

---

---

# The Philosophy of Forensic Scientific Identification

ALLAN JAMIESON\*

[M]ost lawyers have little or no appreciation for the scientific method and lack the ability to judge whether proffered research is good science, bad science, or no science at all.

—David L. Faigman<sup>1</sup>

## INTRODUCTION

This Article will discuss some of the features that make a process scientific, outline the forensic process through which evidence must travel, consider the principles and practice of individualization, and finally describe the difficulties of assessing the significance of any “match,” with particular emphasis on DNA profiling.

### I. THE FORENSIC PROCESS

The “forensic process” is the method by which physical evidence is considered and handled from the crime scene to the court. The aim of the process is to present probative evidence to the court.<sup>2</sup>

The major features can be summarized as:

- (1) Protection
- (2) Recording
- (3) Collection
- (4) Analysis
- (5) Interpretation
- (6) Evaluation
- (7) Presentation

The first three of these generally comprise the process of crime

---

\* Director of the Forensic Institute, Glasgow, UK; Visiting Professor at the faculties of Law and Life Sciences at Napier University, Edinburgh, UK.

1. DAVID L. FAIGMAN, *LEGAL ALCHEMY: THE USE AND MISUSE OF SCIENCE IN THE LAW* 54 (1999).

2. Dan Krane et al., *Sequential Unmasking: A Means of Minimizing Observer Effects in Forensic DNA Interpretation*, 53 J. FORENSIC SCIS. (forthcoming July 2008).

---

---

scene investigation and will not be considered in detail here.<sup>3</sup> It is, in my opinion, vital that we refine the definitions of the processes of analysis, interpretation, and evaluation to facilitate discussion of the important principles that are applied at each step. In particular, “interpretation” and “evaluation” require definition and differentiation when attempts are being made to avoid observer bias.<sup>4</sup>

Evidence is only evidence when it is probative of a story. Without a story there can be no evidence, rather like no shadow without light. Evidence becomes forensic evidence when used in a legal process.<sup>5</sup> Many pages have been written on *how* to collect the evidence, but *what* to collect receives scant attention despite being crucial to the forensic process.

Despite the importance of crime scene investigation in the forensic process, there is no widely accepted common method or agreed practice. Depending on your initial reasoning it may make sense to collect everything, or from a different perspective, almost nothing. The difficulty with crime scene investigation is that it is almost impossible to be sure that the scene has been properly investigated.<sup>6</sup>

In many cases there has been a tendency to identify a suspect and then look for the evidence against him, or assume on cursory examination what has actually occurred and simply seek confirmatory evidence. A large number of biases<sup>7</sup> can then come into play with the result that there seems to be an overwhelming case against the accused and for the desired version of events.

The scientific approach, or method, is purported to be less subject to the biases and prejudices of the investigator and therefore more likely to lead to a higher probability of a correct identification of the story, including the identity of the perpetrator. There is a significant body of evidence that whilst the scientific method may be unbiased, scientists, including forensic scientists, are not.<sup>8</sup>

A crime scene is, in scientific terms, an observation or series of observations from which the investigator will create a hypothesis or story that explains the evidence. But of course, no matter what story the investigator eventually decides upon, there remains the possibility that it is not the true one. The best that the investigator can hope to achieve is a “best fit” or “most likely” story given the evidence. Are the “best fit”

---

3. *Id.*

4. *Id.*

5. *Id.*

6. FAIGMAN, *supra* note 1, at 62.

7. See generally Michael J. Saks et al., *Context Effects in Forensic Science: A Review and Application of the Science of Science to Crime Laboratory Practice in the United States*, 43 *Sci. & Just.* 77 (2003).

8. *Id.*

and “most likely” one and the same? Which is more probative?

#### A. ANALYSIS

Analysis for our purposes is any measurement or observation performed on an item. We observe and measure things routinely. Science’s very rock is the objective measurement of things. Almost all measurement is subject to error. Scientifically, we seek to estimate or measure that error so that we know how much we may trust the result of the measurement. Measurement of uncertainty is an increasingly important concept in analytical science, and has a particular importance in forensic science.

Analysis is a method. The output of analysis is a measure (e.g., concentration, weight), identification of a thing (e.g., drug) or feature (e.g., toolmark), or other result.

