"Testing and challenging DNA evidence to avoid miscarriages of justice"

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Introduction

Used properly, DNA evidence can enhance a criminal investigation. Used properly, DNA evidence can exonerate the innocent. At trial DNA evidence can help convict the guilty. Applied improperly, DNA evidence can lead to significant miscarriages of justice. Developments in both technology and statistical systems, using the advanced computation powers now available, offer opportunities for using DNA in court for noble aims, but they also increase the risk of miscarriages of justice.

I was asked for my thoughts on the most effective way of testing DNA experts, and addressing and avoiding jury misconceptions about DNA evidence, including the so called 'CSI effect.'[2] The aim of this presentation is to alert you to some areas where DNA evidence at trial can lead to miscarriages of justice and help you to help the court avoid such miscarriages.

I embrace that challenge, but I do so with three important qualifications:

> First: In over 10 years as a trial judge of the NSW District Court, I have never had a trial where the admissibility or reliability of the prosecution's DNA evidence was challenged. What challenges have occurred went only to the relevance of the DNA evidence to the facts in issue, and such challenges too have been rare.
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> Secondly: It is a truth, universally acknowledged, that a trial lawyer, on elevation to the bench, becomes a much better advocate and cross-examiner than when they were practicing and actually had to cross-examine.
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> Thirdly, no two trials are the same – it would be absurd to suggest a template for cross-examination – at best I offer some hints about preparation for trial.

[1] The opinions expressed in this paper are my own, and not those of the NSW District Court. If cited back to me, I reserve the right to say of the paper – "Oh Haesler - what would he know!"

[2] In 2007 CSI was the world's most popular TV show with 84 million viewers; *New York Post* 17 June 2008; cited in J. Goodman-Delahunty & L Hewson *Improving jury understanding and use of expert evidence* Australian Institute of Criminology Technical Report 37 *at p 5.*

I urge those of you who need immediate instruction on DNA to go to Annexure A and the publications listed at the end of this paper- Annexure D. I'm pleased to say, the standard NSW Forensic and Analytical Science Service[3] (FASS) annexure to DNA court reports provides an excellent overview. The forensic science community can take the credit for the 'gold standard' appellation often given to DNA evidence, but, and it's an important but, every forensic scientist and legal practitioner must ensure that the over enthusiastic use, or misapplication of, DNA evidence does not result in miscarriages of justice and the consequent devaluation of this important investigative and evidentiary tool.

Nothing set out here is definitive. I hope some of the suggestions will help you focus on the relevance of any proposed DNA evidence to the facts in issue at trial. I hope some of the suggestions will help you test the DNA evidence presented by the prosecution. DNA evidence is too broad a topic for a short presentation.[4] The art of cross-examination is similarly vast. Mastering both however requires only one simple lesson be learnt - prepare!

The Judge's role in preventing miscarriages of justice

Trial judges have only a limited role in preventing miscarriages from occurring. Judges are rarely aware of the tactics or plans of counsel. Judges do not control the way evidence is prepared, presented, proved and tested; that is for the parties.

The judge's role as a 'gate-keeper' of the evidence is determined by whether or not objection is taken to evidence and the proper application the *Evidence Act* 1995, "according to its terms."[5] A judge is required to ensure that only relevant and admissible evidence goes to the trier of fact.[6] Judges must exclude evidence where the potential for unfairness exceeds the impugned evidence's probative value[7] – but only if objection is taken.

Defence counsel have considerable responsibility here; absent a successful incompetence of counsel ground, the Court of Criminal Appeal (CCA) will hold an applicant for leave to appeal bound by the decisions of their lawyers.[8]

[3] Formerly, the Division of Analytical Laboratories (DAL).
[4] My cross-examination starting point has always been Younger I., *The Advocate's Deskbook: The Essentials of Trying A Case*, Prentice Hall Law & Business, 1989
[5] *Adam v The Queen* (2001) 207 CLR 96; [35] & [36].
[6] If DNA evidence is not capable of advancing a prosecution case it not relevant and should not be admitted: *R v Scott* [2020] NSWCCA 81.
[7] See *Volpe v R* [2020] VCA 268; *Fennell v The Queen* (2019) 93 ALJR 1219; [2019] HCA 37.
[8] A difficult task indeed! See *Nudd v R* [2006] HCA 9; (2005) 225 ALR 161; *Hanna v R* [2017] NSWCCA 168 and most recently *Xie v R* [2021] NSWCCA 1.

The opinion rule applies to all trials: “Evidence of an opinion is not admissible to prove the existence of a fact about the existence of which the opinion was expressed.”[9] Evidence about DNA and its impact on a trial will however come from an expert witness giving their opinion, as an exception to that rule.

The expert must, however, only give an opinion if they have specialised knowledge based on their training, study or experience. And, their opinion must be wholly or substantially based on that knowledge.[10] The test is a broad one, and contains no requirement the opinion, or the material it is based on, be reliable: “The focus of attention must be on the words “specialised knowledge”, not on the introduction of an extraneous idea such as “reliability.””[11] A separate presentation would be required to fully explore the issues relating to the admissibility of opinion evidence and the criticism of this approach.[12]

An example comes from Xie v R.[13] The focus of the appeal was on one expert whose techniques and reports about DNA found in a stain on the accused’s garage floor were said to be dodgy. At trial other DNA experts were (over objection) allowed to give evidence about how in their experience the profile derived from the garage floor stain showed a high level of consistency with mixed stains found at the crime scene itself.[14] The opinions the stains were similar was not supported by any statistical comparison or analysis:

> Q. You just - I mean, really this is your evidence: "I've looked at it; I'm an expert and I reckon they are relatively similar"; that's it, isn't it?
>
> A. I would probably summarise it a little differently. I would say that what I am looking at are two objective pieces of scientific data, each of which are highly complex with a high amount of information. To generate any of those complex pieces of data can only occur under a certain limited amount of circumstances.”[15]

