# Likelihood ratio and evidence strength

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## 1 Likelihood ratio as a measure of evidence strength

The fallacies we considered earlier in the book — such as the base rate fallacy, the prosecutor's fallacy, and the defense attorney's fallacy—show how the posterior probability can be misjudged, upwards or downwards, even if the subject gets the likelihoods right. These examples illustrate that the assessment of the posterior probability of a hypothesis given the evidence depends also on the prior probability of the hypothesis. The correctness of such an assessment therefore requires that the priors are chosen sensibly (or that a range of sensible priors is considered) and appropriately put together with the likelihoods involved. Quite crucially, the posterior probability given a piece of evidence should not be confused with the probative value of a given piece of evidence itself with respect to the hypothesis in question.

add crossref

Consider the following examples. Suppose the prior probability of a given hypothesis $H$ is low, say $\mathsf{P}(H) = .001$, but taking evidence $E$ into account brings this probability up to .35, that is, $\mathsf{P}(H|E) = .35$. This is a dramatic upward shift. Even though the posterior probability of $H$ given $E$ is not very high, $E$ strongly favors $H$. Conversely, suppose the prior probability of $H$ is extremely high, say $\mathsf{P}(H) = .999$, but taking evidence $E$ into account brings this probability down to .75, that is, $\mathsf{P}(H|E) = .75$. This is a dramatic downward shift. Even though the posterior probability of $H$ given $E$ is still quite high, $E$ speaks against $H$. Now, let's turn to the blood stain example from **??**.The posterior probability given the match turned out to be an unimpressive .17 (assuming a prior probability of .1). This does not mean that the incriminating evidence was weak. while, the match was not not strong enough to make it very likely that the defendant was the source of the traces, the posterior probability is seventeen times larger than the prior. Similarly, in the Collins case, the posterior probability jumped from the $1/6\times10^6$ prior to .7 after taking the match into account. Still not enough for a conviction but a remarkable increase nonetheless. These examples illustrate how measuring the strength of evidence in terms of the posterior it leads to seems inappropriate.

Fix crossref.

So how do we capture the strength of an item of evidence so that the measure does not depend on the priors and reflects the impact the evidence has on the posterior probability? One measure of the strength of evidence is the likelihood of the evidence compared to the prior of the evidence (this measure is sometimes called the *Bayesian factor*:

$$\mathsf{BF}(E,H) = \frac{\mathsf{P}(E|H)}{\mathsf{P}(E)}. \tag{1}$$

The Bayesian factor is one probabilistic measure of the extent to which the evidence, regardless of the absolute posterior probability, supports or does not support the hypothesis. It is an intuitively plausible measure of evidential strength. Note that by Bayes' theorem

$$\mathsf{P}(H|E) = \mathsf{BF}(H,E) \times \mathsf{P}(H)$$

and so the Bayesian factor is greater than one if and only if the posterior probability $\mathsf{P}(H|E)$ is higher than the prior probability $\mathsf{P}(H)$, $\mathsf{P}(H) < \mathsf{P}(H|E)$. So $E$ *positively* supports $H$ whenever the Bayesian factor is greater than one. The greater the Bayesian factor (for values above one), the greater the upward shift from prior to posterior probability, the more strongly $E$ positively supports $H$. In line with the motivating examples, the posterior probability of $H$ given $E$ could still be low even if the Bayesian factor is significantly above one.

Conversely, again by Bayes' theorem, the probability of $H$ given $E$ is lower than the probability of $H$, $\mathsf{P}(H) > \mathsf{P}(H|E)$ just in casethe Bayesian factor is less than one. So $E$ *negatively* supports $H$

whenever the Bayesian factor is less than one. In general, the smaller the Bayesian factor (for values below one), the greater the downward shift from prior to posterior probability, the more strongly $E$ negatively supports $H$. If $\mathsf{P}(H) = \mathsf{P}(H|E)$, the evidence has no impact on the probability of $H$.

One reason to think the Bayesian Factor is a useful measure of evidential strength is that it appropriately deviates from 1, its point of neutrality. But let us pause a moment to think about the denominator in (1). It can be calculated following the law of total probability:

$$\mathsf{P}(E) = \mathsf{P}(E|H)\mathsf{P}(H) + \mathsf{P}(E|\neg H)\mathsf{P}(\neg H). \tag{2}$$

The catch-all alternative hypothesis $\neg H$ can be replaced by a more fine-grained set of alternatives, say $H_1, H_2, \ldots H_k$, provided $H$ and these alternatives are exclusive and cover the entire space of possibilities (that is, they form a partition). The law of total probability would then read:

$$\mathsf{P}(E) = \mathsf{P}(E|H)\mathsf{P}(H) + \sum_{i=1}^{k} \mathsf{P}(E|H_i)\mathsf{P}(H_i). \tag{3}$$

For simplicity, let's stick to (2) for now, and use it to rewrite (1):

$$\mathsf{BF}(E,H) = \frac{\mathsf{P}(E|H)}{\mathsf{P}(E|H)\mathsf{P}(H) + \mathsf{P}(E|\neg H)\mathsf{P}(\neg H)}. \tag{4}$$

What should be clear from this formulation is that the Bayesian factor fails to satisfy one of our requirements: that the measure of evidential strength should not depend on the prior probability of the hypothesis. Indeed, suppose $\mathsf{P}(E|H) = 1$ and $\mathsf{P}(E|\neg H) = .1$. If $\mathsf{P}(H) = .1$, $\mathsf{P}(E)$, the denominator, is .19 and so the Bayesian Factor is approximately 5.26. If, however, $\mathsf{P}(H) = .2$, the denominator is .28 and the Bayesian Factor is approximately 3.57.

M: check the calculations, we'll hide them later.

```
EifH <- 1
EifNH <- .1
H <- .1

E <- EifH * H + EifNH * (1-H)
E
```

```
## [1] 0.19
```

```
BF <- EifH/E
BF
```

```
## [1] 5.263158
```

```
EifH <- 1
EifNH <- .1
H2 <- .2

E2 <- EifH * H2 + EifNH * (1-H2)
E2
```

```
## [1] 0.28
```

```
BF2 <- EifH/E2
BF2
```

```
## [1] 3.571429
```

A related reason to worry about the denominator of (4) is that assessing the strength of evidence using the Bayesian factor seems to impose too great a cognitive burden on an agent, since it would require estimating $\mathsf{P}(E)$. This rarely can be done directly, and estimation using the denominator of (4) or (3) (in a more complex case) not only requires that the agent sifts through the entire space of possibilities, but also that the agent uses as weights a sensible selection of priors for the hypotheses involved.

For the above reasons, a measure that puts no such cognitive requirements on an agent would be preferrable. Clearly, we should not simply use $\mathsf{P}(E|H)$. For one thing, in most interesting cases this conditional probability will be very close to one and will not allow us to distinguish between the strenghts of pieces of evidence that we should distinguish. For instance, what is the probability that the blood types match if the accussed is the source? Well, one, pretty much. What is the probability that the DNA profiles match if the accussed is the source? Again, one. But obviously a DNA profile match is not on par with a blood type match insofar as strength of evidence is involved. Consider an example

by Robertson, Vignaux, & Berger (2016). In a child abuse case, the prosecutor offers evidence that a couple's child rocks and that only 3% of non-abused children rock, $\mathsf{P}(\text{child rocks}|\text{no abuse}) = .3$. If it is unlikely that a non-abused child would rock, the fact that this child rocks might seem strong evidence of abuse. But this reading of the 3% figure is mistaken. It could well be that 3% of abused children rock, $\mathsf{P}(\text{child rocks}|\text{abuse}) = .3$.ˆ[Note that the two probabilities need not add up to 1. Similarly, learning only that $\mathsf{P}(\text{child rocks}|\text{abuse}) = .3$ does not provide full information needed for evidence evaluation, and one also needs information about $\mathsf{P}(\text{child rocks}|\text{no abuse}) = .3$. In our particular case, given that rocking is equally unlikely under either hypothesis, rocking cannot count as evidence of abuse, and any of the low conditional probabilities involved alone does not allow us to notice this. Thus, in order to avoid exaggerations of the evidence both conditional probabilities need to be involved in the evidence strength evaluation (Royall, 1997, Triggs & Buckleton (2004), ENFSI (2015)).

One issue that these considerations illustrate is that what matters is also the probability of the evidence if the hypothesis is false. If the accussed is not the source, the probability of a blood match if the accussed is not the source, while small, is much higher than the probability of a DNA profile match, and this seems to explain why the latter piece of evidence is stronger. So, both the probability of the evidence given the hypothesis, and the probability of evidence given an alternative hypothesis should be somehow factored into a useful measure of evidential strength.

One straightforward way to implement this is to use the **likelihood ratio**, a comparative measure of whether evidence $E$ supports a hypothesis $H$ more than a competing hypothesis $H'$, in symbols:

$$\mathsf{LR}(E,H,H') = \frac{\mathsf{P}(E|H)}{\mathsf{P}(E|H')}. \tag{5}$$

If the evidence supports $H$ more than $H'$, the ratio would be above one, and if the evidence supports $H'$ more than $H$, the ratio would be below one. So, as with the Bayesian factor, support levels correspond to deviations from one. The greater the likelihood ratio (for values above one), the stronger the evidence in favor of $H$ as contrasted with $H'$. The smaller the likelihood ratio (for values below one), the stronger the evidence in favor of the competing hypothesis $H'$ as contrasted with $H$. The likelihood ratio is a simpler and more workable measure than the Bayesian factor, since it does not require one to think about the probability of the evidence in general, namely $\mathsf{P}(()E)$. This apparent simplicity, however, can often give rise to errors in the assessment of the evidence, especially if the two hypotheses are not chosen carefully. As it will transpire, the choice of the hypotheses that are conditioned upon is crucial. In the most straightforward case, $H'$ is simply the negation of $H$. In many practical contexts such a simplistic set-up, however, is not viable. We will discuss these issues in detail in this chapter later on.

The relationship between likelihood ratio $\mathsf{P}(E|H)/\mathsf{P}(E|H')$ and posterior odds $\mathsf{P}(H|E)/\mathsf{P}(H'|E)$ is apparent in the odds version of Bayes' theorem:

$$\frac{\mathsf{P}(H|E)}{\mathsf{P}(H'|E)} = \frac{\mathsf{P}(E|H)}{\mathsf{P}(E|H')} \times \frac{\mathsf{P}(H)}{\mathsf{P}(H')}. \tag{6}$$

If the likelihood ratio is greater (lower) than one, the posterior odds will be greater (lower) than the prior odds of $H$. The likelihood ratio, then, is a measure of the upward or downward impact of the evidence on the prior odds of two hypotheses $H$ and $H'$.

Experts sometimes testify by offering the likelihood ratio as a measure of the strength of the evidence. An expert, for instance, may testify that the blood-staining on the jacket of the defendant is ten times more likely to be seen if the wearer of the jacket hit the victim (prosecutor's hypothesis) rather than if he did not (defense's hypothesis) (C. Aitken, Roberts, & Jackson, 2010, p. 38). Experts are typically advised not to comment on the posterior odds given the evidence. As this formulation of the Bayes's theorem makes clear, an assessment of the posterior odds will require a judgment about the prior odds, and the latter lies beyond the competence of an expert. A prominent forensic scientist recommends that experts 'not trespass on the province of the jury by commenting directly on the accused's guilt or innocence, ... and should generally confine their testimony to presenting the likelihood of their evidence under competing propositions' (C. Aitken et al., 2010, p. 42).

The idea that both conditional probabilities involved in likelihood ratio should be used in evidence strength evaluation applies generally to all forms of evidence, inclusive of DNA evidence, although it might not always make a practical difference. For suppose an expert testifies that the crime traces

genetically match the defendant and that the **random match probability** is extremely low, say 1 in 100 million. Is the match strong evidence that the defendant is the source of the traces? The random match probability—often interpreted as the probability that someone who is not the source would coincidentally match, $\mathsf{P}(\mathsf{match}|\neg\mathsf{source})$—is a common measure of the strength of a DNA match. The lower this probability, the more strongly incriminating the match. This is sensible because a low random match probability suggests it is unlikely two people could share the same DNA profile. This is, however, also in agreement with the use of likelihood ratio in evidence evaluation, because $\mathsf{P}(\mathsf{match}|\mathsf{source})$ is practically equal to one, so neglecting in in evidence strength reporting does not make any real difference. That $\mathsf{P}(\mathsf{match}|\neg\mathsf{source})$ is low is in such contexts enough to ensure that the likelihood ratio is significantly above one. For practical purposes, then, a suitably low random match probability does capture the idea that the evidence is strongly incriminating evidence. The conceptual point still stands, though. If $\mathsf{P}(\mathsf{match}|\mathsf{source})$ was significantly different from one, reporting only $\mathsf{P}(\mathsf{match}|\neg\mathsf{source})$ would be misleading.

To better appreciate the theoretical virtues of likelihood ratios, it is instructive to look at a case study, DNA evidence, focusing in particular on so-called cold-hit matches.