It is common for analysis, and the measure, to be considered together as “interpretation.” However, it is useful to restrict the definition of interpretation in the forensic environment so that the distinction between the measure (analysis) and the assessment of what this means (evaluation) is clear.

They are of course closely related, but the same measurement can be obtained by different methods of analysis, and the analysis may be, effectively, both interpretation and evaluation. Whatever the method, the result is then the object of the next step—interpretation.

#### B. INTERPRETATION

The vast majority of work in the forensic scientific environment is about establishing a match (i.e., hairs, fibers, paint, DNA, fingerprints, and other marks and impressions). To do this, we take the output of the analytical phase and use the results to make our comparison. It is often not clear how people use the words interpretation and evaluation. It is nevertheless a useful discipline to separate these as they may involve different reasoning and different expertise. For most purposes, interpretation can be regarded as the reporting of the analytical results without any attempt to go further than describe the output of the analysis. Examples of interpretation are: concentration of alcohol, type of drug, and alleles in a DNA profile.

#### C. EVALUATION

In all of these operations the key feature that differentiates interpretation from evaluation is that while interpretation may establish what something *is*, it is evaluation that attempts to establish what it means. Evaluation assesses perhaps what the sample *matches*, and considers the *significance of that in the particular case*. Evaluation is the assessment, *in a specific case*, of the probative value of the interpretation.

This allows us to identify another general guideline about the difference between analysis, interpretation, and evaluation: generally speaking, the required degree of case-related knowledge increases at each stage. Analysis can usually be performed by what have been regarded as technical staff, interpretation in most areas can be performed by someone with a good training and understanding of science, whereas a knowledge of the forensic issues is a requirement for many types of evaluation. Evaluation is obviously an important component of casework. The output of evaluation is the opinion of the expert, usually expressed in a written statement or report.

Evidence evaluation is emerging as one of the most interesting and complex debates in forensic science. One example illustrates the difficulty with what has been a fairly common approach to handling evidence, summarized in the oft-used phrase in expert reports: “[T]his evidence is consistent with . . . .” The current thinking is that this only goes part way to helping the court.<sup>9</sup> The key issue is the other stories the evidence is consistent with, and the relative strengths of each in evidential terms.

Before evidence can be presented to a court it must conform to the jurisdiction’s rules on admissibility.<sup>10</sup> Generally speaking, most jurisdictions will require that admissible evidence is “probative,” meaning providing support to one side of a case or the other.<sup>11</sup>

Probative value will be specific to a case rather than to a specific finding. Assessing the probative value is part of the evaluation of the evidence. Consider the finding of DNA from the suspect in a vaginal swab in a case of alleged rape. Is this evidence probative?

If the defendant accepts that sex occurred but there was consent, is it probative evidence?

In a murder, the blood from the accused is found on of the victim’s clothes and *vice versa*. Is this evidence probative? If the defendant concedes that he visited the victim the day before and a fight occurred that involved both of them shedding blood, then the evidence is not probative. The simple fact that evidence is ‘consistent with’ a particular story provides only a limited value to a court when set out in such terms. This is a crucial element in evidence-based decisions. The issue is not, does the evidence support this story, but, *of all the stories supported by the evidence*, is this one the most likely?

---

9. See, e.g., Allan Jamieson, *Bad Language*, THE JOURNAL, Sept. 2007, at 22, available at <http://www.journalonline.co.uk/pdf/2007-09.pdf>; see also FPT HEADS OF PROSECUTIONS COMMITTEE WORKING GROUP, REPORT ON THE PREVENTION OF MISCARRIAGES OF JUSTICE 115 (2004), available at <http://canada.justice.gc.ca/eng/dept-min/pub/pmj-pej/pmj-pej.pdf>.