[9] The opinion rule -s 76 *Evidence Act*
[10] s 79 *Evidence Act; Honeysett v The Queen* (2014) 253 CLR 122; [2014] HCA 29.
[11] See *Tang v R* [2006] NSWCCA 167 at [137] and *Tuite v R* (2016) 49 VR 196: [2015] VSCA 148.
[12] See Edmund G., “*Forensic science in criminal courts: the latest scientific insights”* (2016); “*Regulating Forensic Science and Medicine at Trial: It’s Time for a Wall, a Gate and some Gate-Keeping*” (2020). A number of papers on the topic by Judges Yehia, Becket, and me can be found on the Public Defender’s site.
[13] *Xie v R* [2021] NSWCCA 1.
[14] *R v Xie No4* [2014] NSWSC 500, Johnson J at [379]-[380].
[15] *Ibid* at [382].

As presently applied s 79 *Evidence Act* allows such evidence. But if a scientific reliability standard were applied the evidence's admissibility would be questionable.[16]

A trial judge's other role is to ensure the jury appreciates the significance of each portion of the evidence presented at trial and the positions taken by each party. Miscarriages occur when judge's get such directions wrong.

Again, defence counsel has considerable responsibility here; if corrections are not sought to judicial jury directions an appeal ground may not be considered.[17] For good or ill, it is presumed that proper judicial direction can ameliorate the unfair misuse of otherwise admissible evidence.[18]

Preparing for trial

While no trial is the same as another there are some 'typical' examples. A typical case involves DNA results that are relatively unambiguous. An expert in such a case can give evidence of the high probability of a DNA profile match, between either:

a. A DNA profile obtained from evidence at the scene of a crime (such as a break and enter) and a profile from the defendant after a buccal swab has been taken and their profile recovered from it.[19]

   or

b. A mixed DNA profile obtained after a complainant in a sexual assault case is medically examined and the DNA profile of a defendant (and the complainant).

A DNA 'match' between profiles with a corresponding high statistical probability[20] gives rise to 3 possible explanations:

1. The person whose profile is matched is the source of the DNA found.

[16] The England and Wales Criminal Procedure Rules and the Criminal Practice Direction stipulate that Expert evidence is admissible only if the court is satisfied that there is a sufficiently reliable scientific basis for the evidence to be admitted.
[17] Rule 4 *Criminal Appeal Rules.*
[18] *The Queen v Glennon* (1992) 173 CLR 592; *DAO v R* [2011] NSWCCA 63.
[19] Often a profile match has already been made after a search of the offender's DNA data base.
[20] The NSW FASS put a conservative cut off of 100 billion when reporting and final match statistic or Likelihood Ratio (LR). Often the numbers generated are much, much, higher. A LR of 100 billion is said to provide "extremely strong support" for one proposition versus the other.

2. Someone with the same profile as the person under suspicion is the source of the DNA found. With modern DNA technology this option may be statistically highly unlikely, unless the person has an identical twin; or,
3. The match is a false positive due to a contamination error.[21]

Not all crimes scene samples give clear and unambiguous DNA profiles. Accordingly, a reported DNA profile "match" from a complex sample may not have the same probative value as that derived from a simple profile. Complexity arises where the DNA recovered came from a variety of sources – for example; while there may be blood on a corpse there may also be skin cells and semen. Complexity arises where less than optimal quantities of DNA were recovered.

Less than optimal quantities are recovered; if not very much the DNA was left at a scene because the cells were left from a touch, or, if they were transferred from another location or source, or, if they have been degraded by exposure to the elements or other environmental factors, such as cleaning products. It is rare in most such cases to determine the type of cell from which the DNA came.

Complex DNA samples can be replete with ambiguity, as can be any reported matches derived from them. If only sub-optimal amounts of DNA are recovered ('trace' DNA)[22] the sensitivity of modern testing techniques can increase the risk of contamination at all stages of the investigation process.[23] New and enhanced anti contamination features have be put in place in all accredited DNA labs, protective clothing can be worn and protocols adhered to; but these protections often are not as stringent at the point of collection, particularly if that point is quite literally a 'crime scene.' Even where an optimal quantity[24] of DNA is recovered if there are multiple sources and or contributors, or relatives in the mix, the techniques used to analyse the results often lack the apparent objectivity that gives DNA evidence about simpler crimes scene samples its probative force.

Often DNA results generated from complex samples give profiles, or partial profiles, that fall below the minimum standard peak heights mandated by laboratories[25] and their verification

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[21] *Forensic DNA analysis: A Primer for Courts* (2017), The Royal Society of Edinburgh and the UK Judicial College; The University of Dundee at [2.4]**;** Gill P, *Misleading DNA Evidence: Reasons for miscarriages of justice*, Elsivier, 2014) p 36; National Research Council, *Strengthening Forensic Science in the United States: A path forward* The National Academies Press 2009 (NRC Report) 1996, p. 88.

[22] These are very small amounts - a few cells, involving qualities measured in picograms; a pictogram "PG' is 1×10^{-12} of a gram.

[23] When testing methods are boosted outside the standard parameters used on such samples, the terms 'trace' or "Low Copy Number (LCN)" are used.

[24] 50 nanograms - a nanogram is 1×10^{-9} of a gram.

[25] See Annexure A.

agencies.[26] Questions can arise when different terms and terminologies are used, or, where different statistical models and associated software are used to give statistical weight to the evidence. Questions can arise about the point at which attempts to interpret such complex samples should even be made; let alone admitted as evidence at trial.[27] It is critical that the results of any DNA analysis be reported in a fair and balanced way?[28]

Miscarriages of justice occur when overzealous experts push the boundaries and fail to apply (or fail to reveal for commercial reasons) scientific method. Scientific method requires:

1. Belief in a hypothesis;
2. Testing the hypothesis by experiment;
3. Reviewing the results to ensure they are reproducible and data can be verified.