## 2 The cold-hit confusion

DNA evidence is one of the most widely used forms of quantitative evidence currently in use. It may be used to corroborate other evidence in a case, or as the primary incriminating evidence. For example, suppose different investigative leads point to an individual, Mark Smith, as the perpetrator. The investigators also find several traces at the crime scene left by the perpetrator. Laboratory analyses show that the genetic profile associated with the traces matches Smith. In this scenario, the DNA match corroborates the other evidence against Smith. In contrast, suppose the police has no other investigative lead except the traces left at the crime scene. Hoping to find the perpetrator, the police run the genetic profile associated with the traces through a database of profiles and find a match, a so-called **cold-hit**.

Cold-hit DNA matches have been the focus of intense discussion in recent years. Since in cold-hit cases there is little or no other evidence, cold-hit matches are often the primary item of evidence against the defendant. Some believe that this circumstance weakens the case. Others disagree. This debate illustrates how probability theory—in particular, the likelihood ratio—can help to assess the strength of evidence at trial. What follows examines some of the main arguments.

For concreteness, consider the California rape and murder case of Diana Sylvester. In 2008, many years after the crime, John Puckett was identified as a unique 9-loci match through a database search of 338,000 profiles. He was the only individual in the database who matched the traces collected from the victim Diana Sylvester in 1972. According to an expert witness, the particular pattern of alleles present in the material was (conservatively) expected to occur randomly among Caucasian men with a frequency of 1 in 1.1 million. This is the **random match probability** (**RMP**). The random match probability—often interpreted as the probability that someone who is not the source would coincidentally match, $\mathsf{P}(\mathsf{match}|\neg\mathsf{source})$—is a common measure of the strength of a DNA match.

The lower the RMP, the more strongly incriminating the match. The rationale here is that a low random match probability suggests that it is unlikely that two people would share the same DNA profile. In line with what we already discussed, strictly speaking, a match is strong evidence that the defendant is the source only if the probability that the person who left the traces (the 'source') would match is significantly greater than RMP. In practice, when it comes to DNA evidence, it is often assumed that $\mathsf{P}(()\mathsf{match}|\mathsf{source})$ is very high.

Although clearly 1 in 1.1 million should not be confused with the probability of Puckett's innocence (see **??** for details),the small figure indicates it is very unlikely that a random person unrelated to the crime would match. The match is therefore strong evidence of Puckett's guilt. Assuming that the probability of a match if Puckett indeed was the source was (practically) 1, the likelihood ratio is simply $1.1 \times 10^6$.

check crossref later

M: check calculation

```
eIfh <- 1
eIfnH <- (1/1.1e6)
lr <- eIfh/eIfnH
lr
```

```
## [1] 1100000
```

During the pretrial hearing, however, Bicka Barlow, the DNA expert for the defense, pointed out that this was a cold-hit case. No evidence tied Puckett to the crime other than the cold-hit match, Puckett's previous rape convictions and the fact that he was in the area at the time of the murder. In order to correctly assess the probative value of the cold-hit match, Barlow argued, the random match probability should be multiplied by the size of the database. The result of such a multiplication is called the **database match probability** (**DMP**). In Puckett's case, the multiplication of $1/1.1\times10^6$ by $338,000$ resulted in a database match probability of approximately .3.

M: check calculation

```
dmp <- 1/1.1e6 * 338e3
1/dmp
```

```
## [1] 3.254438
```

which is a less impressive number than the original RMP (the likelihood ratio for the DMP is approximately 3.25). According to this calculation, it was no longer very unlikely that an unrelated person from the database would match, and so the cold-hit DNA match was no longer strong evidence of guilt. At least, this was Barlow's argument.

Barlow followed a 1996 report by the National Research Council called NRC II (National Research Council, 1996), preceded by an earlier report on DNA evidence called NRC I (National Research Council, 1992). NRC II recommended precisely what Balrow did: that in cold-hit cases RMP should be multiplied by the database size, yielding DMP. The underlying idea was that the larger the size of the dataset, the higher the database match probability, and the lower the strength of the match. This correction was meant to guard against the heightened risk of mistaken matches for the innocent people in the database. To see however, if this was sound advice, we need to look under the hood.

The NRC formed the Committee on DNA Technology in Forensic Science, which issued its first report in 1992. In that report they advised against using cold hit results as evidence, and insisted that only the frequencies related to loci not used in the original identification should be presented at trial, that is, that the evidence used to identify the suspect should not be used as evidence against the suspect.

This recommendation has been criticized by many because it underestimates the value of cold-hit matches. The problem was, given a certain amount of evidence the expert, prior to suspect identification, had to make a somewhat subjective decision of how to divide the evidence into two items: one to be used only in the suspect identification, and one to be used only in the trial itself as evidence against the suspect. This overly limited the utility of the evidence and introduced an unnecessary element of subjectivity.[1]

NRC II withdrew the earlier recommendation. However, the contrast between low RMP and the frequency of DNA matches in actual database searchers was indeed stark. For instance, the Arizona Department of Public Safety searched for matching profiles in a database comprising 65,000 individuals. The search found 122 pairs of people whose DNA partially matched at 9 out of 13 loci; 20 pairs people who matched at 10 loci; and one pair of people who matches at 12 loci. So it is not that unlikely to find two people in a database who share the same genetic profiles (examples of fairly high counts of DNA matches in database searches was actually used by Barlow in the Diana Sylvester case). In light of this contrast, NRC II recommended the use of DMP rather than RMP. NRC II recommended also that in cold-hit cases the likelihood ratio $R$ associated with the DNA match should be divided by $d+1$. Their first recommendation was about a correction of the random match probability, and this second recommendation is about the likelihood ratio.

One argument by NRC employed an analogy involving coin tosses. If you toss several different coins at once and all show heads on the first attempt, this seems strong evidence that the coins are biased. If, however, you repeat this experiment sufficiently many times, it is almost certain that at some point all coins will land heads. This outcome should not count as evidence that the coins are biased. According to NRC II, repeating the coin toss experiment multiple times is analogous to trying to find a match by searching through a database of profiles. As the size of the database increases, so does the number of attempts at finding a match, and it is more likely that someone in the database who had nothing to do with the crime would match.

Another argument provided by NRC II compared a database trawl to multiple hypothesis testing, and

[1] It also opened the gate for multiple testing with various evidence division points, and multiple testing leads to its own statistical problems. But let's put this issue aside.

multiple hypothesis testing should be avoided if possible in light of classical statistical methods.

Third, NRC II was concerned with the fact that in cold-hit cases the identification of a particular defendant occurs after testing several individuals. This concern has to do with the data-dependency of one's hypothesis: seemingly, the hypothesis 'at least one person in a given database matches the DNA profile in question' changes its content with the choice of the database.

We will start with the coin analogy. It is in fact unclear how the analogy with coin tossing translates to cold-hit cases. Searching a larger database no doubt increases the probability of finding a match at some point, but is the increase as fast as the Arizona Department of Public Safety examples and the coin analogy suggest?

Quite crucially, following (Donnelly & Friedman, 1999) we need to pay attention to what hypotheses are tested, what probabilistic methods the context recommends, and what exactly the evidence we obtained is. For instance, one hypothesis of interest is what we will call a *general match hypothesis*:

(General match hypothesis) At least one of the profiles in the database of size $n$ matches the crime sample.

The general match hypothesis is what NRC II seems to have been concerned with. If for each data point RMP= $\gamma$ were held constant, and if random matches with different data points $\mathsf{match}_1, \mathsf{match}_2, \ldots, \mathsf{match}_\mathsf{d}$ excluded each other, the probability of there being at least one random match would be the same as the probability of their disjunction and could be calculated by the additivity axiom:

$$\begin{aligned}\mathsf{P}(\text{at least one match}) &= \mathsf{P}(\mathsf{match}_1 \vee \mathsf{match}_2 \vee \cdots \vee \mathsf{match}_\mathsf{d}) \\ &= \sum_i^d \mathsf{P}(\mathsf{match}_\mathsf{i}) = \gamma \times d\end{aligned}$$

This calculation would result in the outcome recommended by NRC II, if the value of the evidence were to be a function of the probability of (General match hypothesis).

The first question is, whether a directly additive calculation should be applied to database matches. First, notice that in applications DMP does not really behave like probability. Take a simple example. Suppose a given profile frequency is .1 and you search for this particular profile in a database of size 10. Does the probability of a match equal $.1 \times 10 = 1$? The answer is clearly negative. Multiplication by database size would make sense if we thought of it as addition of individual match probabilities, provided matches exclude each other and so are not independent. Here is a coin analogy. Suppose I toss a die, and my database contains $n =$ three *different* numbers: $1, 2$ and 3. Then, for each element of the database, the probability $p$ of each particular match is $1/6$, and the probability of *at least one* match is $1/6 + 1/6 + 1/6 = 1/6 \times 3 = n \times p = 1/2$. We could use addition in such a situation because each match excludes the other matches, a condition that is not satisfied in the database scenario.

Another reason why DMP is problematic can be seen by taking a limiting case. Suppose everyone in the world is recorded in the database. In this case, a unique cold-hit match would be extremely strong evidence of guilt, since everybody except for one matching individual would be excluded as a suspect. But if RMP were to be multiplied by the size of the database, the probative value of the match as measured by DMP should be extremely low. This is highly counter-intuitive.

Even without a world database, the NRC II proposal remains problematic, since it sets up a way for the defendant to arbitrarily weaken the weight of cold-hit DNA matches. It is enough to make more tests against more profiles in more databases. Even if all the additional profiles are excluded (intuitively, pointing even more clearly to the defendant as the perpetrator), the NRC II recommendation would require to devalue the cold-hit match even further. This, again, is highly counter-intuitive.

Perhaps a somewhat more sensible answer is obtained by assuming the independence of $\mathsf{nomatch}$ for the members of the database and deploying a solution similar to the one used in the birthday problem. Here, the idea would be—assuming matches for different data points are independent and have constant RMP — to calculate:

$$\begin{aligned}\mathsf{P}(\mathsf{match}) &= 1 - \mathsf{P}(\mathsf{nomatch}) \\ &= 1 - (1-\gamma)^d\end{aligned}$$

where $\gamma$ is RMP, and $d$ is the database size. This would be in line with using the binomial distribution to calculate the probability of no match:

$$\begin{aligned}\mathsf{dbinom}(0,d,\gamma) &= \binom{n}{0}\gamma^0(1-\gamma)^{d-0} \\ &= 1\times 1\times(1-\gamma)^d\end{aligned}$$

Now, assuming indeed that $\gamma$ is constant and that matches between data points are independent, the dependence of the probability of at least one match on the database size can be pictured as follows:

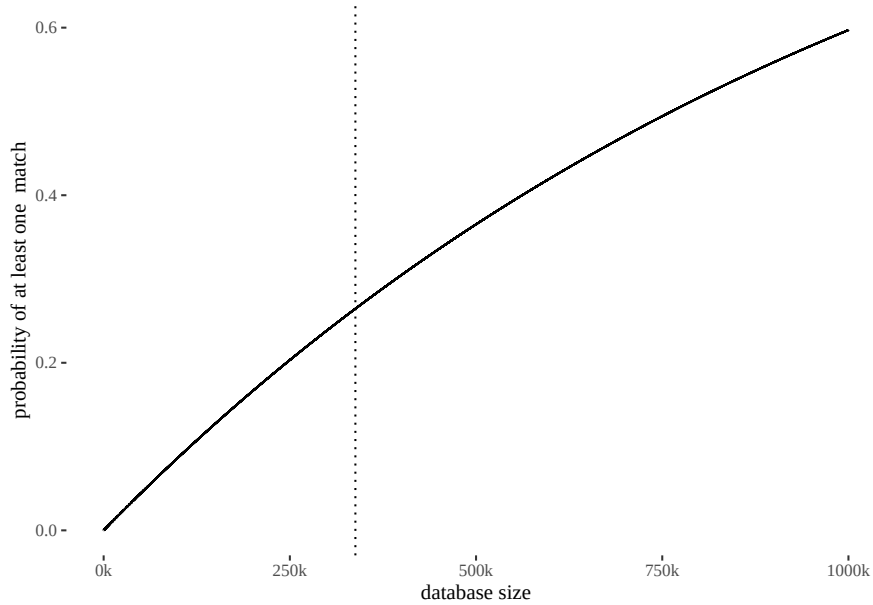


Figure 1: Binomial model of the database search problem. The probability of at least one match depending on the database size, assuming independence and constant RMP used in the Puckett case. The actual database size marked with a vertical line.

If we use the RMP and database size used in the Puckett case, the calculated probability of at least one match is 0.2645501. Not exactly the DMP postulated by the defendant, but pretty close. The question is, should this number be the probability used to evaluate the evidential impact of the cold hit?

One problem is, whether the independence assumption is satisfied in the database search problem is unclear. After all, if you are informed about the match frequencies in the database, and they teach you that since two arbitrary database points quite likely do not match, if the sample matches one of them, it is less likely to match the other one. And the independence assumption is not benign. We will illustrate it with a somewhat distand, but a very striking example, coming from . Suppose you consider whether your effort of casting a vote in the upcoming election is worth it in a context where there are 500k other voters. One of the probabilities you might be interested in is the probability that your vote would make a difference. If we apply the binomial model to the problem, the probability that a candidate will receive exactly $k$ votes if $n$ people vote is supposed to be $\binom{n}{k}p^k(1-p)^{(n-k)}$, where votes of the population members are supposed to be indepent and estimated to have the same probability $p$ of being for the candidate. For instance, if 500k people vote and $p = 0.5$, the probability that the candidate will receive exactly 250k votes is 0.0011284, which is around $1/886$ and much higher than $1/n$. This fairly high chance made some claim that the chance that your voice is decisive if the chances are equal is fairly high in such circumstances. However, note that if $p = .505$, the probability that the candidate will receive exactly 250k votes is $1.5651281 \times 10^{-14}$, which is less than one in a trillion. This lead some to claim that outside of the very specific circumstances, decision-theoretic arguments for the rationality of voting are hopeless. Barnett, however, points out that such a sensitivty to success probability simply makes the binomial model inappropriate for the voting context, observing that its calculations also disagree with empirical estimates which are not too far from $1/n$. This sensitivity arises, because within the binomial model the more trials (voters) there are, the more tightly the results will tend to cluster around the

think about independence again once the section is done

cite Barnett

Brennan and Lomasky, Democracy and Decision, as well as Brennan, The Ethics of Voting, 19.