10. FED. R. EVID. 702.

11. *Id.*

## II. THE SCIENTIFIC METHOD: MATCHING

Much has been written about “the scientific method,” and yet there seems little agreement about what it is. Perhaps the difficulty arises from the possibility that there is not one, but several, scientific methods. Sir Peter Medawar writes: “If the purpose of scientific methodology is to prescribe or expound a system of enquiry or even a code of practice for scientific behaviour, then scientists seem to be able to get on very well without it.”<sup>12</sup> What chance do we have when it is said that, “[i]n science, as in politics, religion, philosophy, etc., our beliefs are consequences of complex historical, psychological and social processes and interactions. The power of these processes and interactions makes the attempt to identify a method for science misleading and unnecessary.”<sup>13</sup>

There is no doubt that scientific breakthroughs sometimes occur in unpredicted and unpredictable ways. We can begin by describing some features that could generally be agreed to make a process scientific. Carl Sagan said: “Science is more than a body of knowledge; it is a way of thinking.”<sup>14</sup> Defining that way of thinking is not easy.

A scientific approach to a problem may comprise the sequence of: (1) observation, (2) measurement, (3) hypothesis creation, (4) hypothesis testing. This simple sequence hides a number of variations on the theme. Observation may be casual and lack measurement, or structured and measured. Either *de novo*, or from observations, a hypothesis can be constructed and tested experimentally. This enables the scientist to either predict what effect will result from a particular cause or, as required of the forensic scientist, work from the observed effect to a cause.

The scientist necessarily uses inductive reasoning in the creation of hypotheses. Unfortunately, there is no intrinsic logical basis for that because no matter how many times it happens, you can never actually know that it will happen the *next* time. Of course the more occasions that the system performs the same way the more we believe that our hypothesis is correct. This is the basis of the Bayesian approach to evidence evaluation; using our prior beliefs in conjunction with evidence to assess hypotheses. However, one failure and the hypothesis will require modification or abandonment: “[S]cience looks like the most courageous activity that a person can undertake. But it also is a tragic one because, in this picture, you can find out that you are certainly wrong, but you can never know that you are certainly right.”<sup>15</sup>

---

12. PETER MEDAWAR, *PLUTO'S REPUBLIC* 78 (1984).

13. BARRY GOWER, *SCIENTIFIC METHOD: AN HISTORICAL AND PHILOSOPHICAL INTRODUCTION* 16 (1997).

14. CARL SAGAN, *THE DEMON-HAUNTED WORLD: SCIENCE AS A CANDLE IN THE DARK* 25 (1997).

15. GALILEO'S COMMANDMENT: 2,500 YEARS OF GREAT SCIENCE WRITING 42 (Edmund Blair Bolles ed., 1999).

---

---

Optical illusions provide a good illustration of the difficulties with simple observation as a guide to reality. We process the information that we receive and this can change our perceived “reality.”

Yet so it is, we see the illiterate bulk of mankind that walk the high-road of plain common sense, and are governed by the dictates of nature, for the most part easy and undisturbed. To them nothing that is familiar appears unaccountable or difficult to comprehend. They complain not of any want of evidence in their senses, and are out of all danger of becoming Sceptics. But no sooner do we depart from sense and instinct to follow the light of a superior principle, to reason, meditate, and reflect on the nature of things, but a thousand scruples spring up in our minds concerning those things which before we seemed fully to comprehend.<sup>16</sup>

As Faigman warns: “The law must be cautious before relying on experience in light of relatively straightforward lessons of history that common sense about the empirical world—even based on extensive experience—is often wrong.”<sup>17</sup>

The scientific method is an attempt to create a consistent model of the universe. Observations are one way for us to test our model, but we do that testing within a framework that attempts to minimize the errors in observation and measurement that every test is subject to.

Individualization is a matching problem, and matching is a population problem. The goal of most forensic matching is to reduce the potential population from which an item could have come, to one. This extreme is the definition of identification. The process that we are more interested in, because of its more common application, is that of *individualization*. Individualization recognises that most scientific evidence is probabilistic, which is to say that we attempt to establish a *probability* or likelihood that two items had a common origin. The single exception to this practice is of course the community of fingerprint experts.

There are three inputs to the match decision:

- (1) Description of the mark (e.g., DNA profile from crime stain).
- (2) Description of the source (e.g., DNA profile from suspect).
- (3) Criteria for a match (e.g., all alleles match—no alleles in crime stain not present in suspect).