The apparent certainty of forensic DNA analysis, and the statistics that often support the weight of DNA profile "matches", often give rise to an "aura of certainty" that DNA evidence at trial does not deserve. That 'aura of certainty' is reflected in judicial statements that endorse the proposition that a high statistical probability of a profile match is evidence of identity.[29] A defence lawyer must understand the limitations and dangers that flow from presumptions of certainty that are not justified. As the UK House of Lords has noted; "Without empirical data about transfer and persistence of DNA interpretations of results by experts must remain subjective."[30]

The defence lawyer must, by carefully considered objection and thorough questioning, convey to both jury and judge that DNA analysis alone can rarely give such certainty, let alone remove all reasonable doubt. A defence lawyer must advance credible reasons why alternative explanations for any prosecution assertions about must be considered.

Despite occasional judicial comments to the contrary[31] I remain staunch; expert opinions about DNA results presented at trial, cannot, in the absence of other evidence, say with certainty:

1. Whose DNA it is!

[26] In Australia, the National Association of Testing Authorities (NATA).
[27] Gill (2014) p 36; And, in my opinion the TruleAllele evidence in Xie- an opinion not shared by the CCA who state it was "clearly" explained to the jury *Xie* CCA NSWCA 1 at [121].
[28] *Forensic DNA analysis: A Primer for Courts* (2017), The Royal Society of Edinburgh and the UK Judicial College; The University of Dundee.
[29] See *Xie v R* CCA at [317] & [318].
[30] Science and Technology Select Committee. Forensic Science and the Criminal Justice system: A blue print for change, UK House of Lords; 2019.
[31] Ibid.

2. What bodily fluid the DNA originated from!
3. How the DNA got there!

Further, even if the results of the analysis have been reported by the experts in a fair and balanced way:

4. Don't presume the results will be understood by the judge or jury in a fair and balanced way.[32]

Accordingly, a DNA profile match alone should never be used to prove an accused's involvement in a crime.[33]

So take care! Uncertainties arise because in most cases:

1. The type of cell from which the DNA sample was obtained can't be identified;[34]
2. It can't be said when the cells were deposited;
3. It can't be said where the cells were first deposited;
4. A mixture of DNA is to be expected;
5. Assessing how many contributors there are mixture is an inexact science;
6. Assessing the proportions from each contributor to the mixture is an inexact science;
7. A contributor to the sample may be masked by other profiles similar to theirs.
8. There may be close relatives in the mix.

Lawyers must adapt to new technology but we must not do so uncritically. Using the more typical binary model for DNA identification all possible profiles in the crime scene sample were first identified before any comparison with the profiles from any reference samples or data bases was attempted.

New techniques, introduced from about 2013, use what is called a continuous probability model to analyse the results generated by DNA testing machines now used. The new techniques are more often used where mixed or degraded crimes scene sample samples have been recovered. Their modelling (deconvolution) determines the probability of all the different genotypes (a set of allele pairs) possible at each loci tested. This can be a huge number. A distribution is then made; from most to least likely. A reference sample can then

[32] *Volpe v R* at [70], *Volpe*, a "shoe print" case is instructive about how s137 can be used to exclude evidence about similarity and the inability of directions to 'cure' the apparent prejudice of expert evidence of a match.
[33] Gill (2014) Page 70; *Forensic DNA analysis: A Primer for Courts* (2017) at 3.1.2. but note *Xie* v R ibid
[34] Although in many cases the source may seem so obvious an educated guess can be made see page 14 below. As the NSW FASS Report Annexure notes even where a differential extraction is performed on sample where spermatozoa and no sperm cells the attempt to separate them may not be successful and mixed DNA profiles can still result.

be compared to the genotypes in the distribution and an LR generated which reflects the fit. The higher the LR, the better the overall fit of the reference sample to the genotypes with the higher probabilities generated by the modelling.

It is only when the reference sample is entered into the model's program that the most probable locus said to "best fit" or match the reference sample is isolated. Such models promise extraordinary results. In *Xie v R* the basis for the science and calculations of probabilities involved in a continuous probability model and "the probability distribution of allele pairs" that resulted were said by the CCA to be "clearly" explicable to judges and jurors.[35] I have my doubts.[36]

Getting the basics right

You could go back to my 2010 papers,[37] but the standard NSW Forensic Science Service annexure to DNA court reports is a good place to start. So too are the Primers put out by The Royal Society of Edinburgh, the UK Judicial College and The Royal Statistical Society. Annexure A sets out some of basic DNA science. Annexure D sets out some extra research resources.

Why Miscarriages Occur

Miscarriages of justices occur when the boundaries of knowledge or advocacy are overstepped and it is implied that evidence has more meaning or relevance than it really does. As humans we are easily seduced by coincidence and tend to down play the role of chance; we are over ready to interpret coincidence as cause and effect. Miscarriages of justice are often associated with a "cascade of errors"[38] or false assumptions. Peter Gill describes four:[39]

1. The association fallacy;
2. The hidden perpetrator effect;
3. The naive investigator effect; and

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[35] At [121].
[36] See Annexure A.
[37] Andrew Haesler SC, "Dealing with DNA in Court: it's Use and Misuse", *Judicial Review* (2008), Vol 8 No. 1; And on the Public Defenders webpage
https://www.publicdefenders.nsw.gov.au/Pages/public_defenders_research/Papers%20by%20Public%20Defenders/public_defenders_papers_pd.aspx
DNA in Court: its Use and Misuse, by Andrew Haesler SC (revised - Sept 2008)
DNA in the Local Court - the CSI Effect, by Andrew Haesler SC (2010).
[38] Gill P. (2014).
[39] Gill P, (2014).

4. The swamping effect.

Each provides a wealth of topics on which to cross-examine a DNA expert and crime scene officer.

