investigative phase of a case where there is no defence yet assigned or the defense may not wish to provide an alternative. In common usage these are usually exclusive but not always exhaustive. The standard definition for two mutually exclusive propositions is that

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[1] "The law of likelihood applies to pairs of hypotheses, telling when a given set of observations is evidence for one versus the other: hypothesis A is better supported than B if A implies a greater probability for the observations than B does. This law represents a concept of evidence that is essentially relative, one that does not apply to a single hypothesis taken alone. Thus it explains how observations should be interpreted as evidence for A vis-a-vis B, but it makes no mention of how those observations should be interpreted as evidence in relation to A alone."

https://doi.org/10.1016/j.fsigen.2020.102406
Received 6 April 2020; Received in revised form 21 September 2020; Accepted 3 October 2020
Available online 22 October 2020

they cannot both be true at the same time. A common definition for exhaustive propositions is that they cover all possibilities. Two (or many) exhaustive propositions cannot both (or all) be false at the same time. For two (or more) mutually exclusive and exhaustive propositions exactly one is always true. An example of two mutually exclusive and exhaustive propositions – considering a single source trace DNA profile - would be 'John Smith is the source of the DNA' and 'John Smith is not the source of the DNA'. However, as outlined by Lindley ([4] @ pg 5) or more recently in [2], such an alternative makes assignment of the probability of the evidence impractical. Indeed, one cannot assign meaningfully a probability of the DNA results given such a vague proposition. Cook et al. [5] also underline that [using] the word "not" lacks transparency as it "*gives the court no idea of the way in which the scientist has assessed the evidence with regard to the second proposition*". One needs to be more precise, even in this simple situation (we will develop this example later on with a DNA mixture). The probability of a corresponding DNA profile will be different if the person -who is the source of the DNA- is John Smith's identical twin brother or an unrelated person.

We start by reiterating the well-known principles of evidence interpretation from [3]:

1) The results should be evaluated within a framework of circumstances: this framework is commonly denoted by 'I', which by convention stands for the task relevant information. By task relevant, we mean the information that is useful for case assessement and evaluation (e.g., the information needed for formulation of propositions and choice of the relevant population).
2) The results should be evaluated with respect to at least two competing propositions.
3) The role of the expert should be to consider the probability of the results given the propositions and not the probability of the propositions themselves: results are commonly denoted 'E', which by convention stands for Evidence.

These principles are based on earlier works by Evett and Weir [6]. All thoughts on proposition setting flow from these three principles.

We largely follow the teachings of Evett (this follows from many publications but we reference one of the earliest [7]). The court is likely to be interested in questions of the type: What is the probability Mr Smith is a donor to this stain? This probability cannot be developed from the DNA evidence alone (this relates to the third principle outlined above). The principles above lead naturally to the evaluation of evidence using an LR[2] . The formula for obtaining this probability is well known.

1.1. The role that the convention on naming proposition has on thoughts about exhaustivity

In "What is the Probability that This Blood Came from That Person? A meaningful Question?" (published 1983) Evett named the two propositions C and $\overline{C}$[3] . The use of these two terms clearly implied two exclusive and exhaustive propositions. This usage persisted until, at least, 1997 [9–11]. However by 1998 common usage had changed to the use of the terms H_p and H_d [12,13]. For example, the DNA Commission [14] (2006) stated: "*A typical analysis of a crime sample has the prosecution hypothesis (H_p) and the* defence *hypothesis (H_d)*." No comment appears in that paper on whether or not these need to be exhaustive.

We provide below some examples of where the topic of the exhaustivity of propositions has been mentioned in guidance documents.

- The UK's Forensic Science Regulator's guidance [15] document on DNA mixture interpretation: "*However, for forensic evaluation it is not necessary that they* [propositions] *be exhaustive. That is, they do not need to cover all possibilities; it is sufficient that they represent the two competing propositions of the prosecution and* defence *within an accepted framework of circumstances.*"
- The ENFSI guideline for evaluative reporting in forensic science [16]: "*Though the considered propositions are those deemed most relevant, they do not need to be exhaustive, so both propositions could be false. The likelihood ratio says nothing about propositions other than the two that were considered.*"
- Practitioner Guide No 4 (UK). Case Assessment and Interpretation of Expert Evidence. Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses [17]: "*The LR is the ratio of two probabilities, conditioned on mutually exclusive (but not necessarily exhaustive) propositions.*"
- The ISFG DNA commission recommendations on proposition setting state [18] "*it will be necessary to account for* defence*'s view of events*", and later "*These do not need to be exhaustive, but should reflect the positions of both parties*."

In other texts it is also stated that the propositions do not need to be exhaustive, but that there are some safeguards that need to be met [19–22]. In Kokshoorn et al. [21], whilst it is stated that the propositions need not be exhaustive, it is noted that "… *if possible this is preferred.*" In Evett et al. [23] or in Taroni et al. [20] it is stated that one of the properties of propositions is that "*Propositions are mutually exclusive and exhaustive*", however the authors then go on to make the note that this requirement only needs be true "*Within the stated framework*." In a similar sentiment Gittelson et al. [24] state "*…propositions need to be mutually exclusive and exhaustive in the context of the case (*i.e. *one should not consider all propositions as default, but only those that are of interest to the court).*" This has been picked up by the Australian and New Zealand Policing Advisory Agency National Institute of Forensic Science in their guideline for evaluative reporting [25].

As outlined in [15] *'The root problem here is that of attempting to use a two proposition framework in a case where there are several potential* defence *propositions.'*

1.2. Goal of this work

Taking these aspects into account, we seek to develop a rational approach to forming propositions when little or no information is available in order to summarise the defense's account of the facts or more generally when multiple propositions need to be considered.

2. Theory

In a purely mathematical sense, propositions do not need to be exhaustive to form a ratio of two probabilities and call that an LR.

It is also easy to write out a pair of exclusive and exhaustive propositions. Let H_p be the proposition that aligns with the prosecution argument and let H_a simply be the complement of this.[4] An example would be:

H_p: Mr Smith is a DNA donor to the stain

H_a: Mr Smith is not a DNA donor to the stain.

[2] Or preferably a Bayes factor (BF). With simple propositions, a BF reduces to an LR. However, with multiple propositions, the BF is a ratio of weighted likelihoods.

[3] Lindley (1985) [4] uses the symbols F and and Good (1950) [8] the symbols H and $\overline{H}$ for the propositions which explicitly implies that they are exclusive and exhaustive. One can also infer from the mathematics in many texts that the authors are treating the propositions as exclusive and exhaustive.

[4] Please note that we need notation only if we use formulae, that is between specialists. In statements, we can simply refer to the propositions as 'Mr Smith is the source of the DNA' and 'An unknown Eurasian person is the source of the DNA'. No notation is needed.