To claim a scientific basis for an expertise, the expert should be able to demonstrate for the technique(s) that they use, as a minimum:

- (1) Reliability studies of analytical technique (validation)

The scientific approach to this problem is normally to put a sample

---

16. BISHOP GEORGE BERKELEY, A TREATISE CONCERNING THE PRINCIPLES OF HUMAN KNOWLEDGE (1710), available at <http://18th.eserver.org/berkeley.html>.

17. FAIGMAN, *supra* note 1, at 80.

through the system to see how often the sample produces the same result. This is the *reproducibility* of the technique; its ability to provide consistent results when applied to the same samples.

(2) Establishment of false positive and false negative rates

Even if the technique is perfect, in many systems there is not a clear difference in the measurement when it is used to separate two or more groups. A false positive occurs when something that does not have the characteristic being sought is classified as actually having them, whereas a false negative is when something should be placed in a particular class but isn't. Generally, systems are designed to minimize the number of false positives and false negatives. However, in many systems the two are inextricably linked and as one attempts to minimize one error, the other increases.

(3) Defined match criteria

This requires a specification for the degree of similarity that two items must have before we declare a match. The specificity or discriminating power of a technique is “[t]he ability of an analytical procedure to distinguish between two items of different origin.”<sup>18</sup> Given that all matches are probable matches this leads to the further requirement to know the

(4) Probability of any match being a true match

As we increase the stringency of the requirements then the more sure we may be that we actually have a match, but at some point we will have made the requirements so tight that even a matching item is not classed as a match because it will differ in some, possibly trivial and irrelevant, way. The opposite effect is obtained when we reduce the stringency of our match criteria so much that almost nothing can be excluded as matching.

In most non-forensic biology, physics, and chemistry there are clear match parameters to enable one to say that sample “A” is or is not a bison, bismuth, or a boson. In forensic science, we can say that something is a bomb, bullet, or buprenorphine, but it gets a little more difficult when we get to the questions such as, “is this the same bomb as that?” or “did this bullet come from this gun?”

Setting aside some of the difficulties in allelic attribution, a DNA profile can be matched to another DNA profile with 100% accuracy (interpretation), and with a precision dependent on the number of loci used in the match (evaluation). The “match criteria” are defined; the numbers must match *exactly*.

---

<sup>18</sup> Scientific Working Group on Materials Analysis, *Forensic Paint Analysis and Comparison Guidelines*, FORENSIC SCI. COMM., July 1999, <http://www.fbi.gov/hq/lab/fsc/backissu/july1999/painta.htm#3.0%20Terminology>.

---

---

Having established the degree to which a match exists (it will rarely be perfect), the forensic scientist must now evaluate the significance of the match.

Another parameter that may be useful to know when assessing an identification system is the sensitivity. In this context, this means how little of the material from the individual that needs to be available to enable an identification. For example, to identify a person only a few molecules of DNA may be required, but a significant area would normally be necessary to allow identification by facial recognition.

If you see only a part of someone's face you may be unsure whether it is who you think it is. As you can see more you become more confident in the identification, until you are sure that it is the person you thought it was. They do not look exactly as you saw them the last time; perhaps they have shaved; their hair is different; they have glasses; they're a little fatter or thinner; yet you are sure that your identification is correct. The closer you look, the less that they will resemble the version of the person you are using as a reference to compare them against. If you saw them only a month ago, and look at the surface of their skin you will find that the cells of the skin are not the same ones that were there a month ago. Their hair is longer, their biochemistry is subtly different. Yet you are sure that this is the same person.

Consider a hair. If I remove a hair from a person's head and cut it in two then if I look at the two pieces with the naked eye they may look identical. I would say that they are the same; a match. This 'match' may even hold when I look at them under a low power microscope. But at some level of detail, it may even be the chemistry of the parts of the hair, I will find a difference; they will no longer match.

How close does a match need to be before we say it's a match? How many differences do you need to come to a conclusion of no match? It is an issue with all evidence based on marks and impressions, or anything where a 'match' is declared. Did the analyst not look close enough to find a difference, or too close to see a match?

The principles underlying the *scientific* use of marks and impressions are no different from any scientific comparison and matching exercise. Whether the *forensic* application of these satisfies those criteria may depend on the history, the practice, the courts, and the practitioners involved in the discipline.