The association fallacy

A crime scene sample may come from a number of sources. The nail on a bloodied finger may also have skin cells under it. [40] A Sexual Assault Investigation Kit (SAIK) sample may have semen, blood and skin cells within it. If a presumptive test for blood comes back positive or semen is seen after a microscopic view of a slide it may be wrongly assumed that any DNA recovered and extracted for analysis has the same source when the evidence could never allow for such discrimination.

In *Jama's case*,[41] cells linked to sperm cells with a DNA profile matching Jama's with a very high probability were found on a slide in the complainant's SAIK.[42] The finding of DNA led to two assumptions; that the complainant had been sexually assaulted and that her assailant was Jama. Both were found to be palpably false. After Jama had spent months in gaol it was accepted that the complainant had not been raped at all. Jama's DNA came to be associated with the crime scene sample from the SAIK, as part of the investigation because of a contamination event whose exact nature was never discovered. But his DNA was associated with another earlier investigation that did not result in charges.

In *Scott's case*,[43] the complainant had had sex with her boyfriend, before being sexual assaulted by an unknown man. A DNA profile matching Scott's' to a very high probability was found in the crime scene samples. As semen was identified in the crime scene sample, the DNA found was presumed to come from Scott's semen, and he was charged and remanded in custody. Scott was innocent. His DNA was in the sample analysed but It was not his semen. A sample of his skin cells had been taken in another town for a quite different and minor offence, but they had contaminated the victim's crime scene evidence. It turned out a lab tray from a robotic testing unit[44] had been inadvertently reused.

The hidden perpetrator effect

The *Scott case* also provides an example of the hidden perpetrator effect. Once his profile

[40] Armstrong v R [2013] NSWCCA 113.
[41] *R v Jama* (unrep, VCA, 7 Dec 2009); Vincent F.H.R., *Inquiry into the circumstances that led to the conviction of Mr Farah Jama.* Melbourne, Department of Justice, 2010.
[42] Sexual Assault Identification Kit (SAIK).
[43] Gill P. (2014) at 102.
[44] The NSW and Queensland DNA labs don't process most crime scene samples rather the samples for testing arrive at the lab in RATS- Robot Acceptable Tubes. The exception is a SAIK taken after a sexual assault complaint. NSW FASS will process SAIKs.

had been identified the statistics giving weight to the "match" were so high that no attempt was made to carefully examine the actual crime scene sample to see if another person's profile could be detected in it.

The naïve investigator

The naïve investigator (or naïve prosecutor/judge/jury) effect, flows from the presumption that once DNA is found, any "match" with a high statistical probability will provide evidence of identity and guilt. This in turn leads to exculpatory evidence being either ignored or not being sought. Once a known person's DNA profile is matched to the crime scene sample, he or she becomes the focus of the investigation. The complete absence of other evidence (or quite significant exculpatory evidence) is subsequently is ignored. In *Scott's case,* this was the fact he had never been anywhere near the town where the offence was committed. As a consequence, Scott spent months on remand and the true offender escaped detection.

The naïve investigator effect also provides an example of "confirmation bias" – where the apparent objectivity of the 'profile match" leads investigators to ignore exculpatory evidence. Confirmation bias can lead to failures in applying scientific method. This is a failure that is not be readily protected against by the test in s 79 *Evidence Act*. Care needs to be taken that an expert's answers are not based on mere intuition but rather on experiment and testing.[45]

Another example is The Phantom of Heilbronn,[46] this mystery arose because the possibility of contamination was ignored because the crime scene's DNA analysis revealed a clear individual profile.[47] Following the murder of a German police officer, a massive hunt was conducted across Europe for a woman whose DNA profile was found at the murder scene. The profile was also found at over 30 of other quite different crimes in a number of European countries. It was eventually discovered that the profile came from a factory worker who made the cotton swabs in the DNA collection kits!

The swamping effect

Evidence at trial is generally either direct or circumstantial. Jury decisions are meant to be reasonable, but Bayesian[48] or probabilistic reasoning is not required by them. The test of

[45] For examples see *Velevski v The Queen* [2002] HCA 4 – Another Haesler SC failure.
[46] https://en.wikipedia.org/wiki/Phantom_of_Heilbronn
http://content.time.com/time/world/article/0,8599,1888126,00.html
[47] Gill P. (2014) page 32 .
[48] See *Xie* [2021] at [149] "The theorem holds that the odds of a hypothesis given certain evidence (the "posterior odds") equals the odds of the hypothesis without that evidence (the "prior odds") multiplied by the ratio between the probability of that further evidence if the hypothesis is true and the probability of that further evidence if the hypothesis is not true (ie, the likelihood ratio) (see D Hodgson, "A Lawyer looks at

"beyond reasonable doubt" has no mathematical or statistical basis. There is no requirement that evidence or even a verdict must be justified to a scientific or statistical certainty. In fact, certainty is not required.

Juries (or judges as triers of fact) decide the practical issue of whether an element of an offence has been proved beyond reasonable doubt and ultimately whether or not to attribute legal responsibility for a crime to the accused. This is not an issue of philosophical or scientific proof. Where only one portion of the evidence is given a statistical weighting or the appearance of mathematical certainty, expert opinions of the likihood of, and thus strength of, that part of the evidence can overwhelm other evidence that is not so blessed with an expert opinion about its weight.

DNA Myths

A number of misconceptions or myths about DNA occupy the popular imagination. The popular imagination must be guarded against, but it can also be utilised by the defence to defeat good science and good evidence (not that I encourage that approach - I do not like "truthiness" in my court).

Most myths arrive because experts are not tested fully, or tested at all on whether their opinions are the result of conclusions reached by applying the scientific method to data. Common DNA 'myths' include:

1. Judges and juries will use their common sense when assessing expert evidence.
2. Big numbers provide proof of identity
3. Every contact leaves a trace/ Absence of evidence is evidence of absence.
4. We can identify the source of the DNA.
5. DNA experts have all the crime scene information; just like the actors CSI!
6. We can prove a case with DNA evidence - The CSI effect.