However practical assignment of the probability of the evidence requires that the propositions be specified more precisely. Biedermann et al. [19] make this point when they state "*Although it is straightforward to obtain a mutually exclusive*, and *exhaustive alternative by the negation of the first proposition, it is not advisable, as such an alternative proposition may be unhelpful in practical terms.*"

Although it may not be immediately obvious, the complementary hypothesis is often comprised of many sub-propositions. For example, if Mr Smith is not a donor, then his brother, or his cousin, or his uncle, or someone completely unrelated to him might be a donor. The net effect of this is that the complementary alternative may encompass many alternatives which may or may not be of interest to the case. Many of these may not be able to be addressed through lack of information or software. The probability of the results given these different sub-propositions will be different. Therefore, the alternative needs to be specified more precisely. In the example introduced above it is necessary to assign the number(s) of contributors and to specify the ethnicity (or ethnicities) and degree(s) of relatedness of the alternate donor(s) to Mr Smith and any other typed persons. These factors are called nuisance variables. They are needed to assign the probability of interest, but they are not of direct interest themselves.

In common practice the values for these nuisance variables are usually assumed. For example, it may be assumed[5] that there are two donors to the stain and that that all donors are unrelated. This leads to a pair of propositions that are not exhaustive in an absolute sense. For example, the set given above could be rewritten as:

H_p. Mr Smith and an unknown person of X ethnic group of Y geography unrelated to Mr Smith are the donors to the stain.

H_a: Two unknown persons, neither of whom are related to either Mr Smith or each other, and selected from the X ethnic group of Y geography are the only donors to the stain.

We have written these out a little pedantically to emphasise that there are other alternative propositions that are not being considered.

Whilst it is appealing to demand a precise alternative to enable practical implementation, the defense are under no obligation to assist the prosecution at all. In most cases it will be necessary to proceed without any specification of a proposition from the defense and with an insistence that the defense are entitled to the union of all propositions consistent with exonoration.

Biedermann et al. [19] stated this nicely by saying "*Instead of absolute exhaustiveness, practice can proceed with an acceptable coverage, that is the omission of no relevant proposition.*"

Taking up Biedermann et al.'s approach we discuss in the following sections the risk of non-exhaustive propositions, how to identify these risks, and how to identify when it is safe to omit a proposition.

2.1. Identifying the risk with propositions that do not exhaust the sample space

Consider that there are three propositions H_1, H_2, H_3 which are mutually exclusive and collectively exhaustive. Let the evidence be, E, and the relevant background information, I. Further consider that only two propositions H_1 and H_2 are considered. It can easily be shown (see appendix A1.1) that the LR for propositions H_1 and H_2 can be greater than one but, when considering all relevant propositions, the posterior probability of H_1 given the evidence decreases with respect to the prior probability.

Balding [26,27] gives, "*If H and G are not exhaustive, it may be that D is very unlikely under both, but highly likely under a third. In that case the probabilities for H and G may both decline as a result of observing D…*".

This is to be expected, and explains why it is so important to disclose case information and assumptions. But, if one can offer a means to cope with the challenge of considering all relevant propositions, then this should be done. This is what we do below.

2.2. Compound propositions

In Section 1.0 we discussed the need to specify the propositions sufficiently explicitly such that the probability of the evidence can be assigned. A useful way to proceed from vague propositions to some that are sufficiently explicit is to use compound propositions (see Appendix section A2.1).

Consider two exclusive and exhaustive propositions H_p and H_a. That is:

$\Pr(H_p \text{ and} H_a) = 0$ and $\Pr(H_p) + \Pr(H_a) = 1$.

Consider that H_a is vague in that there are three different possibilities H_{a1}, $H_{a2,}$ and H_{a3} (think of something such as the offender, if not the POI, is Caucasian, African American, or Hispanic). We can "break up" H_a into these three possibilities. The algebra is simply a use of the third law of probability and is given in the appendix. We will need to assign the probability of each of H_{a1}, $H_{a2,}$ and H_{a3} given H_a is true to use this law.

2.3. The Bayes factor

Consider any $N+1$ propositions H_p, H_{an} $n = 1…N$. The Bayes factor (BF) is the ratio of the posterior to the prior odds. For the proposition, H_p,

$$BF = \frac{\Pr(E|H_p)\sum_{n=1}^{N}\Pr(H_{an})}{\sum_{n=1}^{N}\Pr(E|H_{an})\Pr(H_{an})} \quad (1)$$

Writing $H_a = H_{a1} \cup H_{a2} \ldots H_{aN}$ and noting that $\Pr(H_{an}) \Big/ \sum_{n=1}^{N}\Pr(H_{an}) = \Pr(H_{an}|H_a)$

$$BF = \frac{\Pr(E|H_p)}{\sum_{n=1}^{N}\Pr(E|H_{an})\Pr(H_{an}|H_a)} \quad (2)$$

With the odds form of Bayes' theorem, the prior odds are a separate term from the LR. This allows the scientist to concentrate on the LR and, correctly, to leave the prior odds to the court. With a BF this separation is no longer possible. However, the formulation in equation 2 requires the assignment of terms such as $\Pr(H_{an}|H_a)$. In most cases scientists will need to assign, and disclose, these probabilities.[6]

Note that formulations similar to the BF given above have been suggested for calculating the value of evidence when stratifying across relationship types in a 'unified LR' such as Eq. 1 in [28].

2.4. The interaction of propositions and assumptions

In an evaluative context (i.e., at court) development of propositions should occur within a framework of circumstances but also on a number of assumptions. The assumptions may be explicit or implicit, and may range from very well supported to speculative.

If the assumption is reformulated as an event, say, event A and its complement $\overline{A}$ instead of making an assumption, and thereby treating an event A as having happened or not, one may instead incorporate the uncertainty surrounding the occurrence of the event into the analysis by considering the refined sub-propositions in which A has happened, or not (see Appendix Section A2.2).

[5] These assumptions - like any used in science - are based on information or knowledge, and to be transparent Willis et al. [16] suggest that they are disclosed.

[6] Scientists already assign these conditional probabilities, but usually as 0 (proposition not considered) or 1 (proposition considered), underlying that if new information is available this will change their evaluation.

Box 1
An extended derivation of one of S&C's formulae. We thank S&C for assistance.