This is a time of increasing stringency in the requirements of experts to establish the reliability of the techniques that they use as well as their authority in the use of those. Many systems have been and are being developed that aim to assist the court in assessing such claims. However, most of these have been by a group of experts in the same field forming themselves into some sort of group and deciding for themselves whether

it is expertise, and who they will register or endorse. External validation should be a feature of any such system.

Most professional codes of practice for forensic scientists demand that the scientist is an impartial participant in the legal process.<sup>19</sup> Unfortunately, while science may be impartial in a very restricted sense, it would appear from a considerable body of research that scientists are not. “Forensic scientists have not progressed beyond trying to will the problem [of bias] away by directing themselves not to allow these influences to affect their judgement”<sup>20</sup>

Notice that there is no suggestion here of dishonesty, merely a lack of awareness of the effect of bias.

### III. DNA: A CASE STUDY

Some of the problems emanating from the supposedly objective measurement of DNA profiles can be illustrated by a case study. Insofar as DNA profiling is concerned, the Forensic Process model is applied as:

- (1) Analysis—extraction, amplification, and electrophoresis using the SGM+ kit
- (2) Interpretation—What alleles are present?
- (3) Evaluation—How many contributors are there?

#### A. ANALYSIS

In standard SGM+ genotyping, a known quantity of DNA is subjected to the analytical process. Polymerase Chain Reaction (PCR) is the method used to multiply the number of DNA molecules at the relevant loci to an amount that can be detected by the equipment. This multiplication is called amplification. Different alleles have different lengths of DNA.

Each cycle of PCR approximately doubles the amount of DNA at the relevant loci, producing roughly  $2^n$  copies where  $n$  is the number of repetitions or “cycles.” To separate the different lengths of DNA, the molecular equivalent of a sieve is used. The different sized DNA molecules are detected by a laser that sends a signal to be processed by computer. A chemical trick applied during the amplification process causes the alleles to glow different colors in the laser light and these are reproduced on the densitometric scan (how dense the bands or rungs of the ladder are). This makes it easy to see the different alleles as peaks on a graph. The graph is called an electrophoretogram (epg). Creating the

---

19. See, e.g., Council for the Registration of Forensic Practitioners, Code of Conduct, <http://www.crfp.org.uk/standards/setting/code/code.htm> (last visited Apr. 20, 2008) (“Recognise that your overriding duty is to the court and to the administration of justice: it is your duty to present your findings and evidence, whether written or oral, in a fair and impartial manner.”)

20. Saks, *supra* note 7, at 77–90.

epg is a computer-controlled mathematical operation.

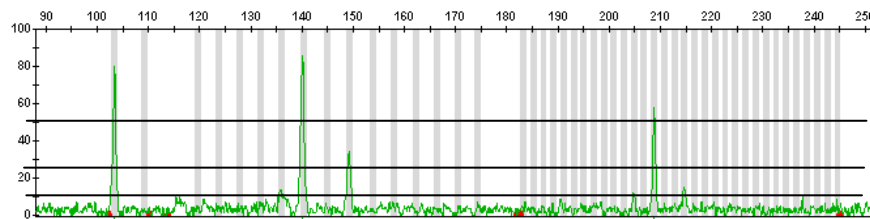
Under ideal circumstances, all of the alleles in a sample will be observed in the epg. When an allele is not observed, the resultant profile is referred to as a “partial” profile. The terms partial and full when applied to profiles are relative terms dependent on the alleles that should be found. A full profile using one type of kit may assess 16 loci, whereas another kit may only be designed to assess 10. A full profile in the latter would only be a partial profile in the former assuming that all of the alleles in the latter were also assessed by the former.

The illustrative case was received by the Forensic Institute in 2007. A profile had been obtained from a surface. It was intended to prosecute person A with a crime that would have resulted in a minimum jail term of five years.

#### B. INTERPRETATION

One part of the epg is shown in Figure I:

FIGURE I: PART OF ELECTROPHORETOGRAM WITH PEAK HEIGHT THRESHOLDS MARKED AT 50, 25, AND 10 RFU'S.