Judges and juries will use their common sense

Not all misconceptions can be cured by judicial direction. To the contrary, some are encouraged by them. In part, this is because we humans are inclined to intuitive decision making. Judges and both defence and prosecution lawyers still exhort a jury to use their

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Bayes Theorem" (2002) 76 ALJR 109 at 109 to 110; cited by Spigelman CJ in *R v Galli* [2001] NSWCCA 504; (2001) 127 A Crim R 493; "Galli" at [55]). The application of Bayes' Theorem by juries to non-statistical evidence or a combination of statistical and non-statistical evidence has been discussed but generally deprecated (Hodgson supra; *R v Denis Adams* [1996] 2 Cr App R 467; *R v Denis Adams (No 2)* [1998] 1 Cr App R 377)"

"common sense." Common sense tells some people the earth is flat, or that Donald J Trump was (or still is) a great President! The term "common-sense", is inherently vague and incapable of measure. Reviews of decisions that are said to be based on a "common sense" evaluation often show that a subjective value judgment was made. Rather than common sense deductions, I prefer rational decisions formed after the evaluation. And, an assessment of all proved or known facts and opinions based on proved facts, in the light of all the evidence at trial.

Big numbers provide proof of identity

A common misconception is that a DNA match establishes to very high, degrees of probability, that the source of the crime scene DNA is the person who committed the crime. Whereas, assuming that the jury are satisfied there is a link between the defendant profile and that in the crime scene sample, the most the DNA expert evidence can do is provide one piece in a circumstantial case.

Reliance on astronomical numbers can lead to such misconceptions. There are various ways of expressing the strength of DNA evidence in non-scientific terms. Some formulations are likely to have greater impact than others; when in fact all the figures do is provide statistical support for one proposition as opposed to another. [49] Put into words that can vary from no support to "extremely strong."[50]

While FASS encourage care and standardisation in the reporting of such statistics there is there is no uniform manner of expressing statistical DNA evidence.[51] The expert interpretation of the DNA evidence whether put as a LR, a frequency ratio, or as exclusion percentage, is exactly the same evidence: "As long as the content of the evidence does not vary."[52]

Problems arise where different reporting techniques are used in the same case. In NSW, the FASS, while it might generate match statistics in the trillions[53] or quintillions[54] has a reporting cut off limit of a hundred billion.[55] Where another system with different reporting technique is used in the same trial, such as TrueAllele®, which reports in the quintillions, the results may give greater than other system's results more apparent weight. "[P]robabilistic genotyping is

[49] As McClellan CJ at CL pointed out in *Aytugrul v R* [2010] NSWCCA 272 at [86]
[50] FASS Standard DNA Report Annexure, page 3
[51] *Xie* (2021) at [334].
[52] *Aytugrul* at [164] and [175] per Simpson J. The High Court later agreed with Justice Simpson: *Ayturul v The Queen* (2012) 247 CLR 170.
[53] 10^{12}
[54] 10^{18}
[55] 10^{11}

inherently different from and not directly comparable to binary interpretation. The weights of evidence that are generated by the two approaches are based on different assumptions, thresholds and formulae."[56]

Even to the most robust and cynical intellects the enormous figures generated give an appearance of certainty that may not be justified. That must not then be carried over into a conclusion that such high match statistics equate to proof of guilt.

Every contact leaves a trace/ Absence of evidence is evidence of absence

Testing is not absolute. Every contact does not leave a trace. A touch or a contact may not be picked up. While we all shed DNA some of us shed more or less DNA than others. It may depend on the environment or what we were doing at the time.

> *QUESTION:* What is the risk that the DNA was transferred to the crime scene sample from another place?
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> *ANSWER:* At each stage of transfer some DNA is lost. Each time you touch something, some of the foreign DNA from the crimes scene sample on your hand will come off onto that item - that's your secondary transfer. And there will be some loss of DNA from the amount originally deposited. At each stage you are losing a certain amount of DNA. With each additional handling it becomes less and less likely that we'll be able to detect a useful amount of DNA…although it does depend on how long you hold an item and the level of DNA deposited. Some people shed more DNA than others or some situations lead to more DNA being shed than others.
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> *QUESTION*: Shedders? Is there such a thing as a good shedder or a bad shedder? Is the more often you hold an item, the more chance there is that you leave some of your DNA behind? Is that right?
>
> *ANSWER*: That's correct, yes. If you hold an item for a lot longer and use it for a longer period, you're more likely to leave DNA than a very brief touch because more of your skin is in contact with that item and for longer. You have more chance to shed those cells from the top layer of your skin.

The physical environment where the crime scene stain was recovered cannot be ignored. As all biological material is inherently fragile; it will degrade.

[56] Scientific Working Group on DNA Analysis Methods (SWGDAM) USA- Guidelines for Validation of Probabilistic Genotyping Systems– FINAL APPROVED 06/15/2015. Available at: www.swgdam.org/publications

QUESTION: Is it the case that over time DNA will degrade?

ANSWER: DNA does degrade over time if it's subject to certain environmental factors, most specifically being sunlight, which contains UV which is detrimental to DNA, moisture exposure, or being rubbed away. These all end up with degraded DNA or removal of DNA.

QUESTION: In relation to the testing of DNA, are you able to determine during the course of testing whether the DNA has been degraded or not?

ANSWER: If we have a degraded sample, we will generally get what's termed a "partial profile", so you will see some aspects of DNA, but not others because the whole entire DNA strand is not intact… So you can mainly see that in the profile, but not entirely.

DNA at a crime scene can be removed or overwhelmed by other material. Biological material moves within an environment. Every transfer of biological material leaves some of it behind, but experiments cannot be duplicated and therefore cannot predict how much DNA will be lost during each transfer event.