Barnett

Andrew Gelman, Gary King, and W. John Boscardin, "Estimating the Probability of Events that Have Never Occurred: When Is Your Vote Decisive?" Journal

probablity of success. To observe how unrealistic that is, keep $p = .505$ and ask yourself how probable it is that the voting result will be between 50.4% and 50.6%. Sure, this outcome might be quite likely, but the binomial certainly overstimates it at 0.8427212. Another unrealistic estimate obtained by the binomial model is the estimate of the probability of an upset (that the leading candidate will lose). With $p = .505$ this is $\mathsf{pbinom}(249999, 500000, .505)$, which turns out to be extremely and unrealistically low: $7.5994495 \times 10^{-13}$. Coming back to our original problem, the binomial estimate of the probability of a match is also quite sensitive to RMP, as illustrated in the following figure:

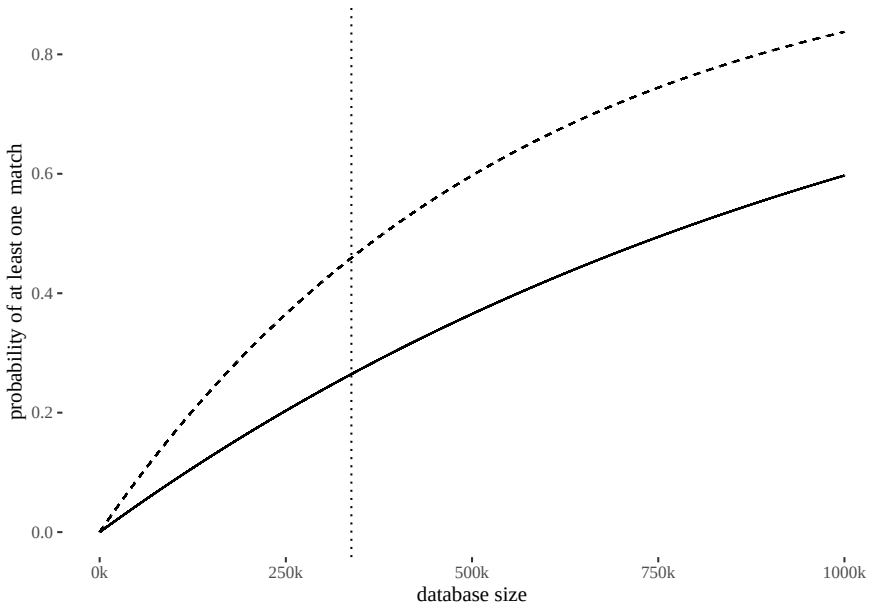


Figure 2: Binomial model of the database search problem. The probability of at least one match depending on the database size, assuming independence and constant RMP used in the Puckett case as compared with the binomial estimate for p=2/1.1e6 (dashed line). The actual database size marked with a vertical line.

The bottom line of the above example is that if we have reasons to think the independence assumption is not satisfied, the binomial model is not appropriate. So, it seems, it is not appropriate for the database match problem either.

The binomial model, however, is useful, in its simplicity, for illustrating an important distinction whose conflation underlies one of the involved arguments. You might have been surprised learning that while the expert testified that RMP on 9 loci for Puckett was 1 in 1.1 million, the Arizona Department of Public Safety found 122 9-loci matches among 65,000 individuals. After all, 122/65000 is 0.0018769, which is much higher than the reported RMP.

Crucially, notice that there is a difference between having a sample and looking for a match in a database of size $n$ and taking a database of size $n$ and checking all pairs that occur within it for a match. In the former case, you are making $n$ comparisons. In the latter case, the number of comparisons is $\binom{n}{2}$, which is much higher. If $n = 65000$, there are $2.1124675 \times 10^9$ pairs to compare, so while the binomial estimate of the probability of at least one match for $n$ comparisons (the former case) is 0.057379, it is approximately 1 for $\binom{n}{2}$ comparisons. For the impact it has on the Arizona Department of Public Safety statistics, consider the binomial estimate of the probability of at least 122 matches among all pairs as a function of the database size, even for relatively low database size range (up to 50000):

From this perspective, it is no surprise there were so many matching pairs among all the pairs from the database. Unfortunatelly, this frequency does not estimate the probability of at least one match in the set-up we are actually interested in. After all, in a cold-hit senario we do have a sample outside of the database and make $n$ comparisons, instead of testing all possible pairs from the database for a match.

Before we move on, note how the Arizona statistics constitute empirical evidence against the adequacy of the binomial model. While the binomial estimate probability of at least 122 matches with an external sample for $n = 6500$ is pretty much 0, the binomial estimate of the probability that multiple pair comparison will result in at least $n$ matches as a function of $n$ looks as follows:

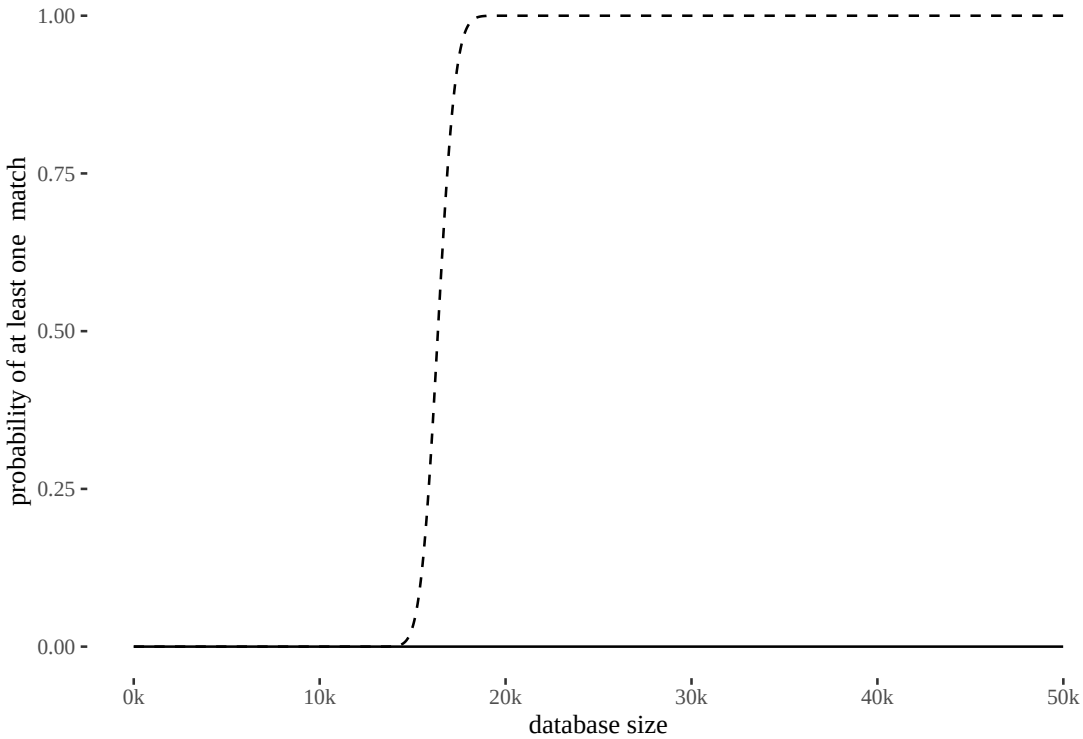


Figure 3: Binomial model of the database search problem. The probability of at least 122 matches depending on the database size for n comparisons, and for all possible pairs among n datapoints (dashed), assuming p=1/1.1e6.

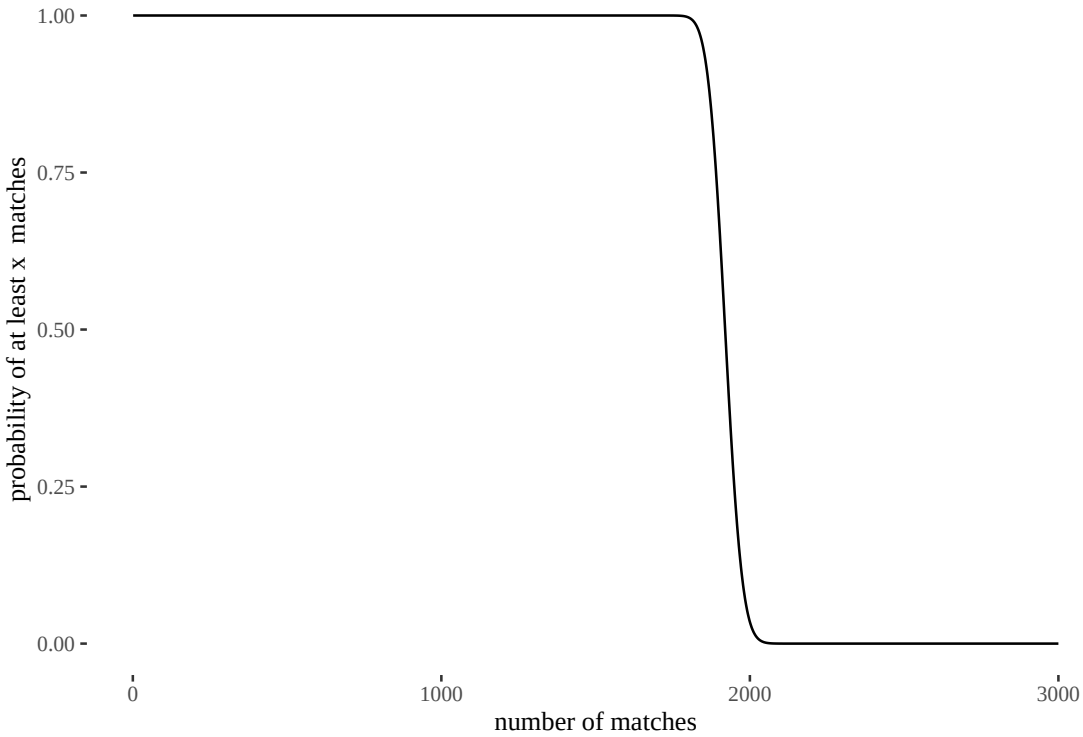


Figure 4: The probability of at least n matches in pairwise comparison within a database of size 65000, assuming p=1/1.1e6.

Moreover, we can take a look at the most likely number of matches if we test $\binom{6500}{2}$ pairs, as estimated by the binomial model. Here it is with an 89% highest density inverval:

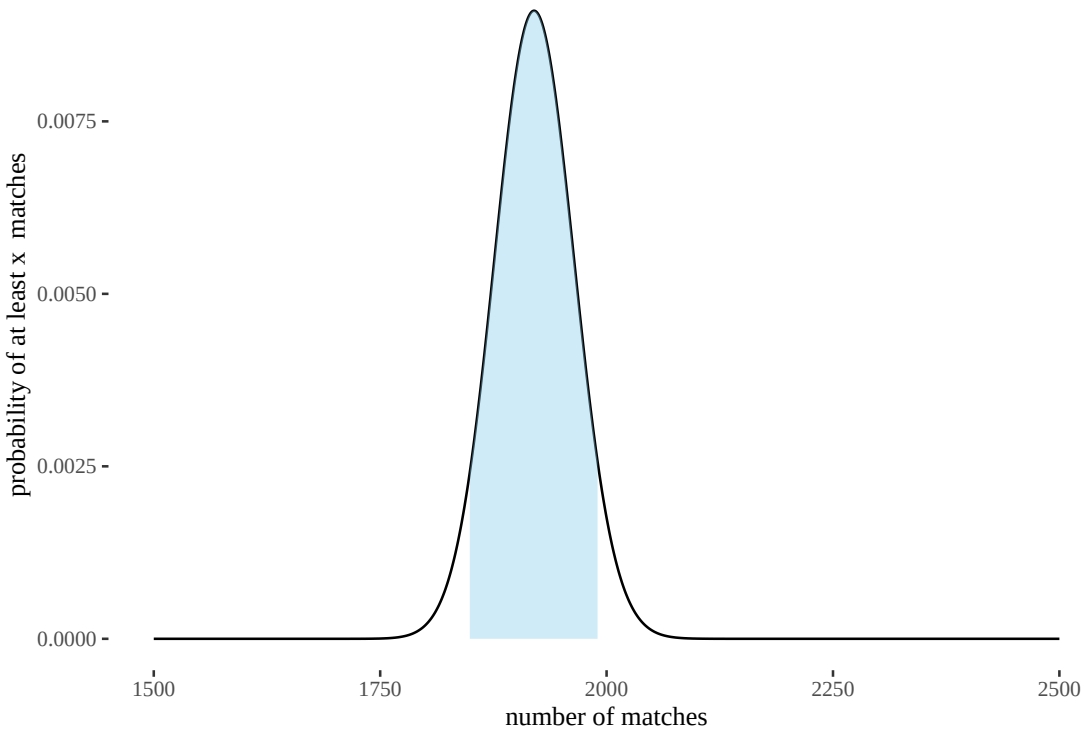


Figure 5: Binomial probability density of n matches in pairwise comparison within a database of size 65000, assuming p=1/1.1e6, with 89% highest density interval = (1849,1990) shaded in blue.