The epg shows molecular size along the x-axis and relative fluorescence units (RFU's) on the y-axis. The locations of known alleles are marked by the grey verticals (known as “bins”). An allele is declared when a peak is located in a bin. The decision as to what is or is not a peak is made using what is known as a peak height threshold. The threshold is the minimum number of RFU's that a peak has to attain before it is considered a ‘true’ peak.

Observation of figure I shows that the baseline is not even. This is, in scientific parlance, noise. The analyst must decide which peaks are noise and which are a signal caused by the presence of allelic DNA. Despite the number of years that profiling such as this has been performed, there is as yet no widely adopted objective method of determining what is signal and what is noise. Gilder et al., for example, have suggested statistical methods similar to those used by analytical chemists who have been faced with similar decisions for many years.<sup>21</sup>

21. Jason R. Gilder et al., *Run-Specific Limits of Detection and Quantitation for STR-based DNA Testing*, 52 J. FORENSIC SCIS. 97, 97 (2007).

The choice of peak height threshold has a significant effect on the number of alleles that are identified in this profile. Table I sets out all of the allelic designations at peak height thresholds of 50, 25, 15, and 10 RFU's. Fifty RFU is a common starting place for analysts to place the peak height threshold; they can then move it apparently according to taste!

If interpretation is the decision as to how many peaks are in a profile it is not difficult to see that there is considerable scope for different analysts to arrive at different conclusions.

The 50, 25, 15, and 10, thresholds result in the finding of 5, 13, 16, and 21 alleles respectively (ignoring the amelogenin, or sex, locus which has an X).

The number of alleles at a locus is the most obvious parameter used to determine the minimum number of potential contributors. Each person has a maximum of two alleles at any locus, one from each parent. When the allele received from each parent is the same the individual is homozygous for the alleles at that locus. When the alleles from each parent are different the individual is heterozygous at that locus. Each allele should have the same amount of DNA and so produce a peak in the epg approximately the same size as its partner allele; a 1:1 ratio. This does not always happen. Most analysts consider that two peaks can be considered as originating from a heterozygote if the smaller peak is no less than about 60% of the height of the larger peak.<sup>22</sup> There is again no set limit for this, and the relationship breaks down at very low amounts of DNA when the peak height imbalance can be any value between 0% and 100%.

The absence of alleles where they should be is termed allelic dropout. For example, at 25 RFU there are no alleles at all at the FGA locus. Only when an entire locus has dropped out, or the expected profile is known can dropout be unambiguously demonstrated, otherwise it is an explanation of an observed effect.

In this case, the simplest interpretation of the 50, 25, and 15 RFU profiles obtained is a single source as there are no more than two alleles at any locus.

The 10 RFU profile (this is a very low threshold) indicates a mixture of at least two individuals because three alleles are found at each of D3 and D21.

---

22. See generally T.M. Clayton et al., *Analysis and Interpretation of Mixed Forensic Stains Using DNA STR Profiling*, 91 *FORENSIC SCI. INT'L* 55 (1998); Carl Ladd et al., *Interpretation of Complex Forensic DNA Mixtures*, 42 *CROATIAN MED. J.* 244 (2001).

TABLE I: EFFECT OF LOWERING PEAK HEIGHT THRESHOLD

	AMEL	D3	vWA	D16	D2	D8	D21	D18	D19	THO1	FGA	INTERPRETATION & EVALUATION
PERSON A	X X	15 17	16 18	9 12	17 18	12 14	29 30	16 18	13 14	7 7	20 21	
PERSON B	X X	14 15	16 17	12 14	17 19	13 15	30 31.2	15 16	14 15	8 9.3	22 23	
THRESHOLD												
50 RFU	X		18			12	30		13	7		Single source, high RMP for A
25 RFU	X	15 17	16 18	12	17	12 14	30	18	13 14	7		Single source, medium RMP for A
15 RFU	X	15 17	16 18	12	17	12 14	30 31.2	18	13 14	7 9.3	23	Single source, not A or B
10 RFU	X	14 15 17	16 18	9 12	17 18	12 14	29 30 31.2	15 18	13 14	7 9.3	23	Mixture, A or B cannot be excluded

## C. EVALUATION

The summary of the evaluation of these profiles is in Table 1.