QUESTION: If two different DNA profiles are detected, the one thing we can't do is to say that the DNA was actually lodged on the item at the same time…can we?

ANSWER: No we can't say that. I can't tell you how the DNA got there or whether multiple profiles were laid down together. It could be two separate events, where I could pick up a cup and then someone else could pick up the same cup, or we could both touch that cup at the same time. There is no way to determine which bit of DNA was deposited first, or how long either of the respective DNA samples had been present.

We can identify the source of the DNA

Tests for bodily fluids are generally presumed not to be definitive, so an assertion of an association between a crime scene sample and a body fluid can never be explicit. However, beware of asking the wrong question!

QUESTION: You don't get buckets of DNA do you? You deal with very tiny amounts of material, yes?

ANSWER: Oh, it depends on the case circumstances. I have had a case of two buckets of urine. But, yes - as a general situation -

JUDGE HAESLER: You asked, Mr 'Defence.'

DNA experts have all the crime scene information; just like the actors CSI!

With the exception of sexual assault cases is now rare for a NSW FASS DNA expert to be asked to analyse more than the electropeheragram (EPG) results.[57] The DNA is most often collected by crime scene examiners and sent to the labs. In NSW they use Robot Acceptable Tubes (RATs). The DNA experts then look at the results and use a computer program to generate statistical results. They don't play CSI.

In order to retain their objectively experts should if possible know nothing about the case under investigation. To bring in two more old TV shows; scientists and investigators may wish to or be asked to apply their techniques to a novel problem. Some are more than prepared to 'boldly go where no one has gone before," with the risk they will stray beyond the 'outer limits' of their expertise.

QUESTION: In relation to the DNA, my understanding, it may be wrong, is that it is an absolute necessity to consider the evidence you've been given in the context of the evidence as a whole. That must be right mustn't it?

ANSWER: As a scientist, I actually don't know the context of the evidence. We very rarely get information about that. Often all we get is the description of those samples and very limited case information. Say, for example, we know the charge, but we probably don't know the scenario of how things are alleged to have happened. I can only interpret the profiles as I see them in front of me. I don't really have any context as to the case as a whole, or any other information that's available…We only get the tubes!

QUESTION: You always have to examine the findings you're making against the wider evidence, and I think you essentially agreed, given the very good explanation as to why that is, yeah?

ANSWER: No! Wrong! I don't - it's not my job – that's for jury.

[57] See Annexure A below.

When the expert is given other information and asked to find a solution problems can arise because of the risks associated with confirmation bias. Some experts want to play CSI too![58] For example; consider these alternatives questions:

1. What does crime scene stain 91 tell us?
2. There is a possibility crime scene stain 91 contains multiple victim samples from the crime scene - what are the odds supporting this proposition?

Question 1, allows for the expert opinion to be given objectively without reference to any information about the crime. Question 2, presumes knowledge of the crime and details of the victims being with the expert. It risks the intrusion of subjective opinions and could result in the expert attempting to prove the prosecution hypothesis presented.

We can prove a case with DNA evidence - The CSI effect

Where a scientific expert gives evidence, there is always a danger that a jury will give the expert opinion more weight than it deserves. This risk can be enhanced because in popular culture, including TV shows like “CSI”, DNA evidence is often portrayed as demonstrating infallible evidence of guilt – hence the term “the CSI effect”.

Well before DNA was popularised by TV shows it was accepted that:

> "There may be unusual cases in which the judge has reason to fear that the jury will be overawed by the scientific garb in which the evidence is presented and will attach greater weight to it than it is capable of bearing:" [59]

What the popularisation of DNA by CSI type shows did was give rise to even greater expectations of, and reliance on, scientific evidence as somehow both essential and infallible. Oddly, that awe is selective. Most of us now accept that aeronautical engineers know what they’re doing and confidently book airline tickets, but many don’t accept the climate change predications of other well qualified scientists. Most people will accept health advice about COVID-19, but many are sceptical about the science of inoculation. Navigating the variety of human responses is the curse and the joy of the jury trial.

A “reverse CSI effect,” can be exploited by the defence: “The scientists are so good that if my client was at the scene his DNA would be there!” The reverse CSI effect exploits the

[58] *Wood v R* [2012] NSWCCA 21.
[59] *R v Duke* (1979) 1 A Crim R 39, King CJ, at 41; Also referred to as the “white coat effect” *Morgan v R* [2011] NSWCCA 257.

myths ‘every touch leaves a trace’ and that ‘absence of evidence is evidence of absence.’ It is an example of what I regard as “truthiness.”

There are dangers when Judges attempt to “correct” such misconceptions. An example comes from the fourth and final trial of Robert Xie. Justice Fullerton asked the jury to be astute and not to expect anything like the scientific certainty that features in fictional police or crime scene dramas.[60] An appeal ground that she was reinforcing and restoring credit to a prosecution expert was rejected.[61]

To state the obvious, reliance on myths not facts can be dangerous. Miscarriages of justice occur when the DNA evidence is given more relevance or weight than it deserves. Not every miscarriage is picked up.

Preparing for trial - have you got a plan?

The absence of a DNA profile can be a powerful persuasive tool with a jury, so some clients may prefer to wait for the services of DNA results before they commit to a version of events. As a practitioner however I was always of the view that the earlier you got a proof of instructions, the better.

The presence of DNA, particularly if it can be associated (if not identified specifically) with a bodily fluid, can be a powerful incentive to the making of concessions: “well – yeah-no - I was there BUT…” Sometime there are no available ‘buts” and a matching DNA profile can be a powerful incentive to the making of admissions and or a guilty plea.

More difficult questions arise if your instructions provide no real answer to prosecution expert evidence that there is a DNA profile match that incriminates your client. How then do you answer the prosecution evidence of a DNA profile match?