$BF = \frac{\sum_i \Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)}{\sum_i \Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)}$. Where

E_c is the crime scene profile

E_p is the genotype of the POI

N is the number of contributors

Change the index notation for the summation variable from i to x in the denominator

$BF = \frac{\sum_i \Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)}{\sum_x \Pr(E_c,E_p|H_a,N=x)\Pr(N=x|H_a)}$ Treat the summation in the denominator as constant with respect to i and take it in to the summation across i. $BF = \sum_i \frac{\Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)}{\sum_x \Pr(E_c,E_p|H_a,N=x)\Pr(N=x|H_a)}$ expand $\times \frac{\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)}{\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)}$

$$BF = \sum_i \left[\frac{\Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)}{\sum_x \Pr(E_c,E_p|H_a,N=x)\Pr(N=x|H_a)\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)} \right]$$

Rearrange $BF = \sum_i \left[\frac{\Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)}{\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)\sum_x \Pr(E_c,E_p|H_a,N=x)\Pr(N=x|H_a)} \right]$

Note $\Pr(N=i|E_c,E_p,H_a) = \frac{\Pr(E_c,E_p|N=i,H_a)\Pr(N=i|H_a)}{\sum_x \Pr(E_c,E_p|H_a,N=x)\Pr(N=x|H_a)}$ equation 3

$$BF = \sum_i \left[\frac{\Pr(E_c,E_p|H_p,N=i)\Pr(N=i|H_p)}{\Pr(E_c,E_p|H_a,N=i)\Pr(N=i|H_a)} \Pr(N=i|E_c,E_p,H_a) \right] \quad (4)$$

The obvious question would be what part H_a plays in this consideration and whether it can be dropped from the conditioning. Our feeling is that it should be retained. It may be valuable to return to this discussion in the example in section 3.5.1

Assume that there is no strong background information informing N such that

$Pr\hat{f}_0(N=i|H_p) = Pr\hat{f}_0(N=i|H_a)$ and writing

$\frac{\Pr(E_c,E_p|H_p,N=i)}{\Pr(E_c,E_p|H_a,N=i)} = LR_i$ and $\Pr(N=i|H_a,E_c,E_p) = w_i$

$$BF = \sum_i LR_i w_i \quad (5)$$

3. Propositions in the DNA setting

3.1. The number of contributors (NoC)

In this example we concentrate on the number of contributors to a profile. If DNA is collected on an object, then often the case information does not allow an inference of the NoC. Let H_p be the proposition that the POI is a donor as before. We let H_a be the proposition that the POI is not a donor (the actual donor is assumed to be unrelated for this example). The number of contributors can be anything from 0 to ∞ and may be different depending on the version of events given by both parties. For practical implementation, in many software, it is currently necessary to pick one or a very few numbers for H_p and H_a and hence assign a prior probability of zero to the vast majority of possible contributor numbers.

If we consider a range of NoC, say 3 or 4, then this specifies two propositions under H_p and two under H_a. We assume in such a situation that maximum allele count (MAC) suggests that there are at least 3 donors but there are some imbalances that suggest the plausible presence of a 4th donor.

Recently a conceptual breakthrough was made by Slooten and Caliebe (S&C [29]). After some reasonable assumptions S&C give that the *BF* is well approximated as the weighted average of *LR*s created with the same NoC under H_p and H_a. Hence if we considered NoC could be three or four, the overall BF is the weighted average of LR_3 and LR_4. In the example described above LR_3 would have NoC = 3 under H_a and H_p. LR_4 would have NoC = 4 under H_a and H_p.

In this section we assume that methods for assigning LR_3 and LR_4 are available. We concentrate on the weights for the averaging. Again S&C have given insight on the analysis of the weights.

The weights for this averaging are the probability that NoC = 3 (or 4) given knowledge of the evidence profile, E_c, and that the POI is not a donor. We will term these weights w_i for the weight for NoC = i.

It is difficult to directly assess these weights. Rearrangement of the terms using Bayes' rule (see equation 3 in Box 1) leads to:

$$\underbrace{w_3}_{\substack{\text{weight for}\\ \text{the LR}_3\\ \text{term}}} = \frac{\Pr(E_c,E_p|N=3,H_a)\Pr(N=3|H_a)}{\underbrace{\Pr(E_c,E_p|N=3,H_a)}_{\substack{\text{probability of the crime and POI}\\ \text{profile if it comes from three donors}\\ \text{none of whom are the POI}}}\ \underbrace{\Pr(N=3|H_a)}_{\substack{\text{probability that there are three}\\ \text{donors before looking at the}\\ \text{crime profile and assuming}\\ \text{the POI is not a donor}}} + \underbrace{\Pr(E_c,E_p|N=4,H_a)}_{\substack{\text{probability of the crime and POI}\\ \text{profile if it comes from four donors}\\ \text{none of whom are the POI}}}\ \underbrace{\Pr(N=4|H_a)}_{\substack{\text{probability that there are four}\\ \text{donors before looking at the}\\ \text{crime profile and assuming}\\ \text{the POI is not a donor}}}}$$

It may be of interest how S&C came to the formulation that has terms such as $\Pr(N=3|H_a)$. We give an extended derivation in Box 1.

The terms in the above formula regarding the probability of the profile given a number of contributors may be assessed either with software or subjectively. In fact this is the term(s) that has been assessed and discussed historically, but often misnamed or misunderstood as the probability of the NoC. w_3 will be the largest term if the profile is well explained by three donors. If there are many imbalances or fewer but larger imbalances, then w_4 will be the largest term. Buckleton et al. [30] showed that it takes considerable imbalances either in size or number to create the situation where w_4 is the larger term.

The remaining terms are the prior probability that there are 3 (or 4) donors informed only by the background information, I, that is, without any inspection of the profile. This consideration has usually been overlooked.

Published work also shows that LR_n and LR_{n+1} are often very similar especially for the major donors to a stain [31–33]. In such a case the weights are close to immaterial.

Caliebe [34] gives a valuable worked example reprising the "hat example" of Biedermann, Taroni and Thompson (BTT 2011) [35]. In this example the profile, if viewed without examining the references, can be explained as a two person mixture. However, POI C is homozygous 1313 at D5S818 which shows 8,111,213 in the sample from the hat.

If we had been presented with this example several years ago the authors would exclude Mr C. Our process would have been to assign NoC blind with respect to the references and then stick with that number. We would have felt that 'adjusting" NoC to 3 to include Mr C was fitting the profiles to the accused. We still feel that reassigning NoC as 3 is wrong, but the insight from S&C is that the uncertainty in NoC can be embraced from the start. If the NoC is assigned as "at least 2″ and we consider NoC = 2 or 3 for simplicity then $LR^2 = 0$ and $LR^3 = 10{,}000$ (where LR^2 is the LR assuming NoC = 2 and LR^3 is the LR assuming NoC = 3). Presenting both these LRs to the court asks them to make the decision which one is relevant. If this is impossible for the scientist then, we suggest it will be impossible for the jury. The most likely outcome in an adversarial environment, we feel, will be to proceed with the lower LR in this case 0. However following S&C the weight w_3 is about 0.69 and $LR^{2\text{ or }3}$ is about 7000. This high weight on NoC = 3 comes as a surprise to us and the resulting LR challenges us. Biedermann informs us that this is a case supplied by Bill Thompson where only allele presence or absence were available with some alleles in parentheses. We assume that the high weight on NoC = 3 arises because height information is unavailable and this profile is actually more likely under NoC = 3 than NoC = 2. BTT 2011 give $\frac{\Pr(E_c|H_a,N=2)}{\Pr(E_c|H_a,N=3)} = 0.44$ giving an LR in favour of $N = 3$ of about 2.