So, if the expert's estimate is adequate and the binomial model is adequate, we indeed should be surprised by the presence of 122 matches. But this is because this number is suprisingly low: instead we should expect a much higher number, around 2000 of them!

Now that we used the imperfect binomial model to clear up at least one confusion, let us put it aside, and focus on an even deeper problem with using the probability of (General match hypothesis) instead of RMP in evidence evaluation. Probabilistic epistemology recommends that once we obtain new evidence, our new degrees of belief should be the probabilities obtained by conditionalizing on this evidence. Crucially, we should update on the total evidence we obtained rather than only on a part of it. Here the question is, does (General match hypothesis) exhaust what we have learned from our database match?

To get us started thinking about this question, consider a coin analogy which Donnelly & Friedman (1999, p. 950) found more adequate than the one proposed by the NRC. Imagine a biased coin whose physical appearance is indistinguishable from the fair coins in a piggy bank. The biased coin is the perpetrator and the piggy bank is the database containing innocent people. After the biased coin is thrown into the bank with the other coins, someone picks out a handful of coins at random and flips each of them twenty times. Each coin lands heads approximately ten times—except for one coin, which lands heads on all twenty flips. The fact that other coins seem unbiased makes the claim that this one is biased better supported.

Coming back to DNA matches, think about the following scenario: first, you identified the suspect by some means other than a database trawl. Then, it turned out his DNA profile matches the crime scene stain. Fine, here it seems uncontroversial that this constitutes strong further incriminating evidence. Now, imagine a further database search for a database not containing this suspect finds no matches. Would you think that this information supports the guilt hypothesis? If your answer is yes, then you do have the intuition that the lack of matches with other people (whose profiles, in this particular case, happen to be in a database) strengthens the evidence.

The key lesson here (and in the complete-world database scenario we already discussed) is that we not only learned that there was a match in the database of size $n$, but also that in $n-1$ cases there was no match, and this information also has evidential value. In line with this, contrary to NRC II, **?** argues

that if potential suspects in the database are excluded as sources, this should increase, not decrease, the probability that the defendant who matches the crime traces is the source. A cold-hit match, then, is stronger and not weaker evidence of guilty than ordinary DNA matches.

Before moving on to a better model that captures how this could be, let us look at another argument put forward by NRC, an analogy to multiple hypothesis testing. NRC claimed that there is an analogy between searching for a match in a database and multiple hypothesis testing, which is a dubious research practice. In classical hypothesis testing, if the probability of type I error in a single test of a hypothesis is 5%, the probability of at least one type I error will increase by testing the same hypothesis multiple times. In analogy—the argument goes— we need to correct for the increased risk of type I error, and just as the Bonferroni correction requires that the $p$-value threshold be divided by the number of tests, NRC II requires that the estimated probability of a random match should be multiplied by the number of comparisons.

This analogy with multiple testing, however, is misplaced. As **?** points out, multiple testing consists in testing the *same* hypothesis multiple times against new evidence. In cold-hit cases, no such multiple testing is involved. Rather, multiple hypotheses—each concerning a different individual in the database—are tested only once and then excluded if the test is negative. From this perspective, for each $1 < i < n$, the following hypothesis is tested:

(Particular match hypothesis) Profile $i$ in the database matches the crime sample.

and the hypothesis that the defendant is the source was one of the many hypotheses subject to testing. The cold-hit match supports that hypothesis and rules out multiple other hypotheses.

## 3 Likelihood ratio and cold-hit DNA matches

To find a better parth towards the resolution of the database search problem, let us look at another recommendation of NRC II, that in cold-hit cases the likelihood ratio $R$ associated with the DNA match should be divided by $n+1$, where $n$ is the database size. This recommendation, too, is questionable. Suppose $R$ is not too high, say because the identified profile is common since the crime scene DNA is degraded and only a few markers could be used. Then, $n+1$ can be greater than $R$, so $R/(n+1) < 1$. The match would then be exculpatory, a very counter-intuitive result.

The recommendation seems mistaken on more general grounds that we already brought up as well. If the defendant on trial is the source, the probability that he would match is practically 1. If he is not, the probability that he would still match equals the random match probability. Neither of these probabilities change because other suspects have been tested in the database search. In fact, if potential suspects are excluded as potential sources, this should increase, not decrease, the probability that the defendant who matches the crime traces is the source.

A more principled way to assess cold-hit matches based on the likelihood ratio, exists. The proposal draws from the literature on the so-called **island problem**, studied by (Dawid, 1994; Dawid & Mortera, 1996; Eggleston, 1978). Let the prosecutor's hypothesis $H_p$ be The suspect is the source of the crime traces and the defense's hypothesis $H_d$ be The suspect is not the source of the crime traces. Let $E$ be the DNA match between the crime stain and the suspect (included in the database) and $D$ the information that none of the $n-1$ profiles in the database matches the crime stain. The likelihood ratio associated with $E$ and $D$ should be (Balding & Donnelly, 1996; Taroni, Biedermann, Bozza, Garbolino, & Aitken, 2014):

$$V = \frac{\mathsf{P}(E,D|H_p)}{\mathsf{P}(E,D|H_d)}.$$

Since $\mathsf{P}(A \wedge B) = \mathsf{P}(A|B)\mathsf{P}(B)$, for any statement $A$ and $B$, this ratio can be rewritten as:

$$V = \frac{\mathsf{P}(E|H_p,D)}{\mathsf{P}(E|H_d,D)} \times \frac{\mathsf{P}(D|H_p)}{\mathsf{P}(D|H_d)}. \tag{7}$$

The first ratio in (7) is roughly $1/\gamma$, where $\gamma$ is the random match probability. The second ratio— call it the **database search ratio**—requires some more work. Consider first the denominator $\mathsf{P}(D|H_d)$. If the

suspect is not the source ($H_d$), someone else is, either someone who is in the database or someone not in the database. Let $S$ stand for The source is someone in the database. By the law of total probability,

$$\mathsf{P}(D|H_d) = \mathsf{P}(D|S,H_d)\mathsf{P}(S|H_d) + \mathsf{P}(D|\neg S,H_d)\mathsf{P}(\neg S|H_d). \tag{8}$$

If the source is someone in the database ($S$) and the suspect is not the source ($H_d$), it is very unlikely that no one in the database would match ($D$), so $\mathsf{P}(D|S,H_d) \approx 0$. The equality in (8) therefore simplifies to:

$$\mathsf{P}(D|H_d) = \mathsf{P}(D|\neg S,H_d)\mathsf{P}(\neg S|H_d),$$

The database search ratio would therefore be:

$$\frac{\mathsf{P}(D|H_p)}{\mathsf{P}(D|H_d)} = \frac{\mathsf{P}(D|H_p)}{\mathsf{P}(D|\neg S,H_d)\mathsf{P}(\neg S|H_d)}.$$

Note that $\mathsf{P}(D|H_p) = \mathsf{P}(D|\neg S,H_d)$ because whether the suspect is the source ($H_p$) or not ($H_d$) does not affect whether there is a match in a database that does not contain the source ($\neg S$). Let the probability that no person in the database other than the suspect would match ($D$), assuming the suspect was in fact the source, be $\psi_{n-1}$. Notice that $\mathsf{P}(D|\neg S,H_d)$ is the probability that no one other than the suspect matches in the database that does not contain the real source, if the suspect is not the source. So this conditional probability can also be estimated as $\psi_{n-1}$.[2] Let $\mathsf{P}(S|H_d) = \varphi$. The database search ratio then would reduce to

$$\frac{\mathsf{P}(D|H_p)}{\mathsf{P}(D|H_d)} = \frac{1}{1-\varphi}.$$

As the database gets larger, $\varphi$ increases and the database search ratio also increases. This ratio equals one only if no one in the database could be the source, that is, $\varphi = 0$.

Since the likelihood ratio $V$ of the cold-hit match results by multiplying the likelihood ratio of the DNA match and the database search ratio, $V$ will always be greater than the mere likelihood ratio of the match (except for the unrealistic case in which $\varphi = 0$) . Thus, a cold-hit DNA match should count as stronger evidence than a DNA match of a previously identified suspect.

Dawid & Mortera (1996) study different database search strategies and consider the possibility that information about the match is itself uncertain, but the general point remains. Under reasonable assumptions, ignoring the database search would give a conservative assessment of the evidentiary strength of the cold-hit match. Donnelly & Friedman (1999), with slightly different assumptions, derived the formula $R \times [1 + md/N]$, where $R = 1/\gamma$, $d$ is the database size, $N$ the number of people in population not in database, and $m$ is an optional multiplier reflecting how much more likely persons in the database are though to be the source when compared to the rest of the population. The expression cannot be less than $\gamma$. If no other profile has been tested, $d = 0$ and LR is simply the regular DNA match LR. If $N$ is zero, that is, everyone in population is in the database, the result is infinitely large.

This proposal is able to accommodate different competing intuitions. First, consider the intuition that as the size of the database grows, it is more likely that someone in the database would match. This intuition is captured by the fact that $\varphi$ increases proportionally to the size of the database even though this increase does not imply that the evidential value of the cold-hit match should decrease.

Second, there is intuitive resistance to basing a conviction on a cold-hit match, although this resistance is less strong in case of an ordinary match (more on this later in Section **??**).This preference for convictions based on an ordinary DNA match seems in tension with the claim that a cold-hit match is stronger evidence of guilt than an ordinary match. There is a way to make sense of this, though. The key is to keep in mind that the evidentiary strength—measured by the likelihood ratio—should not be confused with the posterior probability of guilt given the evidence. Even if a cold-hit match is stronger evidence of guilty, this fact does not imply that the posterior probability of the defendant's guilt should be higher.

Fix crossref later

[2] If the prior probability that the perpetrator is in the database was high, the calculations would need to be different. But normally, this prior is not too high.

If the cold-hit match is the only evidence of guilt, the posterior probability of guilt may well be lower compared to cases in which other evidence, such as investigative leads, supplements the DNA match. This lower posterior probability would justify the intuitive resistance towards convictions in cold-hit cases, despite the fact that a cold-hit match alone is stronger evidence than a dna match obtained otherwise and taken on its own.

## 4 Likelihood ratio and hypothesis choice

As the preceding discussion shows, the likelihood ratio is a fruitful conceptual framework for assessing the strength of the evidence, even in complex cases such as cold-hits.

One major difficulty, however, is the choice of the hypotheses $H$ and $H'$ that should be compared. Generally speaking, the hypotheses should in some sense compete with one another—say, in a criminal trial, $H$ is the hypothesis put forward by the prosecution and $H'$ is the hypothesis put forward by the defense. Presumably, the two hypotheses should be something that the two parties disagree about. But this minimal constraint offers too little guidance and leaves open the possibility for manipulations and misinterpretations of the evidence. What follows outlines some of the main arguments in the literature on this topic.

Consider a stylized DNA evidence case. Suppose the prosecutor puts forward the hypothesis that the suspect left the traces found at the crime scene. This hypothesis is well supported by laboratory analyses showing that the defendant genetically matches the traces. The defense, however, responds by putting forward the following *ad hoc* hypothesis: 'The crime stain was left by some unknown person who happened to have the same genotype as the suspect.' Since the probability of the DNA match given either hypothesis is 1, the likelihood ratio equals 1 (Evett, Jackson, & Lambert, 2000). The problem generalizes. For any item of evidence and any given prosecutor's hypothesis $H$, there is an *ad hoc* competing hypothesis $H^*$ such that $\mathsf{P}((\,)E|H)/\mathsf{P}((\,)E|H^*) = 1$. Hypothesis $H^*$ is simply a just-so hypothesis, one that is selected only because it explains the evidence just as well as hypothesis $H$ does (Mayo, 2018). If no further constraints are placed on the choice of the competing hypotheses—it would seem—no evidence could ever incriminate a defendant. This is unsettling.

But this conclusion need not be so damning in practice. Judges and jurors, however, will often recognize *ad hoc* hypotheses for what they are—artificial theories that should not be taken seriously. Perhaps, the reasonable expectations of the participants in a trial will suffice to constrain the choice of hypotheses in just the right way. At the same time, real cases can be quite complex, and it is not always obvious whether a certain choice of competing hypotheses, which are not obviously *ad hoc*, is legitimate or not.

Here is an example that illustrates how even when the competing hypotheses are not obviously *ad hoc*, the absence of a clear rationale for their choice may create confusions in the assessment of the evidence. In R. v. Barry George (2007 EWCA Crim 2722). Barry George was accused of murdering TV celebrity Jill Dando. A key piece of evidence at play was:

$E$ A single particle of firearm residue (FDR) was found one year later in George's coat pocket and it matched the residue from the crime scene. This was the key incriminating evidence against him.