At the risk of stating the obvious, you will need to consider:

1. Whether your instructions are wrong, either deliberately or unknowingly.

[60] *R v Xie* fourth trial Summing Up; “You should not penalise the Crown if you think there are questions left unanswered by the crime scene analysts, or if you think the physical evidence…in the crime scene itself does not provide the level of certainty you might have thought it should.” *Xie* [2021] at [449].
[61] *Xie* [2021] at [464].” There may be room for debate as to whether the direction was necessary. We certainly should not be taken as stating that it is desirable that a direction of this nature be given in all cases involving complex scientific evidence. However, for the reasons we have given, whether the direction was necessary or otherwise it did not result in a miscarriage of justice.”

No lawyer likes drawing attention to a case they lost, nor to their own fallibilities but the Armstrong cases from 2010 to 2014 illustrate my point. [62]

2. Whether there has been a contamination event.

   Contamination involves the introduction of extraneous DNA to the scene, exhibit or sample. Whether contamination can be investigator-mediated in the police exhibit room, in the lab or data base or in the equipment used also requires consideration.[63] Has the DNA match skewed the investigation toward your client and away from the real culprit? Did the police start with the DNA profile match and go looking for other evidence? Has there been cognitive bias?

3. Does the DNA corroborate other evidence? Does other evidence corroborate the DNA evidence?

   In many dodgy DNA cases the DNA did not add very much to the prosecution case. The question has to be asked whether calling the impugned DNA evidence was worth it? [64]

There is another equally obvious point to be made. Even the best preparation may not result in an acquittal if the prosecution have a better and equally well prepared case - *Western Australia v Edwards* is a case in point. [65] For a short summary see Annexure C.

Conference the prosecution expert

It should be obvious, but it's often not done! Sometimes, sadly, it appears that whether or not the expert was conferenced prosecution, defence or both, failed to understand or chose not to understand, the expert opinion about the DNA evidence.[66]

Speaking to the scientist can help you distinguish expert opinion based on scientific knowledge from guesswork and experiment and help you help them to them focus on their responsibilities to the court without the need to cross-examine them back to proper scientific

[62] In the interests of transparency see; *R v Armstrong* [2010] NSWSC 800 (sentence after trial); *Armstrong v R* [2013] NSWCCA 113 (successful CCA appeal) and *R v Armstrong* [2014] NSWSC 700 (second sentence after guilty plea).
[63] See *R v Hillier* [2010] ACTSC 33; the Jama case, the Adam Scott case, and the Phantom of Heilbronn case.
[64]For example *Aytugrul*. Or possibly Xie; was calling evidence about the garage floor stain evidence worth the risk of miscarriage of justice inherent in using new technology and models of such complexity?
[65] See Annexure C.
[66] Defamation laws prevent me giving examples.

propositions. Your focus must be on first, learning as much as you can from them and then getting as much objectivity from them as possible.

Speak to the prosecution

What precise use do the prosecution wish to make of the expert evidence about DNA? Or, to put it in *Evidence Act* terms, what fact in issue is the expert's opinion about DNA said to prove, or assist in proving? Can the proposed DNA evidence be limited in its scope?

Does the expert need to be called at all? Can the DNA evidence be the put before the jury, either as admissions (s 184 *Evidence Act*) or as agreed facts (s 191 *Evidence Act*) or as a written chart or summary (s 50 *Evidence Act*).

I**s there a need challenge the evidence?**

In many cases, a DNA profile match and a calculation of its statistical strength will not give any information about how, when and in what circumstances, the DNA was deposited or transferred, and, if transferred, whether that transfer was passive or active. Nor can it deal with any issues about persistence; where, and in what circumstances, the DNA found was deposited, and at what rate the DNA could have dissipated since it was deposited.

> *QUESTION*: You can't actually date DNA can you?
>
> *ANSWER*: Absolutely not, nor is there a test that can determine how old that sample is, or when it was deposited.

As a consequence the evidence may be either neutral (something that should be pointed out in opening address) or irrelevant to a fact in issue, and thus inadmissible.[67]

Objections to the DNA evidence

The fact that aspects of the scientific evidence, (including DNA analysis and statistical match probability opinion evidence) may be complex is not a reason to exclude it.[68] Absolute certainty of result or unanimity of scientific opinion is not required for admissibility.[69]

Before evidence can be admitted it is essential the techniques and methods used be explicable, validated, independently verified by an agency such as FASS which has been

[67] ss 55 & 56 *Evidence Act.*
[68] *R v. Lissoff* [1999] NSWCCA 364.
[69] *R v Gilmore* [1977] 2 NSWLR 935 at 939-94.

accredited by a standardisation body such as the National Association of Testing Authorities NATA. Known guidelines and limitations set out in them should be used, and available for review, as should the assumptions and statistical methods used in any computer software applied to the analysis. If the guidelines or thresholds are exceeded, such as occurs when LCN DNA results are obtained, what was done must be made known. The questions asked of the expert by the prosecution must be disclosed.

While some experts may adopt a never say never approach when dealing with police or prosecutors a point must be drawn when the mix is too complex for the results to be meaningful. Examples include; where the number of contributors cannot be ascertained or the proportions contributed cannot be assessed or if there are too many relatives in the mix or if the quantity of DNA is too small or the quantity of DNA from some contributors is too small to produce any meaningful results. If no meaningful results can be obtained the evidence is not relevant and if not relevant the results are inadmissible.

As DNA techniques and science develop experts will push to, reach and then go beyond the outer limits of theory and practice as currently understood. Section 79 *Evidence Act* is not a brake on such potential excess. That said the objections must be made and limits of new developments known and then subject to rigorous testing before they are used as evidence in court.

This paper's focus is on challenging the weight that might be attached to DNA evidence admitted at trial, not the admissibility of that evidence. But where a novel, untested or commercial in confidence, procedure was used an important pre-trial question is: why? It must then be asked - does the new technique push too far? Has it been verified? Has it gone beyond the outer limits of known science?