This raises an issue that is tangential to this paper but important: if the mathematical analysis gives a result for an LR that one feels is too high (or too low) does the scientist subjectively overrule that. Caliebe notes in her paper that "*because the prior distribution is uncertain and to be conservative, it would make sense to arrive at an overall LR which is somewhat lower,* e.g. *around* 5000."

In this case we would feel comfortable with the LR of 7000 only if there was a strong indication from peak heights that $N = 3$. In the absence of this we would subjectively class this analysis as uninformative. In the adversarial environment of the US any subjective intervention that does not favour the defense will almost certainly lead to strong argument in court. Even if it does favour the defense the obvious argument arises: has the subjective intervention been sufficient.

As stated this is an important subject but tangential to this paper. We do not feel we have any particular insight into what to do.

The number of contributors, then, is a situation where propositions are always non-exhaustive since it would be impossible to consider NoC values up to infinity. But, it would often be acceptable coverage to use a single term and the consequences of considering a subset of propositions are small and readily manageable.

3.2. *Considering the possibility of a sibling as the donor*

Consider a single source DNA profile from a crime scene that is to be compared with the POI. We compare the use of the proposition set 1:

H_p: The POI is the donor

H_a: An unknown person is the donor.

With set 2 where there are two H_a:

H_{a1}: An unknown person unrelated to the POI is the donor (the unrelated proposition), and

H_{a2}: A sibling of the POI is the donor (the sibling proposition).

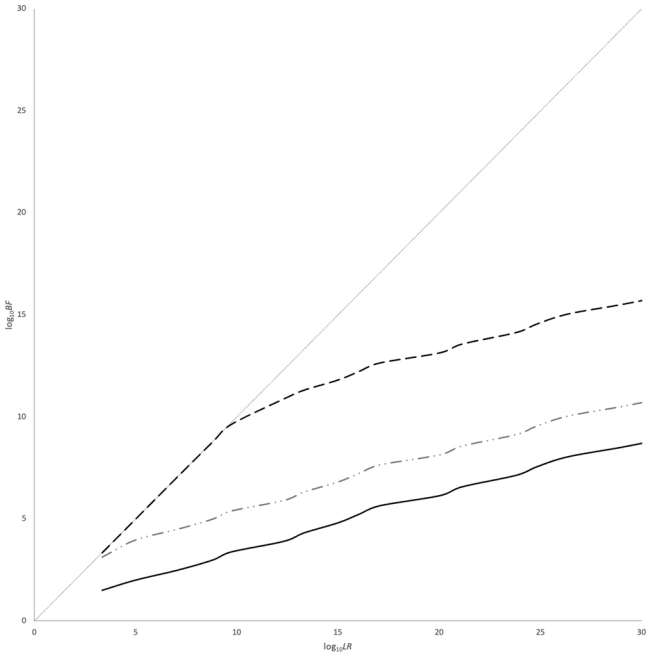

Fig. 1. A plot of $\log_{10}$BF vs $\log_{10}LR$ for a situation where the POI and the brother are sampled from a population of 10^8 (dashes), 10^3 (dashes and dots), or 10^1 (solid) equally likely persons and $\Pr(E|H_p) = 1$, $\Pr(E|H_{a1}) = \Pr(E|H_a) = 2p_{a1}p_{a2}$, and $\Pr(E|H_{a2}) = \frac{1+p_{a1}+p_{a2}+2p_{a1}p_{a2}}{4}$ at each locus where p_{a1}, p_{a2} are sampled from U[0,1/3].

This is obviously a very incomplete set of possibilities but it does actually bring out the core principles and effects. We examine this difference by comparing the *LR* with the BF. Unfortunately the sample space of variables is huge. We examine here the very specific situation where the POI and the brother are sampled from a population of 10^8 persons (or 10^3 or 10^1) who collectively represent the total population from which the offender must have come with each person having an equal probability of being the donor. We further assume that $\Pr(E|H_p) = 1$, $\Pr(E|H_{a1}) = \Pr(E|H_a) = 2p_{a1}p_{a2}$, and $\Pr(E|H_{a2}) = \frac{1+p_{a1}+p_{a2}+2p_{a1}p_{a2}}{4}$ at each locus where p_{a1}, p_{a2} are sampled from U[0,1/3] These are plausible values for many loci. We vary the number of loci between 1 and 30. This is simply to get a range of different probabilities for the three propositions.

In Fig. 1 we plot the BF for proposition set 2 vs the *LR* for proposition set 1.

These three lines could alternatively be interpreted as being based on the prior probabilities of the sibling being the donor (if the alternative proposition is true) are 10^{-8}, 10^{-3}, or 10^{-1}. We vary the number of loci, *l*, between 1 and 30. We also plot the lines $x = y$ (the expected line for the unrelated proposition only).

In the example shown in Fig. 1 we judge consequence of ignoring the possibility of a sibling being a donor as not serious when the prior on the sibling is 10^{-8} and the *LR* is below about 10^{13}. At higher *LR* the BF and *LR* differ but both expressions of evidential value are large.

For a prior probability of a sibling being 10^{-3} or 10^{-1} the difference between the *LR* and BF may be considerable. Although, it is well known that relatives share part of their DNA, it is educational to see the effect of our prior probability of the sub-proposition given the alternative is true ($\Pr(H_{ai}|H_a)$ illustrated in Fig. 1. Previously Balding [27] and Buckleton and Triggs [36] warned about the negative consequences of omitting a consideration of relatives.

3.3. Assumed contributors

Consider a sexual assault with a DNA profile generated from a relevant item (we deliberately leave vague the provenance of this item at this point). There is no dispute that the sexual assault took place, and the DNA work seeks to inform on the identity of the attacker. We omit the matter of relatedness for simplicity and to expose the underlying principles.

Consider four propositions. Let the person of interest be P, the potentially assumed contributor be V, $H_p = H_{VP} \cup H_{Pa}$, $H_d = H_{Va} \cup H_{aa}$, $H_V = H_{VP} \cup H_{Va}$, and $H_{\overline{V}} = H_{Pa} \cup H_{aa}$ where:

H_{VP}: V and P are the donors to the DNA,

H_{Pa}: P and an unknown person are the donors to the DNA,

H_{Va}: V and an unknown person are the donors to the DNA,

H_{aa}: Two unknown persons are the donors to the DNA.

Ideally, we would need to consider all the propositions in light of the case information. But, let us suppose that there is very little information or the information is not helpful. For example, let us now say that the item was a tissue found near the scene of the attack and thought potentially to have been used by the attacker to clean himself after commiting the assault. One can approximate the value of the results given all these propositions, especially if some of the sub-propositions (given the main proposition is true) have a low prior probability compared with the others or if the probability of the results given some sub-propositions are relatively small.