The defense argued that, since it was only one particle, there must have been contamination. The experts for the prosecution, however, testified that it was not unusual that a single particle would be found on the person who fired the gun. George was convicted, and his first appeal was unsuccessful.

After the first appeal, Dr. Evett from the Forensic Science Service worried that the evidence had not been properly assessed at trial. The jurors were presented with the conditional probability $\mathsf{P}(\mathsf{residue}|H_d)$ of finding the firearm residue in George's coat given the defense hypothesis $H_d$ that George *did not* fire the gun. This probability was estimated to be quite low, indicating that the evidence spoke against the defense's hypothesis. But the jurors were not presented with the conditional probability $\mathsf{P}(\mathsf{residue}|H_p)$ of finding the same evidence given the prosecutor's hypothesis $H_p$ that George *did* fire the gun that shot Dando.

$H_d$ BG did not fire the gun that shot JD.

$H_p$ BG fired the gun that shot JD.

An expert witness, Mr. Keeley, was asked to provide both conditional probabilities and estimated them to be $1/100$, which indicated that the firearm residue had no probative value.

After new guidelines for reporting low level FDR in 2006, the FSS re-assessed the evidence and

concluded that it was irrelevant. George appealed again in 2007, and relying on Keely's estimates, won the appeal.

At first, this case seems a good illustration of how likelihood ratios help to correctly asses the value of the evidence presented at trial. But this reading of the case would be overly optimistic. In fact, a close study of the trial transcript shows that Keeley's choice of hypotheses lacked coherence and the likelihood ratio based on them was therefore meaningless (Fenton, Berger, Lagnado, Neil, & Hsu, 2014).

For instance, Mr Keeley is reported to have said:

> It was necessary to balance the likelihood that the particle came from a gun fired by the appellant and the likelihood that it came from some other source. Both were unlikely but both were possible.

On one occasion, Keeley compared the hypothesis that the particle found in George's pocket came from a gun fired by George himself, and the alternative hypothesis that the particle came from another source. At the same time, Keeley said that the prior probabilities of both hypotheses should be low, which is mathematically impossible if they were exhaustive and exclusive.

On another occasion, Keeley took the prosecutor's hypothesis to be The particle found in George's pocket came from the gun that killed Dando. But the conditional probability of the evidence given this hypothesis should not be low. It should actually be one.

Note that here the persecution hypothesis is taken to be: the particle found in BG's pocket came from the gun that killed JD. Now, $E$ is a logical consequence of this hypothesis, and so this likelihood should be 1. In some other contexts, Keeley took the defense hypothesis to be The particle on George's pocket was inserted by contamination, but again, the conditional probability of the evidence given this hypothesis should be one. The most charitable reading of the trial transcript suggests that the expert had in mind the hypotheses George was the man who shot Dando and The integrity of George's coat was corrupted. But these hypotheses are neither exhaustive nor exclusive, and Keeley gave no clear criterion for why these hypotheses should be compared in the likelihood ratio (see Fenton et al., 2014 for further details).

#### 4.0.0.1 Exclusive and exhaustive?

The confusion in the Barry George case is attributable to the absence of clear rules for choosing the hypotheses in the likelihood ratio. One such rule could be: pick competing hypotheses that are exclusive (they cannot be both true) and exhaustive (they cannot be both false). In this way, the parties would not be able to pick *ad hoc* hypotheses and skew the assessment of the evidence in their own favor. % %One of the competing hypotheses in the likelihood ratio does not have to be the negation of the other. In some cases, they could both be false (hence, not exhaustive), and in some they could both be true (hence, not mutually exclusive).

% Besides blocking partisan interpretations of the evidence, there are other principled reasons to follow the exclusive-and-exhaustive rule, specifically, the fact that when the hypotheses are not exclusive or exhaustive, the likelihood ratio delivers counterintuitive results. %andconfusions in the assessment of the strength of the evidence often arise. % %but it is not obvious that the hypotheses selected should always be exclusive and exhaustive. %Whether this rule would be a good guiding principle, however, is not clear-cut. %

If two competing hypotheses %$H_p$ and $H_d$ are not mutually exclusive, it is possible that %the evidence supports them to an equal extent %they both make the evidence equally likely (the likelihood ratio is one), and yet the posterior probabilities of the hypotheses given the evidence are higher than their prior probabilities. For instance, let $H_p$ stand for `The defendant is guilty' and $H_d$ for`The defendant was not at the crime scene'. Both hypotheses might be true. %Say the prior probability of both is 50%. Let $E$ stand for `Ten minutes before the crime took place the defendant---seen at a different location--- was overheard on the phone saying \emph{go ahead and kill him}.' %$E$ supports both $H_p$ and $H_d$, and It is conceivable that the likelihood ratio should equal one in this context, yet the posterior probabilities of each hypothesis, given $E$, should be higher than the prior probability. So, intuitively, the evidence should positively support each hypothesis, contrary to what the likelihood ratio would suggest. % Further, when the two competing hypotheses are not exhaustive, the likelihood ratio may once again clash with our intuitions. %The likelihood ratio

This was wrong. Fixed.

might then equal one even though the evidence lowers their posterior probability. For example, suppose Fred and Bill attempted to rob a man. The victim resisted, was struck on the head and died. Say $H_p$ stand forFred struck the fatal blow' and $H_d$ stand for Bill struck the fatal blow.' The hypotheses are not exhaustive. A missing hypothesis isThe man did not die from the blow.' Suppose $E$ is the information that the victim had a heart attack six months earlier. The likelihood ratio $\mathsf{P}(()E|H_p)/\mathsf{P}(()E|H_d)$ equals one since $\mathsf{P}(()E|H_p) = \mathsf{P}(()E|H_d)$. Yet $E$ reduces the probability of both $H_p$ and $H_d$. So, in this case, the evidence should negatively support each hypothesis, contrary to what the likelihood ratio suggests.

Despite these problems, however, always relying on exclusive and exhaustive hypotheses is not without complications either. For consider an expert who decides to formulate the defense hypothesis by negating the prosecution hypothesis, say, the defendant did not hit the victim in the head.' This choice of defense hypothesis can be unhelpful in assessing the evidence because the required probabilities are hard to estimate. For instance, what is the probability that the suspect would carry such and such blood stain if he did not hit the victim in the head? This depends on whether he was present at the scene, what he was doing at the time and many other circumstances. %Similarly, in a rape case, it is hard to estimate the probability of the matching evidence if the suspect did not have the intercourse with the victim. Instead, what is considered is the hypothesis that someone else, unrelated to the suspect, had intercourse with the victim. As \citet{evett2000MoreHierarchyPropositions} point out, the choice of a particular hypothesis to be used in the evaluation of the strength of the evidence %of, say, the lack of semen in a rape case, will depend on contextual factors. %Sometimes it will be \emph{intercourse did not take place}, sometimes it will be \emph{the intercourse took place, but the complainant used a vagina douche}, or sometimes \emph{another sexual act took place}. More often than not, the hypotheses chosen will not be mutually exclusive. % Comparing exclusive and exhaustive hypotheses can also be unhelpful for jurors or judges making a decision at trial. %is not required for the application of Bayes' Theorem, is not the usual practice, and could lead to a In a paternity case, for example, % in which the results of DNA profiling are to be evaluated, the expert should not compare the hypothesesThe accused is the father of the child' and its negation, but rather, The accused is the father of the child' andThe father of the child is a man unrelated to the putative father' (**?**). The choice of the latter pair of competing hypotheses is preferable. Even though the relatives of the accused are potential fathers, considering such a far-fetched possibility would make the assessment of the evidence more difficult than needed %Similarly, for a given DNA mixture, strictly speaking for any $n$ there is a hypothesis that covers the suspect and $n$ other unkown sources, but for sufficiently large $n$ these are usually discarded as unrealistic. % %At the same time, if the defense hypothesis is too specific, *ad hoc* and entails the evidence, it won't be of much use. For example, take The crime stain was left by some unknown person who happened to have the same genotype as the suspect.' %The probability of a DNA match given this hypothesis would be 1. %But usually the probability of the DNA match given the prosecution's hypothesis, sayThe crime stain was left by the suspect,' is also 1. This would result in a rather uninformative likelihood ratio of 1 %For example, consider the prosecution hypothesis The probability of a match given this hypothesis is practically 1.% Another feature of such specific explanations is that it's hard to reasonably estimate their prior probability, and so hard to use them in arguments between opposing sides. (**?**).

#### 4.0.0.2 Variability

Any choice of competing hypotheses lies between two extremes. For one thing, exclusive and exhaustive hypotheses guard against arbitrary comparisons and ensure a more objective assessment of the evidence. The drawback is that exhaustive and exclusive hypothesis cover the entire space of

possibilities, and sifting through this space is cognitively unfeasible. So, in this respect, comparing more circumscribed hypotheses is preferable. The danger of doing so, however, is slipping into arbitrariness as likelihood ratios heavily depend on the hypotheses that are compared. The more latitude in the choice of the hypotheses, the more variable the likelihood ratio as a measure of evidentiary value. %It is hard not to view this variability as a sign of arbitrariness. %% R; this last sentence was too much

Here is a particularly troubling %example phenomenon. %Competing hypotheses can concern any factual dispute, from minute details such as whether the cloth used to suffocate the victim was red or blue, to ultimate questions such as whether the defendant stabbed the victim.

changed, because this wasn't really an example.

As it turns out, the likelihood ratio varies across hypotheses formulated at different levels of granularity: offense, activity and source level hypotheses (on this distinction, see earlier in **??**). It is even possible that, at the source level, the likelihood ratio favors one side, say the prosecution, but at the offence level, the likelihood ratio favors the other side, say the defense, even though the hypotheses at the two levels are quite similar. Further, a likelihood ratio that equals 1 when source level hypotheses are compared may tip in favor of one side or the other when offence level hypotheses are compared (**?**). This variability makes the likelihood ratio a seemingly arbitrary—and easily manipulable—measure of evidentiary value. This is not to say that it is unhelpful. Expert witnesses often rely on the likelihood ratio when they assess the probative value of many forms of evidence (**?**).

% The likelihood ratio can be misleading, but this risk is mitigated when its assessment is accompanied by a careful discussion of a number of issues, such as: which hypotheses are being compared; how they are formulated; their level of granularity (that is, source, activity and offense level); why the hypotheses are (or are not) exclusive and exhaustive; why other hypotheses are ruled out as unworthy of consideration.

%the choice of the hypotheses to be compared, their level, their being exclusive and exhaustive (or not), the formulation of the evidential statement, and the reasons not to use other hypotheses in the evidence evaluation.

%%M: Great, nice summary. I changed a few things here and there

Revised this paragraph a bit, take a look again.

% %

%It is unclear, however, how the analogy translates to cold-hit cases. Searching a larger database no doubt increases the probability of finding a match at some point. But judges and jurors should not be concerned with %the probability of the statement %The NRC II recommendation pertained to the probability of the statement %`At least one of the profiles in the database %of size $d$ would randomly match the crime sample.' %Call it the general match hypothesis. %This statement has probability $(d+1)\times p$, where $p$ is the random match probability and $d+1$ is the database size. \todo{Is this right? You have d+1. Why?} % %are interested in whether a particular defendant is the source of the crime traces. %They are concerned with the statement`The profile of the particular defendant on trial would randomly match the crime sample.'Call this the particular match hypothesis. %and the probability of at least one false positive. %So what is of interest is the probability of the particular, not the general match hypothesis. % This is in line with the general idea that one should update on total available evidence: the claim that the defendant's profile match entails but is not entailed by the claim that at least one of the database profiles match, and so it is the former and not the latter that the fact-finders should rely on. % %Rather, they should be concerned with %the probability of the statement 'The profile of the defendant on trial would randomly match the crime sample.' The probability of finding a match between the particular defendant and the crime sample does not increase because other people in the database are tested. %

%NRC II was concerned with the fact that in cold-hit cases the identification of a particular defendant occurs after testing several individuals. This concern has to do with the data-dependency of one's hypothesis. But, as **?** points out, the problem of data-dependency arises when the same hypothesis is tested multiple times against new evidence. In cold-hit cases, however, there is no multiple testing. %there is no multiple hypothesis testing involved here. %Rather that the hypothesis about the suspect being formulated after the test, %Rather, multiple hypotheses—each concerning a different individual in the database—are tested only once and are excluded by a negative match. %before the search multiple individual hypotheses about each of potential suspects in the database are formulated, and each of them is tested once during the search. %From this perspective, the hypothesis that the defendant is the source was one of the many hypotheses subject to testing. The cold-hit match supports that hypothesis and

rules out the others.

%Perhaps, there is a better analogy here %(**?**, p. 950). Imagine a coin that is known to be biased but whose physical appearance makes it indistinguishable from the fair coins in a piggy bank. The biased coin is the perpetrator and the %piggy bank is the database containing innocent people. %After the biased coin is thrown into the bank with the other coins, someone picks out a handful of coins at random and flips each of them twenty times. Each coin lands heads approximately ten times—except for one coin, which lands heads on all twenty flips. The fact that other coins seem unbiased makes the claim that this one is biased better supported since at least one coin in the bank must be biased.%

% %Contrary to NRC II, **?** argue that if potential suspects in the database are excluded as sources, this should increase, not decrease, the probability that the defendant who matches the crime traces is the source. A cold-hit match, then, is stronger and not weaker evidence of guilty than ordinary DNA matches.