At 50 RFU the profile matches person A with a fairly high random match probability (i.e., the probability that the DNA came from someone else; poor evidential value). If the 50 RFU profile is from a single source, then person B is excluded as the source. Even though they match at four out of five alleles, they have no 18 allele at the vWA locus. At 25 RFU the profile also matches person A with a lower random match probability (i.e. higher evidential value). Dropout has certainly occurred in both of these results as entire loci are missing from the profiles. At those loci showing at least a single allele it is only by reference to a known profile, such as person A or person B, can dropout be said to occur. Furthermore, it can be proposed that these profiles are a mixture of A and B, not a single source, which has been subject to considerable dropout. This is 'consistent with' the observation.

Interesting things begin to happen at 15 RFU. This is also apparently a single source profile using the number of alleles. However, if this is so, then the profile could NOT have originated from A or B; it could be a single source, the unknown person C. If A is the accused, then this leaves the prosecution with a difficulty in that the 25 RFU profile could now be:

- (1) Person C (not A)
- (2) Person A and another
- (3) Person B and another
- (4) Two people with unknown profiles capable of producing the observed result.

Clearly it is not possible to establish from the profiles alone which of these is true.

Proponents of the Bayesian approach would have to concede that the most likely explanation for the observation at 15 RFU in this case is also the simplest: this is a single source profile from an unknown person who is not A.

Lowering the peak height threshold to 10 RFU, admittedly an unusually low threshold, produces yet further possibilities. There are two loci that show three alleles, indicative of a mixture of at least two people.

The possibilities are now a:

- (1) Mixture of A and another (could be B, C, or another)
- (2) Mixture of B and another (could be A, C, or another)
- (3) Mixture of C and another (could be A, B, or another)
- (4) Mixture of two or more unknowns.

The phrasing used in reports, at least in the UK, would be that A, “cannot be excluded as a potential contributor.” The court is not told how many other people, “cannot be excluded.”

In the actual case in question, the prosecution scientist set the peak height threshold at 25 RFU, the threshold offering the best evidence against A. No explanation was offered why this was the chosen threshold.

When dropout occurs it is essential that great caution is used in the interpretation and evaluation of profiles. Worryingly, it is possible to obtain what would normally be interpreted as a partial or full single source profile from a mixture. The example in Table 2 is based on another case involving three unrelated people. The ‘mix’ profile is derived from counting only those alleles that occur at least twice in the profiles of the contributors. If the limit of detection (sensitivity) of DNA used to analyze this mixture requires at least a ‘double dose’ of two alleles to produce a signal, or the amount of DNA in the sample is reduced for any reason, then it is possible that the resultant profile will have the appearance of a full or partial single source profile identical or very similar to the ‘mix.’

Two obvious consequential errors arise from this profile. First, it was a mixture that has been identified as most likely a single source. Second, the resultant profile does not belong to any of the contributors.

TABLE II: A MISLEADING MIXTURE

PERSON	D3	VWA	D16	D2	D8	D21	D18	D19	THO1	FGA
X	17	16	11	24	12	30	13	15	9	18
	17	17	12	25	15	30.2	15	15	9.3	22
Y	13	15	11	17	13	29	15	13	9.3	22
	18	18	12	17	16	30	16	15	9.3	24
Z	14	17	11	24	13	28	16	13	6	22
	16	17	13	24	16	29	17	14	6	22
Mix	17	17	11	17	13	29	15	13	6	22
			12	24	16	30	16	15	9.3	22

Having established how the occurrence of dropout can lead to gross errors in the evaluation of the number of contributors, and the contributors' profiles, we can return to the example case. It has been demonstrated that, even accepting the prosecution's interpretation that a peak height threshold of 25 RFU is appropriate and the number of alleles is 13, it is entirely possible that this is neither the profile of the source of the DNA, nor the correct number of contributors.

It could be argued that there is only a very small probability that such an error will produce a profile that matches a suspect by chance. Mixtures produce specific problems in that once alleles from different sources are mixed it is impossible to know which allele was associated with which source. The major exception to this is the finding of what is known as a major-minor mix; a mixture with a large amount of DNA from one person and a very much smaller amount from another. Again, there are no experimental studies to show at what level it is safe to separate the major and minor profile. How does one interpret a mixture which shows a clear major-minor separation except at a single locus? Two?