Following Slooten and Caliebe [29] if $\Pr(H_v|H_p) = \Pr(H_v|H_d)$ then:

$$LR = LR_{H_V}\Pr(H_V|E, H_d, I) + LR_{H_{\overline{V}}}\Pr(H_{\overline{V}}|E, H_d, I) \quad (6a)$$

When $LR_{H_V} = \frac{\Pr(E|H_{VP})}{\Pr(E|H_{Va})}$ and $LR_{H_{\overline{V}}} = \frac{\Pr(E|H_{Pa})}{\Pr(E|H_{aa})}$

Where $\Pr(H_{\overline{V}}|E, H_d, I)$ is small then $LR \approx LR_{H_V}$. $\Pr(H_{\overline{V}}|E, H_d, I)$ is small when $\frac{\Pr(E|H_{\overline{V}}, H_d, I)\Pr(H_{\overline{V}}|H_d, I)}{\Pr(E|H_V, H_d, I)\Pr(H_V|H_d, I)}$ (equation 6b) is small.

There are therefore two considerations: First, does the background information (not the DNA evidence) give strong reason to prefer some of the propositions ahead of the others. For example, if the background information suggests that V cannot possibly be a donor then H_{Pa} and H_{aa} are preferred over H_{VP} and H_{Va} and $\frac{\Pr(H_{\overline{V}}|H_d, I)}{\Pr(H_V|H_d, I)}$ is large.

Does the profile support the presence of DNA from V? If so $\frac{\Pr(E|H_{\overline{V}}, H_d, I)}{\Pr(E|H_V, H_d, I)}$ is small.

If the profile is well explained by V and P and there are no strong reasons to prefer some of the propositions from the background information then a good approximation to the *LR* will:

For P:

$$LR = \frac{\Pr(E|H_{VP})}{\Pr(E|H_{Va})} \quad (6c)$$

This approximation has been developed considering V either as a contributor or not. Hence, strictly one does not assume that V's DNA is in the mixture, it is simply that this term ends up dominating the analysis. Nor does this approximation have anything to do with whether or not the defense agreed to the inclusion of V in the sense of consulting a defence barrister. In most cases the analyst will have to make this call with the limited information within *I* that they have.

For V (if the presence of P is well supported):

Again following S&C $LR = LR_{H_P}\Pr(H_P|E, H_x, I) + LR_{H_{\overline{P}}}\Pr(H_{\overline{P}}|E, H_x, I)$

$H_x = H_{Pa} \cup H_{aa}$

When

$$LR_{H_P} = \frac{\Pr(E|H_{VP})}{\Pr(E|H_{Pa})} \quad (6d)$$

and

$$LR_{H_{\overline{P}}} = \frac{\Pr(E|H_{Va})}{\Pr(E|H_{aa})}$$

Where $\Pr(H_{\overline{P}}|E, H_x, I)$ is small then $LR \approx LR_{H_P}$.

$\Pr(H_{\overline{P}}|E, H_x, I)$ is small when $\frac{\Pr(E|H_{\overline{P}}, H_x, I)\Pr(H_{\overline{P}}|H_x, I)}{\Pr(E|H_P, H_x, I)\Pr(H_P|H_x, I)}$ is small.

This approximation has been developed considering P either as a contributor or not. Hence, strictly one does not assume that P's DNA is in the mixture, it is simply that this term ends up dominating the analysis. Again in most cases the analyst will have to make this call with the limited information within *I* that they have.

The defense have every right to state what case information they consider impacts the proposition (or propositions). Hence, the case information will impact the formulation of propositions (e.g., H_{Va} or H_{aa}.

In appendix 3.3 we discuss when the evidence poorly supports or excludes the presence of the victim.

SWGDAM 2017 [37] suggest: "*Assumed contributor: an individual whose DNA on an item of evidence is reasonably expected.*" The DNA commission [18] state: "*in a situation where an individual's DNA is assumed to be present under both views (Therefore, not contested by either party.)*" The mathematics above apply in cases where V is not as strongly associated with the item of evidence as described in the DNA Commission statement quoted above. The presence of V's DNA just needs to be one of the options. For example we suggest the consideration of such propositions for discarded items such as the tissue in the above example or a blanket on which P is alleged to have assaulted V. This will generally have a high impact on the value of the results.

Neither the SWGDAM nor the DNA commission statements directly preclude the approach we suggest which requires only a small alteration to existing advice.

Suggestion 1: For mathematical purposes, a contributor should be assumed to be present under both H_p and H_a if there is a reasonable prior probability of their DNA being present and their inclusion is supported by the profile. This *LR* should be reported.

This approach is not findings led, all propositions are considered, but some of the terms (relative to the others) have little impact on the *LR* and are thus omitted. The main assumption regards the assignment of the probability of the sub-proposition if the main proposition is true (e.g., Pr ($H_{p1}|H_p$,*I*) and Pr($H_{p2}|H_p$,*I*)). This should be disclosed in the statement.

Suggestion 2: An alternate we have had suggested is to report both of $LR \approx \frac{\Pr(E|H_{pV})}{\Pr(E|H_{Va})}$, $LR \approx \frac{\Pr(E|H_{Pa})}{\Pr(E|H_{aa})}$ and advise on weighting these based on an assignment of $\frac{\Pr(E|H_{\overline{V}},H_d,I)}{\Pr(E|H_V,H_d,I)}$.

We acknowledge the candor of suggestion 2, but one should be aware that there is a high risk that propositions will be chosen on the basis of the *LR*, whereas propositions ought to be based on case information only. If there is no case information, the scientist will be in a difficult situation as the first principle of interpretation is that 'The results should be evaluated within a framework of circumstances". If there is some case information, and that multiple propositions need to be considered, then we recommend suggestion 1 so that propositions are exhaustive in the context of the case. For evaluation purposes (i.e., in court) scientists should strive to give one *LR* for each person whose DNA presence is an issue.

3.4. The two-POI problem

Consider a case where a two-person stain has been analysed that can be explained as a mixture of the two persons. We identify four propositions:

H_{12}: P_1 and P_2 are the donors to the DNA,

H1a. P_1 and an unknown person are the donors to the DNA,

H2a. P_2 and an unknown person are the donors to the DNA,

H_{aa}: Two unknown persons are the donors to the DNA.

The analysis proceeds very similarly to the assumed contributor section (section 3.3 and appendix section A3.3) and arrives at a similar conclusion.

If there are no strong reasons to prefer some of the propositions, and if the profile is well explained by P_1 and P_2 then a good approximation to the value of the evidence regarding P_1 with or without P_2 assumed will be:

$$LR \approx \frac{\Pr(E|H_{12})}{\Pr(E|H_{2a})} \tag{7a}$$

A good approximation to the evidence regarding P_2 with or without P_1 assumed will be

$$LR \approx \frac{\Pr(E|H_{12})}{\Pr(E|H_{1a})} \tag{7b}$$

Suggestion 1: If there are no strong reasons to prefer some of the propositions, and if the profile is well explained by P_1 and P_2 then Eq.s 7a and 7b are suitable for reporting.

If using Eq.s 7a and 7b it may be useful to run 8a and 8b as a preliminary to confirm the conclusion that the profile is well explained by the inclusion of P_1 or P_2.