% %This can be made clear by relying on the likelihood ratio as a measure of the evidential strength of the cold-hit DNA match. If the defendant on trial is the source, the probability that he would match is practically 1. If he is not, the probability that he would still match equals the random match probability. Neither of these probabilities change because other suspects have been tested in the database search. In fact, if potential suspects are excluded as potential sources, %this should increases, not decrease, the probability that the defendant who matches the crime traces is the source.[3] % %Since the focus should not be on the particular, not the general match hypothesis, the coin tossing analogy does not work. %In a DNA trawl you're not repeating an experiment to reject a general hypothesis. Rather, you consider a particular hypothesis (*the defendant is the source of the material*) and test once for *the defendant's profile matches the crime sample*, and once for each claim of type *person i in the database does not have a matching profile*.

%moved this bit to a footnote

%NRC II made another recommendation. They recommended that in cold-hit cases the likelihood ratio $R$ associated with the DNA match should be divided by $d+1$. Their first recommendation was about a correction of the random match probability (that is, to multiply it by the size of the database), and this second recommendation is about the likelihood ratio (that is, to divide it by $d+1$). This has counterintuitive consequences. Suppose $R$ is not too high, say because the identified profile is common since the crime scene DNA is degraded and only a few markers could be used. Then, $d+1$ can be greater than $R$, so $R/(d+1) < 1$. The match would be exculpatory, a very counter-intuitive result.

%Moreover, NRC II would entail that if the police pick a random person from the database, test their profile and it is a match (call this *lucky strike* )and don't test other members of the database, this evidence — if we follow NRC II — should be stronger than a unique hit in a systematic database trawl, which also does not seem too convincing. % %Interestingly, the frequentist argument focused on a different hypothesis than the likelihood one. The former assessed the probability that at least one profile in the database would match the crime sample by chance, the latter focused on the hypothesis that exactly one profile would match. %In the case of frequency, multiplication by $D+1$ results in a conservative and imprecise estimate, while in the case of likelihood, division by $D+1$ is supposed to give a precise calculation of the likelihood of a cold hit. %

% %emphasized that, in cold-hit cases, the likelihood ratio should taken into account that the suspect is identified only after the search not before. If this fact is not taken into account the likelihood ratio would be data dependent. % %who argued that the hypotheses proposed by the critics of NRC II are data dependent, because the suspect is identified only after the search (see Subsection **??** for further details). %

%Commented this out, perhaps, this is not needed

%(3 CT 669, 675; 5 CT 1093.)11

% How do we square the supposedly extremely low DNA profile frequency with the seemingly high match frequency in empirical studies on existing databases? The key difference is between the probability of a particular previously selected profile matching one in the database, and the probability of the database containing *some* match. % [MARCELLO'S COMMENTS: YES, YOU MADE THIS POINT EARLIER WHEN YOU CRITICIZED THE USE OF DMP, SO I DON'T THINK THIS SHOULD BE REPEATED HERE. MAYBE YOU CAN JUST CLARIFY WHAT YOU SAID EARLIER

[3] Of course, a classical statistician might refuse to rely on Bayesian reasoning, and rely on classical hypothesis testing instead. There are various good reasons not to do so, but we'll just point out that in such a case they simply have nothing to say about the posterior probability of the identity claim.

WHEN YOU DISTINGUISHED DMP FROM RMP?]

% Continuing with the die example, say I pick number one as my `suspect,'' and my database has $n=5$ with individual`profile frequency in the population" of $1/6$. On the assumption that the database is randomly drawn from the population (with replacement), the probability of one of the numbers in the database being 1 is $\approx 1-0.6=0.4$ (notice this time the database can contain repetitions and the sampling was random and so we can't use addition to calculate $\mathsf{P}(()$no match with 1)). % [MARCELLO'S COMMENT: I REALLY LOST YOU HERE. NOW YOU SEEM TO BE ADDRESSING A DIFFERENT PROBLEM THAN COLD-HIT MATCHES. ]

% In contrast, there are $6^5$ possible states of the database, and $6\times5\times4\times3\times2$ of them contain no repetitions, so $\mathsf{P}(()$no match) is $\approx 0.093$ and the probability of *a* matching pair being present in the database is $\approx 0.91$. Intuitively, the difference arises because now we're searching through $\binom{5}{2}=10$ different pairs looking for any of the 6 possible profile matches, instead of searching through 5 profiles looking exactly for one profile.[4] % [MARCELLO'S COMMENTS: OK, SO HERE YOU SEEM TO BE ADDRESSING ANOTHER PROBLEM, SUCH AS BIRTHDAY PROBLEM AND RELATED. I WONDER IF THIS IS ANOTHER PROBLEM, NOT IMMEDIATELY HAVING TO DO WITH COLD-HIT DNA MATCHES. CAN THIS GO INTO A SEPARATE SUBSECTION? THAT MIGHT HELP ORIENT THE READER AND NOT MAKE THIS ONE SUBSECTION SO LONG.]

%

### 4.1 Sensitivity of LR to hypothesis choice and NRC II

%This approach has also been defended defended by %**?** who points out that since the suspect is identified after the databases search, the hypothesis is formulated *ad hoc*. Without the correction, then, the likelihood ratio would be data-dependent.

%Recalling the discussion of sensitivity of the likelihood ratio to the choice of hypotheses, let's take a look at an interesting attempt to defend NRC II by **?**. He insists that hypotheses such as *JS was one of the crime scene donors* are evidence-dependent in the case of database search, "since we had no way of knowing prior to the search that Smith would be the person that matched" (p. 672). Instead, Stockmarr insists, we should evaluate LR using hypotheses that can be formulated prior to the search, such as *the true perpetrator is among the suspects identified from the database*. And indeed, the likelihood of this hypothesis is as NRC II suggests, $k/np$, where $k$ is the number of matching profiles, $n$ the database size, and $p$ the random match probability (see **?**, for a derivation).

%Dawid, in a discussion with Stockmarr (**?**) points out that Stockmarr's hypotheses, while not depending on the result of the search, depend on the data themselves (because they change with the database size). More importantly, he also indicates that Stockmarr's hypotheses are composite and the assessment of LR therefore requires additional assumptions about the priors. Once these are used with Stocmarr's own LR, the posterior is the same as the one obtained using the methods proposed by the critics of NCR II. The phenomenon is a particular case of the one we already discussed, because Stockmarr's hypothesis and the one originally used in the database search problem are equivalent conditional on the evidence. This turns out to be another example of how LR on its own might be insufficiently informative, especially when it is unclear what the involved hypotheses are.[5]

%

### 4.2 Resolving the Database Search Problem

%So we know not to use DMP. But the question remains: what's the relation between the value of a DNA match in a cold hit case as compared to a DNA match for a previously and independently identified suspect? After all we need to have a justified stance on cold hit evidence, and there seems to be no hope of reaching one without the tools provided by legal probabilism.

%Various versions of probabilistic calculations have been developed, depending on what idealizations and additional complexities are being considered. %In order to better understand how to properly assess a cold-hit match, it is instructive to consider a simple scenario, the *island problem*, studied by **?**, **?**, and **?**.

M: Nowhere do you talk about the island problem. Did you delete something here?

[4] This is a reformulation of the well-known birthday problem, it's just we discussed it using smaller numbers to make the considerations more intuitively compelling.

[5] See however, Stockmarr's own reply (*ibidem*).

%%Let $H_p$ stand for `The suspect is the source of the crime traces'` and `$H_d$ for`The suspect is not the source of the crime traces'. Let evidence $E$ be the DNA match between the crime stain and the suspect (included in the database) and $D$ the information that no one among the $N-1$ profiles in the database matches the crime stain. The likelihood ratio associated with $E$ and $D$ should be (**??**): %

$$V = \frac{\mathsf{P}(()E,D|H_p)}{\mathsf{P}(()E,D|H_d)}$$

% %Since $\mathsf{P}(()A \wedge B) = \mathsf{P}(()A|B)\mathsf{P}(()B)$, for any statement $A$ and $B$, this ratio can be written as %

$$V = \frac{\mathsf{P}(()E,|H_p,D)}{\mathsf{P}(()E|H_d,D)} \times \frac{\mathsf{P}(()D|H_p)}{\mathsf{P}(()D|H_d)}$$

% %The ratio $\mathsf{P}(()E,|H_p,D)/\mathsf{P}(()E|H_d,D)$ is roughly $1/\gamma$, where $\gamma$ is the random match probability. The ratio $\mathsf{P}(()D|H_p)/\mathsf{P}(()D|H_d)$ is called the *database search ratio*. To determine this ratio, consider first the denominator $\mathsf{P}(()D|H_d)$. If the suspect is not the source, someone else is, either someone who is in the database or someone not in the database. Let $S$ stand for 'The source is someone in the database.' By the law of total probability, %

$$\mathsf{P}(()D|H_d) = \mathsf{P}(()D|S,H_d)\mathsf{P}(()S|H_d) + \mathsf{P}(()D|\neg S,$$

% %Note that if the source is someone in the database ($S$) and the suspect is not the source ($H_d$), it is nearly impossible that no one in the database would match ($D$). %the probability of $D$ that no one other than the suspect would match can be set to zero. %So $\mathsf{P}(()D|S,H_d) \approx 0$. The above equation %therefore simplifies to: %

Is this right? I elaborated what you had. Please check!

$$\mathsf{P}(()D|H_d) = \mathsf{P}(()D|\neg S,H_d)\mathsf{P}(()\neg S|H_d)$$

% %Let $\mathsf{P}(()D|H_p)$ %be $\psi_{N-1}$. %Notice that $\mathsf{P}(()D|\neg S,H_d)$ %is the probability of a random match in a database of size $N-1$ not containing the the real source, and can also be estimated as $\psi_{N-1}$. If $\mathsf{P}(()S) = \varphi$, then the second ratio in our calculation of $V$ therefore reduces to: %

I don't follow the reasoning. Can you clarify? Why do these two probabilities equal the same thing?

$$\frac{\psi_{N-1}}{\psi_{N-1}(1-\varphi)} = \frac{1}{1-\varphi}$$

% %As the database gets larger, $\varphi$ increases and the database search ratio also increases. This ratio equals one only if no one in the database could be the source, that is, $\varphi = 0$.

%Since in order to obtain the likelihood ratio $V$, the likelihood ratio of the DNA match is multiplied by the database search ratio, the result will alwaysbe greater than the mere likelihood ratio of the match (except for the unrealistic case in which $\varphi = 0$) . Thus, a cold-hit DNA match should count as stronger evidence than a DNA match of a previously identified suspect. **?** study variations of the database search problem, with different search strategies and including the possibility that information about the match is itself uncertain, but the general point remains. Under reasonable assumptions, ignoring the search errs on the side of caution.[6]

%Think about the following scenario: first, you identified the suspect by some means. Then, it turned out his DNA profile matches the crime scene stain. Fine. Now, imagine further database search for a database not containing this suspect finds no matches. Would you think that this information supports the guilt hypothesis? If your answer is yes, then you do have the intuition that the lack of matches

[6] **?**, with slightly different assumptions, derived the formula $R \times [1 + mD/N]$, where $R = 1/\gamma$, $D$ is the database size, $N$ the number of people in population not in database, and $m$ is an optional multiplier reflecting how much more likely persons in the database are though to be the source when compared to the rest of the population. The expression cannot be less than $\gamma$. If no other profile has been tested, $D = 0$ and LR is simply the regular DNA match LR. If $N$ is zero, that is, everyone in population is in the database, the result is infinitely large.

with other people (whose profiles, in this particular case, happen to be in a database) strengthens the evidence.

%The fact that, compared to an ordinary DNA match, a cold-hit DNA match is stronger evidence of guilty does not imply that the posterior probability of the defendant's guilt should be higher in cold-hit cases. The other evidence used to first identify the suspect, jointly with the DNA match, might result in a higher posterior probability of guilt, even if the likelihood ratio of the cold-hit match is higher. This different in the posterior probability of guilt accounts for the intuition that in cold-hit cases we should resist conviction so long as the evidence only consists of a DNA match. The resistance toward conviction should be less strong in other cases so long as the DNA match is supplemented by other incriminating evidence.

%What about the intuition that we'd be uneasy about a conviction based solely on a cold hit match, much less than about a DNA-match based conviction of a previously and independently identified suspect? We think so because now we're thinking about the posterior probability given total evidence.

### 4.3 Levels of Hypotheses

Consider using the stuff that was commented out! I left percentage signs.

Difficulties in assessing probabilities go hand in hand with the choice of the hypotheses of interest. To some approximation, hypotheses can be divided into three levels: offence, activity, and source level hypotheses. At the offence level, the issue is one of guilt or innocence, as in the statement `Smith intentionally attacked the victim with a knife'. At the activity level, hypotheses do not include information about intent but simply describe what happened and what those involved did or did not do. An example of activity level hypothesis is`Smith bled at the scene.'Finally, source level hypotheses describe the source of the traces, such as 'Smith left the stains at the crime scene,' without specifying how the traces got there. Overlooking differences in hypothesis level can lead to serious confusions.

To illustrate, consider a case in which a DNA match is the primary incriminating evidence. In testifying about the DNA match at trial, experts will often assess the probability that a random person, unrelated to the crime, would coincidentally match the crime stain profile %For a survey of developments and complications of this model, see (**?**). The random match probability is often an impressively low number, say 1 in 100 million or lower, at least excluding the possibility that relatives or identical twins would coincidentally match (**?**).