In mixtures without such an easy separation it is impossible to know the actual contributors. All that can be done is to reduce the population to those who *could have* contributed. Dropout again complicates this in that, if dropout has occurred, it is impossible to exclude *anyone* as a potential contributor. Combining this with the fact that dropout is frequently only invoked when comparing a profile with a *known* profile, and therefore this is rather begging the question with crime-stains, dropout should be considered to render mixture interpretation almost impossible.

By way of illustration, if one locus has four alleles, A, B, C, and D, and originated from only two people, the contributors could have genotypes, AB and CD, AC and BD, or AD and BC. Across ten loci, with two alleles per contributor, there are over one million ways to interpret a mixture of two contributors. Put a different way, a mixture of DNA from two people could produce a million possible profiles which could have caused it. It is frequently not obvious how a scientist derives

the opinion that favors one of these options over any of the others. At the very least, the possibility of other interpretations should feature in reports but, sadly, do not. In casework, we frequently come across DNA reports that all but ignore any other possible interpretation than the one that provides the best probative value against the accused; the case example illustrates the point. The most obvious explanation is that the scientist has been influenced by knowledge of the profiles of those involved, whether it is the complainer or the suspect.

This type of bias has been the subject of a meeting in Washington in 2007 at which it was concluded, “forensic DNA analysts often must resolve ambiguities, particularly when interpreting difficult evidence samples such as those that contain mixtures of DNA from two or more individuals, degraded or inhibited DNA, or limited quantities of DNA template. . . . [they] are commonly aware of submitted reference profiles when interpreting DNA test results, creating the opportunity for a confirmatory bias, despite the best intentions of the analyst.”<sup>23</sup>

The solution suggested was that the analyst should have no knowledge of a suspect’s profile until they had completed the interpretation (i.e., number of alleles, number of contributors, possible profiles of contributors) before having knowledge of the suspect’s profile. This process was termed sequential unmasking.<sup>24</sup>

As more mixtures are recovered with the increasing sensitivity of testing, and the number of profiles submitted to databases increases, the probability of chance matches to a particular profile increase. This should affect the probative value of the evidence yet no attempt seems to be made to incorporate this in scientific reports.

#### CONCLUSION

The influence of DNA not only in criminal investigation, but on the whole practice of forensic science, cannot be understated. Many of the features that have made DNA evidence so robust (e.g., laboratory validation, population databases, statistical evaluation, input from the wider scientific community) have created a scientific standard for practices within other areas of expertise associated with producing evidence of individualization. Some have taken this challenge up with more enthusiasm than others, and are suffering for it. Only the protection of some courts has prevented some expertise associated with marks and impressions from being sent back to the drawing board.

The better definition of interpretation and evaluation within the Forensic Process has been clarified here to facilitate sensible discussion of the separate but linked processes involved in all scientific assessment

---

23. Krane et al., *supra* note 2.

24. *Id.*

---

---

of evidence. In particular, this separation makes it easier to implement, practically and theoretically, the sequential unmasking process suggested by Krane et al. in the analysis of DNA.

Although many of the technical difficulties in producing DNA profiles have been overcome, the correct approach to interpretation and evaluation of DNA profiles is still very much a matter for debate. Some of these have been discussed herein. Many of the arguments presented here are deliberately incomplete, for which I make no apology. My purpose is to stimulate thought and debate about concepts that appear to have been taken for granted. Some of the material is new, some will be familiar to those in the field.

In questioning scientists how they know that their interpretation of profiles is the correct one, we are frequently told that it is their 'case experience' that validates the opinion. Returning to the difficulty of working from observed effect to cause, it is entirely unclear how a forensic scientist can use such uncontrolled and unsatisfactory information as that associated with criminal casework to be able to say with any confidence at all that a particular type of profile is 'caused' by the specific circumstance of the case is a cause of great concern. Only data from properly controlled experimental work can produce the confidence and the expertise to support such opinion. "Clearly we learn from experience but it is the way that we learn that distinguishes the scientific from the unscientific."<sup>25</sup>

---

25. I.W. Evett, *Expert Evidence and Forensic Misconceptions of the Nature of Exact Science*, 36 SCIENCE & JUSTICE 118, 122 (1996).