The 2018 DNA commission [18] states, at recommendation 3: "*When the issue regards the possible presence of DNA from several persons of interest, effort should be made to evaluate the profiles separately … this can be achieved by considering the result of the comparison between the given person and the trace and calculating individual LRs for each person.*"

This suggests that a possible solution is to assign *LR*s for individuals separately using the proposition sets implicit in these *LR*s:

$$LR \approx \frac{\Pr(E|H_{1a})}{\Pr(E|H_{aa})} \tag{8a}$$

and

$$LR \approx \frac{\Pr(E|H_{2a})}{\Pr(E|H_{aa})} \tag{8b}$$

Use of Eq.s 8a and 8b is prevalent. Their inclusion in the DNA commission [18] document was motivated by concern that the set of propositions H_{12} and H_{aa} might be used leading to:

$$LR \approx \frac{\Pr(E|H_{12})}{\Pr(E|H_{aa})} \tag{8c}$$

Use of Eq. 8c, if unjustified, may have some seriously adverse effects. A strong major aligned with, say, P_1, will 'carry' P_2 to an unreasonably high *LR* if P_2 aligns even approximately with the minor. It is also possible to have a high *LR* using 8a and 8b but a 0 *LR* using 8c.

Suggestion 2: We suggest here that Eq. 8c should only be used when the background information strongly suggests that the donors are either both or neither of P_1 and P_2. This proposition should be set based on the case information and before comparing the profiles.

In practice, if P_1 and P_2 do explain the profile well[7], then usually Eq.s 8a and 8b produce smaller *LR*s than 7a and 7b, thus if multiple propositions need to be considered results will be less discriminating.

If using Eq.s 8a and 8b, then we recommend a check of $LR \approx \frac{\Pr(E|H_{12})}{\Pr(E|H_{aa})}$ (Eq. 8c) to ensure that P_1 and P_2 do explain the profile well together.

We briefly consider when, if at all, it might be reasonable to use Eq. 8c. One reasonable suggestion is that that P_1 and P_2 are the two victims of a crime. The transfer is alleged to be to the accused. Since it is unlikely that the defense would accept that the DNA is from one of the victims but not the other, propositions used for Eq. 8c would be the most meaningful. In such a case we can infer that $\Pr(E|H_{1a})$ and $\Pr(E|H_{2a})$ are low compared with $\Pr(E|H_{12})$

However, Eq.s 8a and 8b do have a higher adventitious match rate. In many cases they are a pragmatic solution so that the scientist may decide to report them while indicating that the 2 persons explain the mixture. We would however not report the number of 8c, as research has shown that laypersons have difficulties in combining probabilities [39]. We also see difficulties when reporting conflicting results (i.e., the mixture cannot be explained by both persons, but that both 8a and 8b support prosecution's view). But, for very complex mixtures and multiple POI they may be the only practical solution.

Suggestion 3: An alternate suggestion that we have received is to give the results of 7a, 7b, 8a, 8b, and 8c.

Again we leave the reader to form an opinion between the simplicity of suggestion 2 and the candor of suggestion 3, keeping in mind that propositions should be exhaustive in the context of the case and be based on case information. One must not choose the propositions based on the value of the results (i.e., chose the smallest or largest *LR*)[8] .

3.5. The interaction of sub-source and activity level considerations

A very valuable insight was provided in the late 90 s by a group of scientists at the now defunct UK Forensic Science Service [5,23,40] who organised propositions into a hierarchy. In modern DNA usage this hierarchy has five levels but for this discussion we only need to consider two of these:

1 Sub-source level propositions consider the source of the DNA, and

[7] A difficult situation arises when it is not so clear whether a combination of individuals explain the profile well. The treatment of proposition setting for complex scenarios is discussed in [38].

[8] Having different values for the same DNA comparison reminds us of a situation where the same object would have different prices. In our university restaurant, menus have different prices depending on whether you are a student, staff or an extern. It is fine to say, I am a student so I pay the lowest price. But, you cannot say, this is the smallest price, I will take the proposition that I am a student. So, the facts determine the value and not the reverse!

Table 1
A list of the allelic peaks in the stain from the hat and the genotype of POI C.

Locus	Stain from the hat				POI C	
D3S1358	14	15	16		14	15
vWA	15	16	17		16	16
FGA	19.2	23	24	25	19.2	23
D8S1179	12	14	15		14	15
D21S11	28	29	30	32.2	30	30
D5S818	8	11	12	13	13	13
D13S317	9	11	12		9	11

electropherogram can be explained as a two-person mixture if the victim but not the consensual partner is assumed.

The two-person solution excludes POI reference 3A, the brother. The three-person solution includes him. Both solutions exclude the non-contributor POI reference 3B.

Given these case circumstances should we expect a three-person mixture of the victim V, the consensual partner CP and the offender? Is there sufficient belief that DNA from CP should be present to use V and CP in the conditioning and hence force the three-person solution? We think there is from what is known on observation of sperm in the vagina

Table 2
A summary of the profile for NIST MIX13 case 3. This was amplified using Identifiler™ Plus and run on an ABI 3130 CE instrument with an AT of 50 rfu. Also provided is the genotype of the victim which may be assumed to be present in this mixture.

Locus	Allele	Height	Victim	Locus	Allele	Height	Victim	Locus	Allele	Height	Victim
	12	659	1		11	925	1		6	202	
D8S1179	14	521		D13S317	12	1375		TPOX	8	309	
	15	669	1		13	367	1		9	788	1
	28	234			8	120			11	714	1
D21S11	30.2	83			9	1254	1		12	550	1
	31.2	1351	2	D16S539	10	498		D18S51	13	850	1
	35	249			11	55			16	226	
	9	61			12	905	1		10	351	
D7S820	10	1121	2		16	237		D5S818	11	747	1
	11	135		D2S1338	17	88			12	996	1
	10	606	1		19	113			20	616	1
CSF1PO	11	513	1		20	1363	2	FGA	23	95	
	12	226			13	130			26	656	1
	13	126		D19S433	14	1974	2		27	206	
D3S1358	14	2373	2		14.2	84					
	18	355			14	83					
	7	390		vWA	15	1790	2				
TH01	8	333			17	324					
	9.3	1717	2		21	316					

Table 3
Manual interpretation comments of NIST MIX13 case 3.

Locus	Comment
D13S317	Alleles 11 (925 rfu) and 13 (367 rfu) cannot pair without overlap with another contributor, allele 12 (1375 rfu) looks far too big to be the minor (the victim appears to be the major)
D2S1338	Imbalance between the alleles 16 (237 rfu) and 17 (88 rfu)
FGA	Imbalance between the alleles 23 (95 rfu) and 27 (206 rfu)

2 Activity level propositions consider the activity that deposited the DNA.

It is not surprising from a forensic point of view, that case information (and the alleged activities) affect the development of sub-source level propositions and that there is a risk when considering sub-source level propositions without consideration of the context (in particular the activities). We examine an example that outlines the challenge; NIST MIX 13 case 3 [41,42].