%This low probability indicates that it is extremely unlikely that a random person would match.

%The match should count as strong evidence against the defendant % See %This presentation is similar to classical hypothesis testing. In such a context one starts by setting up a chance hypothesis, often called the null $H_0$, and then calculates the probability of the evidence (or data obtained) being such as it is or more extreme on the assumption that $H_0$ holds. If this probability is small (conventionally, below 0.01 or 0.05), this counts as evidence against %$H_0$. But note that just because $\mathsf{P}(()E|H_0)$ is small, it does not follow that, for any alternative hypothesis, $H_*$ $\mathsf{P}(()E|H_*)$ is large. The latter probability could be equally low.

% %A DNA profile consists of pairs of alleles at several loci. Individual allele probabilities are used to calculate the expected frequency of a given profile $\Gamma$ in a relevant population, so that we obtain the genotype probability $\gamma$. Assuming the so-called Hardy-Weinberg equilibrium, $\gamma$ can be obtained by multiplying the allele probabilities. Very roughly, the probability of a match at any particular locus is around $1/10$, and so the probability of a match on all 20 loci used by the FBI CODIS system should be $(1/10)^{20}$. % %Such calculations, however, are a bit simplistic. One factor is that given the crime stain, we already know that at least one population member has profile $\Gamma$, and the observation of a gene increases the chance of another of the same type. Actual calculations are quite complicated, (see **?**), as we'll discuss in the section on BNs for DNA evidence evaluation. % %In legal context, $\gamma$ — the so-called Random Match Probability (RMP), that is, the probability that a random person from the population matches the crime stain profile — is taken to be the probability that the suspect is a match if in fact he is innocent and is usually estimated as the frequency of a given profile in the relevant population. % % is not the probability of innocence (see **??** for details), it % %And yet, in what way the match counts as evidence against the %defendant is not straightforward. %Here it is paramount to avoid a number of confusions. % % %First, the random match probability is not the posterior probability of innocence

since $\mathsf{P}(()\mathsf{match}|\mathsf{innocence})$ should not be confused with $\mathsf{P}(()\mathsf{innocence}|\mathsf{match})$. %The random match probability speaks to the former, not the latter probability. %To confuse the two would be to commit the prosecutor's fallacy (see **??** for details). %Second, %Since the random match probability low probability indicates that it is extremely unlikely that a random person would match. It is tempting to equate the random match probability to $\mathsf{P}(()\mathsf{match}|\mathsf{innocence})$ and together with the prior $\mathsf{P}(()\mathsf{innocence})$ use Bayes' theorem to calculate
the posterior probability of innocence $\mathsf{P}(()\mathsf{innocence}|\mathsf{match})$. But this would be a mistake. % Applying Bayes' theorem is of course recommended and helps to avoid the prosecutor's fallacy, the conflation of $\mathsf{P}(()\mathsf{innocence}|\mathsf{match})$ and $\mathsf{P}(()\mathsf{match}|\mathsf{innocence})$. %(see **??** for details). The problem lies elsewhere. Equating the random match probability with $\mathsf{P}(()\mathsf{match}|\mathsf{innocence})$ overlooks the difference between offense, activity and source level hypothesis. It is hasty to assume that, in one way or another, a DNA match can speak directly to the question of guilt or innocence. Even if the suspect actually left the genetic material at the scene—source level proposition—the match does not establish guilt. %The match could be the result of a laboratory error. Or Even if the defendant did visit the scene and came into contact with the victim, it does not follow that he committed the crime he was accused of. %So even if the random match probability is usually very low, it does not follow that the posterior probability of innocence is near the random match probability given by the expert. %It is true, however, that in many circumstances the random match probability and the posterior probability of innocence given a match would both be very low.

Few forms of evidence can speak directly to offense level hypotheses. Circumstantial evidence that is more amenable to a probabilistic quantification, such as DNA matches and other trace evidence, does not. Eyewitness testimony may speak more directly to offense level hypotheses, but it is also less easily amenable to a probabilistic quantification. This makes it difficult to assign probabilities to offense level hypotheses. Experts are usually not supposed to comment directly on offense level hypotheses, but they often comment on activity level and source level hypotheses. In moving from source to activity level, however, additional sources of uncertainty come into play. %(**?**). % The assessment of activity level hypotheses depends on additional variables other than those on which the assessment of source level hypotheses depends. %For example, is this the kind of staining that would occur if the suspect kicked the victim in the head? For example, the probability of finding such and such quantity of matching glass if the suspect smashed the window depends on how the window was smashed, when it was smashed, and what the suspect did after the action. Another problem arises due to recent improvements in DNA profiling technology (**?**). Since today investigators are able to obtain profiles from minimal amounts of genetic material, transfer probabilities become more difficult to assess as more opportunities of transfer arise. If small traces such as dust speckles can be used as evidence, the possibility that the traces were brought to the scene accidentally becomes more likely. For this reason, moving beyond source level hypotheses requires a close collaboration between scientists, investigators and attorneys (see **?**, for a discussion). %The hypotheses themselves are up for revision as evidence is obtained or facts about what happened are accepted (**?**).

% % % %Since the likelihood ratio might change with the choice of the hypotheses, the clarity on the choice of the hypotheses, and their level in particular, is crucial. For instance, % % %

## 4.4 The two-stain problem

Also, worth a discussion as an illustration

A case study that further illustrates both advatanges and limitations of the likelihood ratio as a measure of evidentiary strength is the two-stain problem, originally formulated by **?**. The key limitation is due to the combination of two circumstances: first, that likelihood ratios vary depending on the choice of hypotheses being compared; second, that it is not always clear which hypotheses should be compared. To illustrate what is at stake, what follows begins with Evett's original version of the two-stain problem (which does not pose any challenge to the likelihood ratio) and then turns to a more complex version (which suggests that likelihood ratios, in and of themselves, are insufficiently informative).

#### 4.4.0.1 Evett's two-stain problem

Suppose two stains from two different sources were left at the crime scene, and the suspect's blood matches one of them. More precisely, the two items of evidence are as follows: %

$E_1$ The blood stains at the crime scene are of types $\gamma_1$ and $\gamma_2$ of estimated frequencies $q_1$ and $q_2$ respectively.

$E_2$ The suspect's blood type is $\gamma_1$.

% Let the first hypothesis be that the suspect was one of the two men who committed the crime and the second hypothesis the negation of the first. %

$H_p$ The suspect was one of the two men who committed the crime.

$H_d$ The suspect was not one of the two men who committed the crime.

% **?** shows that the likelihood ratio of the match relative to these two hypotheses is $1/2q_1$ where $q_1$ is the estimated frequency of the characteristics of the first stain. Surprisingly, the likelihood ratio does not depend on the frequency associated with the second stain.

To understand Evett's argument, consider first the likelihood ratio:

$$\frac{\mathsf{P}(()E_1 \wedge E_2|H_p)}{\mathsf{P}(()E_1 \wedge E_2|H_d)} = \frac{\mathsf{P}(()E_1|E_2 \wedge H_p)}{\mathsf{P}(()E_1|E_2 \wedge H_d)} \times \frac{\mathsf{P}(()E_2|H_p)}{\mathsf{P}(()E_2|H_d)}.$$

Notice that the suspect's blood type as reported in $E_2$ is independent of whether or not he participated in the crime, that is, $\mathsf{P}(()E_2|H_p) = \mathsf{P}(()E_2|H_d)$. So the likelihood reduces to:

$$\frac{\mathsf{P}(()E_1 \wedge E_2|H_p)}{\mathsf{P}(()E_1 \wedge E_2|H_d)} = \frac{\mathsf{P}(()E_1|E_2 \wedge H_p)}{\mathsf{P}(()E_1|E_2 \wedge H_d)}.$$

The numerator $\mathsf{P}(()E_1|E_2 \wedge H_p)$ is the probability that one of the stains is $\gamma_1$ and the other $\gamma_2$ given that the suspect is guilty and has profile $\gamma_1$. The probability that one of the stains is $\gamma_1$ is simply 1, and assuming blood type does not affect someone's propensity to commit a crime, the probability that the second stain is $\gamma_2$ equals its relative frequency in the population, $q_2$. So the numerator is $1 \times q_2 = q_2$. % Next, consider the denominator $\mathsf{P}(()E_1|E_2 \wedge H_d)$. If $H_d$ is true, %the fact that the suspect has profile $\gamma_1$ is irrelevant for the crime scene profiles. the crime was committed by two randomly selected men with profiles $\gamma_1$ and $\gamma_2$. %who can be seen as two random samples from the general population as far as their blood profiles are concerned. There are two ways of picking two men with such profiles ($\gamma_1, \gamma_2$ and $\gamma_2, \gamma_1$), each having probability $q_1 q_2$. So the denominator equals $2q_1 q$. By putting numerator and denominator together, %

$$\frac{q_2}{2q_1 q_2} = \frac{1}{2q_1}.$$

% which completes the argument. In general, if there are $n$ bloodstains of different phenotypes, the likelihood ratio is $1/nq_1$, or in other words, the likelihood ratio depends on the number of stains but not on the frequency of the other characteristics.

#### 4.4.0.2 A more complex two-stain problem

Consider now a more complex two-stain scenario. Suppose a crime was committed by two people, who left two stains at the crime scene: one on a pillow and another on a sheet. John Smith, who was arrested for a different reason, genetically matches the DNA on the pillow, but not the one on the sheet. What likelihood ratio should we assign to the DNA match in question? **?** argue that there are three plausible pairs of hypotheses associated with numerically different likelihood ratios (see their paper for the derivations). The three options are listed below, where $R$ is the random match probability of Smith's genetic profile and $\delta$ the prior probability that Smith was one of the crime scene donors. %

| $H_p$ | $H_d$ | LR |
|---|---|---|
| Smith was one of the crime scene donors. | Smith was not one of the crime scene donors. | $R/2$ |
| Smith was the pillow stain donor. | Smith was not one of the crime scene donors. | $R$ |
| Smith was the pillow stain donor. | Smith was not the pillow stain donor. | $R(2-\delta)/2(1-\delta)$ |

Two facts are worth noting here. First, even though the likelihood ratios associated with the hypotheses in the table above are numerically different, the hypotheses are in fact equivalent conditional on the evidence. After all, Smith was one of the crime scene donors just in case he was the pillow stain donor, because he is excluded as the stain sheet donor. Smith was not one of the crime scene donors just in

case he was not the pillow stain donor, because he is excluded as the sheet stain donor.
% %Second, the example illustrates that sometimes the likelihood ratio is sensitive to the prior probability (after all, $\delta$ occurs in the third likelihood ratio in the table). % In addition, even though the likelihood ratios are numerically different, their posterior probabilities given the evidence are the same. To see why, note that the prior odds of the three $H_p$'s in the table should be written in terms of $\delta$. Following **?**, the prior odds of the first hypothesis in the table are $\delta/1-\delta$. The prior odds of the second hypothesis are $(\delta/2)/(1-\delta)$. The prior odds of the third hypothesis are $(\delta/2)/(1-(\delta/2))$. In each case, the posterior odds — the result of multiplying the prior odds by the likelihood ratio — are the same: $R \times \delta/2(1-\delta)$. So despite differences in the likelihood ratio, the posterior odds of equivalent hypotheses are the same so long as the priors are appropriately related (this point holds generally).

**?** cautions that the equivalence of hypotheses, conditional on the evidence, does not imply that they can all be presented in court. He argues that the only natural hypothesis for the two-stain problem is that Smith is guilty as charged. **?** reply that focusing on the guilt hypothesis is beyond the competence of expert witnesses who should rather select pairs of hypotheses on which they are competent to comment. Some such pairs of hypotheses, however, will not be exclusive and exhaustive. When this happens, as seen earlier, the selection of hypotheses is prone to arbitrariness. To avoid this problem, **?** recommend that the likelihood ratio should be accompanied by a tabular account of how a choice of prior odds (or prior probabilities) will impact the posterior odds, for a sensible range of priors (for a general discussion of this strategy called sensitivity analysis, see earlier discussion in **??**). In this way, the impact of the likelihood ratio is made clear, no matter the hypotheses chosen. This strategy concedes that likelihood ratios, in and of themselves, are insufficiently informative, and that they should be combined with other information, such as a range of priors, to allow for an adequate assessment of the evidence.[7]

% and prior odds needed to calculate LR in cases in which LR depends on priors are available. % %\footnote{Further discussion of the phenomenon is quite interesting. %

#### 4.4.0.3 Likelihood ratio variability in cold-hit cases

%The sensitivity of the likelihood ratio to the choice of hypotheses is not confined to the two-stain problem or alike scenarios.