3.5.1. NIST MIX 13 case 3

The National Institute of Standards and Technology, NIST, created this three-person mixture from a vaginal swab collected from a female (complainant, V), and a pair of real brothers, brother #1 (consensual partner, CP) and brother #2 (POI, reference 3A) in a 7:2:1 ratio[9] . A non-contributor was provided as a POI reference (reference 3B). The agreed facts are that the victim and consensual partner had sex12 hours prior to the alleged assault. The time between the alleged assault and sampling, which can be crucial, was not provided in the scenario. The [43].

This example necessitates activity level considerations about B in order to inform sub-source level proposition setting. Specifically, we see that w_3 is certainly non-zero and plausibly three is the most probable NoC.

We return here to the matter we deferred from section 3.4. That was to discuss the presence of H_a in the conditioning in the term $\Pr(N = 3|H_a)$. In most of the probability terms in this paper there is the background information, I, in the conditioning. We have suppressed it for simplicity but we reintroduce it here. The term is therefore, $\Pr(N = 3|H_a, I)$.

3.5.2. NIST MIX 13 case 3 without background information

In the section above we discussed the observation that the background information supports an expectation of a three person mixture. In this section we rework the analysis as if there was no task relevant case information except the expectation that the victim's DNA was on her own intimate sample.

In Tables 1,2 we give a summary of the profile information in this case.

When we first blindly[10] assigned the NoC for this case we assumed the victim and the consensual partner. That blind analysis is, therefore, no use for this section. Returning to this example we are no longer blind. In Table 3 we give some comments on our analysis if this mixture is assigned as NoC = 2.

We feel that the three loci discussed in Table 2 may be enough to underpin a subjective assignment of NoC = 3. Using NoC = 2 POI A is falsely excluded.

[9] STRmix™ assessed this as 69:28:3.

[10] We were blind to the correct answer but knew the reference genotypes and case circumstances.

Table A1
Arbitrary values for probability of the evidence, prior and posterior probabilities for three different propositions.

H_i	Likelihood $Pr(E\|H_i,I)$	Prior $Pr(H_i,I)$	Posterior $Pr(H_i\|E,I)$
H_1	2w	x	$2x/2x+y+101z$
H_2	w	y	$y/2x+y+101z$
H_3	101w	z	$101z/2x+y+101z$

However, let us imagine that there is no background information indicating NoC = 3 and the initial assignment is NoC = 2. This is not fanciful since 11 participants in the NIST 13 exercise excluded POI A. This lets us introduce a situation encountered occasionally in casework where a POI is excluded when assuming $N = n$, but there is a strong representation of their alleles in the evidence electropherogram (epg), so that if the profile was analysed as originating from $N = n+1$ an $LR > 1$ would result.

Simply adjusting the assumption of the number of contributors so that $N = n+1$ is rightly viewed with strong aversion.

Yet we do not know for certain that $N = n$. It is certainly possible that $N = n+1$. If we limit ourselves to two possibilities, then consider S&Cs Eq. 5 from Box 1 above:

$$BF = LR_n w_n + LR_{n+1} w_{n+1}$$

In the above discussion $LR_n = 0$ and $LR_{n+1} > 1$. We assume that the analyst assigned $N = n$ for good reason and hence w_n is high, say 0.95 and w_{n+1} is low say 0.05. We can see that this avoids the unpleasant aspects of simply adjusting the assumption of the number of contributors, and downweights LR_{n+1} in a reasonable way.

STRmix v2.6 and higher allows a range of NoCs to be examined. For NIST 13 case 3 this gives $LR_2 = 0$, $LR_3 = 2.12 \times 10^6$, and $LR_{2\text{ or }3} = 2.04 \times 10^6$ (for NoC = 2, 3, and 2 or 3 respectively). Noting that:

$LR_{2\text{ or }3} = Pr(N = 2|H_a, E_c)\, LR_2 + Pr(N = 3|H_a, E_c)\, LR_3$, where $Pr(N = 2|H_a, E_c) + Pr(N = 3|H_a, E_c) = 1$ this implies that STRmix assigns[11] $Pr(N = 3|H_a, E_c) = 0.96$ and $Pr(N = 2|H_a, E_c) = 0.04$.

This example does show that using exhaustive propositions, in this case considering NoC = 2 or 3, allows a sensible treatment even when multiple possibilities exist. The weights, $Pr(N = 3|H_a) = 0.96$ and $Pr(N = 2|H_a) = 0.04$ are difficult to obtain numerically by subjective examination.

4. Conclusions

In the strict mathematical sense, if propositions used for assessing the evidence are not exhaustive in the context of the case, then there is a theoretical risk that an *LR* greater than one may be associated with a proposition in the numerator that actually has - after consideration of the evidence - a lower posterior probability when considering all meaningful propositions.

We consider a number of common situations and present solutions that enable to have an acceptable coverage of the propositions to be considered.

Considering relatedness, the limited analysis reported here suggests the effect of an omission of consideration of relatedness is dependent strongly on the prior that a relative is a donor.

When considering whether a contributor, say a victim or the habitual wearer of clothing, should be assumed under both *propositions*, it is likely that non-exhaustive propositions will eventuate. However, there is very little risk of a misleading interpretation if some guidelines are applied. We suggest that a contributor should be assumed to be present under both *propositions* if there is a reasonable prior probability of their DNA being present and their inclusion increases both $Pr(E|H_p)$ and $Pr(E|H_a)$. This is not finding based, but a simplification of the BF formula by discounting very small probabilities. We suggest this approach even when there is a non-zero prior probability that the assumed donor's DNA is be present, but we suggest that there is no requirement for it to be as strongly associated with the possible assumed donor as has historically been the case. For example, we do not require that the sample is an intimate sample, or from the clothing of the habitual wearer, simply that the assumed donor's presence is reasonable.

When considering two POI who collectively explain a crime profile well we suggest the use of Eq.s 7a and 7b. These equations "look" as if they represent an assumption that the other POI is present but actually develop from an approximation where the other POI is considered either present or not. The use of Eq.s 8a and 8b, while not ideal, is acceptable as long as both POI are a good fit to the profile separately and together. We suggest that the value of the *LR* with Eq. 8c is not reported except unless one can infer from the case information that either both or none of the POI contributed to the DNA mixture.

For evaluation purposes (i.e., in court) scientists should strive to give one *LR* for each person whose DNA presence is an issue.

The *LR* reported should be based on propositions that are meaningful in the case and not on the *LR* value.

When considering the number of contributors, the propositions will always be strictly non-exhaustive. However, S&C have shown that the overall BF is the weighted average of *LR*s with the same NoC under both propositions. The weights involve both an assessment of the crime profile and the plausibility of this NoC given the background information.