A similar conclusion holds for DNA matches in cold-hit cases. When the suspect is identified through a database search of different profiles, **?** and **?** have argued that the likelihood ratio of the match %— which usually equals $1/\gamma$ where $\gamma$ is the random match probability— should be adjusted by the database search ratio (see earlier in 3 for details). This proposal tacitly assumes that the hypothesis of interest is something like `the defendant is the true source of the crime traces.'` `%This assumption is eminently plausible but not uncontroversial.` `%The National Research Council (NRC II) recommended in 1996 that that the likelihood ratio of the match 1/$\gamma$ be divided by the size of the database. In defending this proposal, In contrast, \cite{stockmarr1999LikelihoodRatiosEvaluating}, who defends the NRC II 1996 recommendation, argues that the likelihood ratio of the match in cold-hit cases should be divided by the size of the database. He points out that the hypothesis`the defendant is the true source of the crime traces' is evidence-dependent because the investigators had no way of knowing prior to the search that anyone in particular would match. % (p. 672). Accordingly, Stockmarr believes we should evaluate the likelihood ratio using hypotheses that can be formulated prior to the database search, such as 'The true source of the crime traces is among the suspects in the database.' The likelihood associated with this hypothesis and its negation is $k/np$, where $k$ is the number of matching profiles, $n$ the database size, and $p$ the random match probability (see **?**, for a derivation).

In response to this argument, Dawid points out that even though Stockmarr's hypothesis does not depend on the result of the search, it still depends on the data themselves (because it changes with the database size) (**?**). Dawid also points out that Stockmarr's hypothesis is composite and thus the assessment of the likelihood ratio requires additional assumptions about the priors. Once these assumptions are made clear, the posterior of Stockmarr's hypothesis is the same as that of other hypotheses. %obtained using others methods.

[7] The reference class problem is lurking in the background. **?** argues that, in order to calculate the probability of a match given the evidence, the class of possible culprits should be identified, and different choices of such a class might lead to different likelihood ratios. On the problem of priors, see **??**. On the reference class problem, see **??**.

This phenomenon is a particular case of what we discussed earlier since the hypothesis 'The true source is among the suspects in the database' (Stockmarr's) and the hypothesis 'The defendant is the true source of the crime traces' (Taroni's) are equivalent conditional on the evidence. %%This is another example of how likelihood ratios on their own might be insufficiently informative to allow for an adequate assessment of the evidence.

I changed this is a bit. Is this correct?

Yes, there was a minor confusing one passage before, fixed.

### 4.5 LR & relevance, small-town murder etc.

The U.S. Federal Rules of Evidence define relevant evidence as one that has 'any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence' (rule 401). This definition is formulated in a probabilistic language. Legal probabilists interpret it by relying on the likelihood ratio, a standard probabilistic measure of evidential relevance (**?????**). The likelihood ratio (initially introduced in **??** and more extensively in Section **??**) is the probability of observing the evidence given that the prosecutor's or plaintiff's hypothesis is true, divided by the probability of observing the same evidence given that the defense's hypothesis is true.

Let $E$ be the evidence, $H$ the prosecutor's or plaintiff's hypothesis, and $H'$ the defense's hypothesis. The likelihood ratio $\%LR(E,H,H')$ is defined as follows: %

$$LR(E,H,H') = \frac{P(E|H)}{P(E|H')}$$

% On this interpretation, relevance depends on the choice of the competing hypotheses. $\%H_p$ and $H_d$ are used as examples, but other competing hypotheses $H$ and $H'$ could also be used. %When there are no ambiguities, $LR(E,H_p,H_d)$ will be shortened into the less cumbersome $LR(E)$. % A piece of evidence is relevant—in relation to a pair of hypotheses $H$ and $H'$—provided the likelihood ratio $LR(E,H,H')$ is different from one and irrelevant otherwise. For example, the bloody knife found in the suspect's home is relevant evidence in favor of the prosecutor's hypothesis because we think it is far more likely to find such evidence if the suspect committed the crime (prosecutor's hypothesis) than if he didn't (defense's hypothesis) %(**?**, 7) (**?**). In general, for values greater than one, $LR(E,H,H') > 1$, the evidence supports the prosecutor's or plaintiff's hypothesis $H$, and for values below one, $LR(E,H,H') < 1$, the evidence supports the defense's hypothesis $H'$. If the evidence is equally likely under either hypothesis, $LR(E,H,H') = 1$, the evidence is considered irrelevant.

### 4.6 The Small Town Murder objection

This account of relevance has been challenged by cases in which the evidence is intuitively relevant and yet its likelihood ratio, arguably, equals one. Here is one of them: %One such case is *Small Town Murder*

> *Small Town Murder:* A person accused of murder in a small town was seen driving to the small town at a time prior to the murder. The prosecution's theory is that he was driving there to commit the murder. The defense theory is an alibi: he was driving to the town because his mother lives there to visit her. The probability of this evidence if he is guilty equals that if he is innocent, and thus the likelihood ratio is 1 ... Yet, every judge in every trial courtroom of the country would admit it [as relevant evidence]. (The difficulty has been formulated by Ronald Allen, see the discussion in **?**)

Counterexamples of this sort abound. Suppose a prisoner and two guards had an altercation because the prisoner refused to return a food tray. The prisoner had not received a package sent to him by his family and kept the tray in protest. According to the defense, the prisoner was attacked by the guards, but according to the prosecution, he attacked the guards. The information about the package sent to the prisoner and the withholding of the tray fails to favor either version of the facts, yet it is relevant evidence (**?**). %Counterexamples of this sort abound.

- In response to an eyewitness testimony the defendant claims that his identical twin is the culprit. The testimony is unable to favor any of the two options and yet is considered relevant.
- Suppose the evidence at issue is that a fight occurred and the only dispute is over who started it.

- Or suppose the defendant was stopped because of speeding three minutes after an aborted bank robbery and $1/2$ a mile away from the site. The prosecution says this is evidence of guilt: it shows the defendant was escaping. The defense responds that this is evidence of innocence: no bank robber would speed and attract attention.
- Or, in a murder case, the defendant is the victim's son. Is that relevant to show he's guilty? Is it relevant to show he's innocent? The answer seems to be yes, to both questions. This example is due to Samuel Gross and is discussed in (**?**).

%In general, there seem to be numerous examples in which evidence is, intuitively relevant, and the evidence supports neither side's theory over the other side's theory. How is such evidence to be judged relevant from the probabilist perspective?

%

### 4.7 Replies to the overlapping evidence objection

%In response (inspired by the ideas put forward in the discussion by David Kaye, Bruce Hay and Roger Park), note that

It is true that if a piece of evidence $E$ fits equally well with two competing hypotheses $H$ and $H'$, then $P(E|H) = P(E|H')$ and thus $LR(E,H,H')$ will equal 1. But the likelihood ratio may change depending on the selection of hypotheses. Rule 401 makes clear that relevant evidence should have 'any tendency to make the existence of *any fact that is of consequence* [emphasis ours] to the determination of the action more probable or less probable'. So the range of hypotheses to compare should be quite broad. Just because the likelihood ratio equals one for a specific selection of $H$ and $H'$, it does not follows that it equals one for *any* selection of $H$ and $H'$ which are of consequence to the determination of what happened. In *Small Town Murder*, whether the suspect was in town at all is surely of consequence for determining what happened (if he was not in town, he could not have committed the crime). The fact that he was seen driving is helpful information for establishing whether or not he was in town.

But if the range of hypotheses $H$ and $H'$ to compare in the likelihood ratio $LR(E,H,H')$ is quite broad, this may raise another concern. The choice of hypotheses needed to determine the relevance of an item of evidence might depend on other items of evidence, and so it might be difficult to determine relevance until one has heard all the evidence. This fact — Ronald Allen and Samuel Gross argue in (**?**) — makes the probabilistic account of relevance impractical. But, in response, David Kaye points out that deciding whether a reasonable juror would find evidence $E$ helpful requires only looking at what hypotheses or stories the juror would reasonably consider. Since the juror will rely on several clues about which stories are reasonable, this task is computationally easier than going over all possible combinations of hypotheses (**?**).

%

### 4.8 Small Town Murder and bayesian networks

Legal probabilists can also offer a more principled response to *Small Town Murder* and related problems based on Bayesian networks. %rather than a reasonable choice of the competing hypotheses. %The emphasis on the logical relations between the hypotheses have been used by Fenton to address the . Let $H_p$ be the prosecutor's hypothesis that the defendant committed the murder, and $H_d$ the defense's hypothesis that the defendant was visiting his mother. Let $E$ be the fact that the defendant was seen driving to the town prior to the murder. Further, suppose the prior probabilities of $H_d$ and $H_p$ are 50%, and the conditional probability of $E$ on each of those hypotheses is 70% (nothing of what will be said depends on this particular choice of values). Crucially, while indeed the evidence supports both hypotheses, this example is based on a pair of hypotheses that are neither mutually exclusive nor exhaustive. A Bayesian network can be used to calculate other likelihood ratios for hypotheses that are exclusive and exhaustive.

%

Figure 6: Graphic model of Small Town Murder

Figure 7: Probability distribution of $E$

%

Following the calculations in (**?**), for exclusive and exhaustive hypotheses, $LR(E, H_d, \neg H_d) = 1.75$, and similarly, $LR(E, H_p, \neg H_p) = 1.75$, since $P(E|H_d) = 0.7$ and $P(E|\neg H_d) = 0.4$. The likelihood ratio of the evidence, if it is measured against exclusive and exhaustive hypotheses, is not equal to one.[8] Such considerations should also generalize to other paradoxes of relevance.
% %For instance, in the twins problem, the LR is 1 if the hypotheses are: `the suspect committed the crime', and`the suspect's twin brother committed the crime', but is not 1 f we consider the fairly natural hypothesis that the defendant is innocent. %Similarly, %In the food tray example, Bayesian network analysis shows that the value of the evidence 'prisoner withholds tray' for the question who started the fight depends on a range of uncertain events and other pieces of evidence (such as whether indeed a parcel he was supposed to obtain was withheld; whether the prisoner inquired about this; whether and how this inquiry was answered). Considered in this context, the piece of evidence will not have a likelihood ratio of one with respect to at least some choice of sensible hypotheses. %

The general problem with the paradoxes of relevance is that in complex situations there is no single likelihood ratio that corresponds to a single piece of evidence. The problematic scenarios focus on a single likelihood ratio based on non-exclusive or non-exhaustive hypotheses. However, evidence can be relevant so long as it has a probabilistic impact on a sub-hypothesis involved in the case, even without having a recognizable probabilistic impact on the prosecutor's or defense's ultimate hypotheses. When this happens, it is relevant, in agreement with Rule 401 of the Federal Rules of Evidence. Bayesian networks help to see how pieces of evidence can increase or decrease the probability of different sub-hypotheses **?**.

%recommend relying on a Bayesian network to investigate in an orderly manner the way in which pieces of evidence and hypotheses interact.%in an orderly manner.

no one said the interact in an orderly manner. ;)

## References


Aitken, C., Roberts, P., & Jackson, G. (2010). Fundamentals of probability and statistical evidence in criminal proceedings (Practitioner Guide No. 1), Guidance for judges, lawyers, forensic scientists and expert witnesses. *Royal Statistical Society's Working Group on Statistics and the Law*.

Balding, D. J., & Donnelly, P. (1996). Evaluating DNA Profile Evidence When the Suspect Is Identified Through a Database Search. *Journal of Forensic Sciences*, *41*(4), 13961J.

Dawid, A. P. (1994). The island problem: Coherent use of identification evidence. In P. Freeman & A. Smith (Eds.), *Aspects of uncertainty: A tribute to D. V. Lindley* (pp. 159–170). John Wiley & Sons, New York.

Dawid, A. P., & Mortera, J. (1996). Coherent Analysis of Forensic Identification Evidence. *Journal of the Royal Statistical Society. Series B (Methodological)*, *58*(2), 425–443.

Donnelly, P., & Friedman, R. D. (1999). DNA Database Searches and the Legal Consumption of Scientific Evidence. *Michigan Law Review*, *97*(4), 931.

Eggleston, R. (1978). *Evidence, proof and probability* (Vol. 2). Weidenfeld; Nicolson London.

ENFSI. (2015). *Guidelines for evaluative reporting in forensic sciences*.

Evett, I., Jackson, G., & Lambert, J. (2000). More on the hierarchy of propositions: Exploring the distinction between explanations and propositions. *Science & Justice*, *40*(1), 3–10.

Fenton, N., Berger, D., Lagnado, D., Neil, M., & Hsu, A. (2014). When "neutral" evidence still has probative value (with implications from the Barry George Case). *Science & Justice*, *54*(4), 274–287.

Mayo, D. (2018). *Statistical inference as severe testing*. Cambridge University Press.

National Research Council. (1992). *DNA technology in forensic science* [NRC I]. Committee on DNA technology in Forensic Science, National Research Council.

National Research Council. (1996). *The evaluation of forensic DNA evidence* [NRC II]. Committee on DNA technology in Forensic Science, National Research Council.

Robertson, B., Vignaux, G., & Berger, C. (2016). *Interpreting evidence: Evaluating forensic science in the courtroom*. John Wiley & Sons.

Royall, R. M. (1997). *Statistical evidence: A likelihood paradigm*. Chapman; Hall/CRC.

Taroni, F., Biedermann, A., Bozza, S., Garbolino, P., & Aitken, C. (2014). *Bayesian networks for*


[8] **?** offer a slightly different solution to the problem. They construct a Bayesian network with three hypotheses, also exhaustive and exclusive: in town to visit mother, in town to murder, out of town.

*probabilistic inference and decision analysis in forensic science* (2nd ed.). John Wiley & Sons.

Triggs, C. M., & Buckleton, J. S. (2004). Comment on: Why the effect of prior odds should accompany the likelihood ratio when reporting DNA evidence. *Law, Probability and Risk*, *3*, 73–82.