Acknowledgements

This work was supported in part by grant 201-DN-BX-K451 from the US National Institute of Justice, United States of America. Points of view in this document are those of the authors and do not necessarily represent the official position or policies of their organizations. We gratefully acknowledge comments by Johanna Veth and Stuart Cooper which greatly improved this document.

Appendix A

A1.1 The risk with propositions that do not exhaust the sample space

Consider three propositions H_1, H_2, H_3 which are mutually exclusive and collectively exhaustive. Let the evidence be, *E*, the relevant background evidence, *I*. Let the values for the probability of the evidence given the proposition and the prior probability of the proposition be those in Table A1. *w* is an arbitrarily chosen constant, and *x*, *y*, and *z* are equally arbitrary probabilities. The posterior probability of the proposition given the evidence is then also given in Table A1 using the general form of Bayes' theorem:

[11] This assumes that $Pr(N = 2) = Pr(N = 3)$ before consideration of the DNA evidence

$$\Pr(H_i \Big| E, I) = \frac{\Pr(E|H_i, I)p(H_i|I)}{\Pr(E|I)} = \frac{\Pr(E|H_i, I)p(H_i|I)}{\sum_{j=1}^{3} \Pr(E|H_j, I)p(H_j|I)}$$

In much of this discussion we suppress the term I but occasionally reintroduce it when it is necessary for our discussion.

There is no need to know w and it is not necessary, and indeed unlikely, that $104w = 1$. $x + y + z = 1$.

It can be easily shown that H_2 is less probable, and H_3 is equal to or more probable after observation of the evidence for any given values of x, y, and z. The behaviour of H_1 however depends on the value for y and z. If x, y and z are equal (i.e. $x = y = z = 1/3$), then H_1 is about 17 times less probable after observation of the evidence.

The above analysis is well known. Let us now consider that proposition H_3 has a non-zero prior probability but is not considered in the analysis.

If the propositions are H_1 and H_2 then $LR = \frac{\Pr(E|H_1)}{\Pr(E|H_2)} = 2$.

However, this analysis is incomplete and potentially unsafe if $z \neq 0$.

This example can be used to emphasise the risk inherent in using non-exhaustive propositions (i.e. making an inappropriate assumption that assigns $z = 0$)[12] . Let us imagine that the prosecution allege H_1 in Table A1 and consider the alternative as H_2. The reported LR may be 2 suggesting support for H_1. However, H_1 is less probable after consideration of the evidence for many values of x, y, and z. For example, if $x = y = z = 1/3$, then the probability has dropped from 1/3 to 2/104. This significant drop has happened because there is a proposition chosen by neither the prosecution nor the defense that has a significant posterior probability. A similar example is given by Biedermann et al. [2].

A2.1 Compound propositions (see also Good [8] pg 68)

Consider two exclusive and exhaustive propositions H_1 and H_2. $\Pr(H_1) + \Pr(H_2) = 1$. Next consider a different set of exclusive and exhaustive propositions P_1, P_2, and P_3. $\Pr(P_1) + \Pr(P_2) + \Pr(P_3) = 1$. For example

H1. Mr Smith is the source of DNA,

H2. Mr Smith is not the source of DNA,

and

Ha1. The donor is Caucasian,

Ha2. The donor is Hispanic,

Ha3. The donor is African American.

Assume, incorrectly, that H_{a1}, H_{a2}, and H_{a3} are exclusive and exhaustive.

Since H_1 and H_2 are exclusive and exhaustive we can write $LR = \frac{\Pr(E|H_1)}{\Pr(E|H_2)}$ and know that we do not run the risk, outlined above, of missing an important proposition. Further assume that, in order to compute $\Pr(E|H_1)$ and $\Pr(E|H_2)$ we need to know H_{a1}, H_{a2}, and H_{a3}. Then

$$BF = \frac{\sum_i \Pr(E|H_1, H_a i)\Pr(H_a i|H_1)}{\sum_i \Pr(E|H_2, H_a i)\Pr(H_a i|H_2)} \tag{9}$$

We observe that $BF \leq \frac{\sum_i \Pr(E|H_1, H_a i)\Pr(H_a i|H_1)}{\max_i \Pr(E|H_2, H_a i)}$

Without any specific case information on the ethnicity of the donor, a sensible choice of prior probabilities for ethnicity may be based on population proportions of each ethnicity in the local region. If case information is provided that gives information on the ethnicity of the donor (remember that there is a hidden 'I' in the conditioning) then this may cause an assignment of 0 to all but one prior probability on ethnicity and the sums in the LR contract to a single term.

A2.2 The interaction of propositions and assumptions

Current development of propositions often occurs within a framework of circumstances and these circumstances often underpin a number of assumptions. The assumptions may be explicit or implicit, and may range from very well supported to questionable. The use of the word assumption has the likelihood of attracting attention in court. We believe this stems from a view by the legal community of assumptions as generally speculative. Of course assumptions may be very well supported. For example "I assume that the sun will rise again tomorrow" or "one of my children will ask for money in the next year."

In this section we reformulate the idea of an assumption as an event. We will therefore have two events A and $\overline{A}$. Event A will be that a certain assumption is true. $\overline{A}$ is the complement of this.

Following S&C and assuming $\Pr(A|H_p) = \Pr(A|H_a)$:

$$LR = \frac{\Pr(E|H_1, A)}{\Pr(E|H_2, A)} \Pr(A \Big| E, H_2) + \frac{\Pr(E \Big| H_1, \overline{A})}{\Pr(E \Big| H_2, \overline{A})} \Pr(\overline{A} \Big| E, H_2) \tag{10}$$

If $\Pr(A|E, H_2)$ is high relative to $\Pr(\overline{A} \Big| E, H_2)$ then $LR \approx \frac{\Pr(E|H_1, A)}{\Pr(E|H_2, A)}$.

[12] This also outlines why it is important to underline in our statements that if the information changes, so will our evaluation.

Formulating assumptions as events allows a formal focus on when such assumptions may be acceptable.

A3.3 Assumed contributors

Where V is poorly supported by the profile $\frac{\Pr(E|H_{\overline{V}},H_d,I)}{\Pr(E|H_V,H_d,I)} \approx 1$ and the weights for Eq. 6a, repeated here, $LR = LR_{H_V}\underbrace{\Pr(H_V|E,H_d,I)}_{weight} + LR_{H_{\overline{V}}}\underbrace{\Pr(H_{\overline{V}}|E,H_d,I)}_{weight}$ are dominated by the $\frac{\Pr(H_{\overline{V}}|H_d,I)}{\Pr(H_V|H_d,I)}$ which are the prior odds on V being not a donor vs being a donor.

Where V is excluded as a donor to the profile then $\Pr(H_{PV}) = \Pr(H_{Va}) = 0$. In such a case a high *LR* for H_{Pa} relative to H_{aa} still supports the presence of DNA from P on the tissue but the strong association with the "cleaned up after" proposition is reduced and the presence of one other person's DNA will lead to valid questions.

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