But rather than keep such evidence away from juries, the practice in *Evidence Act* jurisdictions has been to leave it to the defence counsel to challenge and explore the evidence in the presence of the jury. The ultimate weight to be attached to the evidence, and the conclusions to be drawn from it, are matters for the jury. This can be frustrating for appeal Judges. In *Tuite No1,* the Victorian Court of Appeal rejected a challenge to the reliability and veracity of DNA evidence.[70] When the matter came back to them after Mr Tuite lost his second trial, they expressed their exasperation that the defence had dared to challenge the reliability of the DNA at trial!

[70] *Tuite v R* [2015] VSCA 148; Tuite v R [2020] VSCA 318.

The potential scope and range of DNA use as an investigative tool is apparently unlimited. We can now use DNA profiles to make predictions about a donor's physical appearance and biogeographical ancestry. Once used to investigate crime, attempts will then be made to introduce such evidence at trial. As each new advance is made challenges will need to be made to the efficacy and reliability of the new techniques used.

There is, nor should there be, any closed categories where evidence cannot be placed before a jury. "It would be wrong to deny to the law of evidence the advances to be gained from new techniques and new advances in science with particular reference, in this context, to DNA evidence."[71] To date most new DNA advances have survived challenges from the evidence admitted. Some examples include:

- *R v Karger* [2001] SASC 64; 83 SASR 1, where Mullighan J, allowed Profiler Plus evidence.
- *R v McIntyre* [2001] NSWSC 311, Bell J considered the admissibility of opinion evidence regarding DNA results using the Profiler Plus system.
- *R v Fuller* [2013] SADC 150, where a challenge to STRMix® evidence was rejected.
- *R v MK* [2012] NSWCCA 110; 223 A Crim R 572, where the Court of Criminal Appeal allowed a Crown appeal from the exclusion by a trial Judge of mixed DNA evidence involving a major component and a weak minor component, with the Profiler Plus kit having been used, as well as Y-Filer testing.
- R v Xie (no 4) [2014] NSWSC 500, where Johnson J allowed evidence derived from the TrueAllele® program. And the CCA determined it was "verified" and relevant and admissible as expert opinion.[72]

Opening

Jury (and judicial) decisions are largely deductive and intuitive. Such decisions are prone to cognitive biases. From the outset - that is your defence opening address - you should raise and provide the jury/judge with mental (or if you're power point competent, actual) bullet points to give them a catalyst to consider the apparent strength of the prosecution's DNA

[71] *R v Reed* [2009] EWCA Crim 2698; [2010] 1 Cr App R 23 at [111].

[72] There is some confusion in terminology used in the Xie decisions. There was evidence at the final trial that that FASS has "validated" True Allele® for a 4 person mixture: Xie CCCA at [113] Fourth trial TT 4058. But FASS witnesses also spoke of the process of evaluation or process of validation: Xie CCa [271] Fourth trial TT 4056. As understand it however, NSW FASS have not completed the validation of TrueAllele® for casework: it did carry out and wrote up an evaluation of the system but that evaluation did not include 5 person mixtures.

evidence. Unless you are confident the prosecution case is going to collapse around them or you don't actually have a defence, the sooner you raise the possibility of exculpatory evidence, and signal any questions about potential problems with the DNA aspect of the case, the better.

While there will be judicial directions as to how the jury may or may not use the DNA evidence, they will come at the end of the trial. When a prosecution opening has planted an early seed that gives the proposed evidence the appearance of objectivity by using numbers in the billions and trillions, the defence must sew doubts early on. The challenge is: How to frame a narrative that created such doubts or neutralises the prosecution DNA evidence. Otherwise, the jury may have trouble focusing on later exculpatory evidence or challenges to the strength and/or relevance of the DNA evidence.

Stopping the inquisitive judge

If there is an agreement between defence and prosecution about the scope of the DNA evidence, or if there is nothing in issue relating to the DNA evidence, PLEASE let the judge know in advance. Judges can get bored and/or want to show off to the jury. As a consequence, they can send a trial off the rails if they butt in where it is not wanted or needed.

On the other hand, if there is agreement about the DNA evidence and an expert is not required, do NOT allow the FASS report and its annexure to be given to a jury. Not all jurors are sufficiently literate to follow and take in all that is set out in such reports. Frankly, for most simple cases, they contain too much information. Unless you actually want the jury to be distracted because of flaws in the defence case, prepare a script or dot points – and ask the Judge to explain it to the jury.

Cross-examination – Simple DNA profiles

A simple DNA profile involves the review of recorded results to see how many possible contributors to the sample there are, and then analysing peak heights which correspond to the loci on the DNA strand being examined.

By reviewing the EPG and the maximum number of potential peaks at a locus and dividing them by two, an estimate number of contributors can be made. If proper inferences are available, results using a different number of assumed contributors can be calculated. Similarly, if there is a possibility that a relative may be in the mix that too can be accounted for.

If a contributor is known or assumed, such as a complainant from whom a vaginal swab was taken, their reference sample can be used to reduce the unknown loci in the result.

Care needs to be taken if there is a dispute about the evidence: What regard was had to the integrity of the exhibits? An illustration was exposed by experiments by Goray and Van Orschott and others.[73] DNA was placed on a knife handle and then the knife was stored in a standard police exhibit tube, put in car and driven around for a while. On later analysis, it was found that some of the DNA had moved from where it was originally deposited.[74] Other experiments were carried out on stained clothing, with similar results.[75]

QUESTION: Why can't you tell me?

An expert who understands their obligations to the court will admit uncertainty, particularly about how and when. By asking questions that get "we don't know" answers, the risk of a jury placing too much weight on the DNA evidence can be reduced.

You need to ask the preparation question - is the source of the profile relevant to a fact in issue?

There is a difference from semen to sperm head cells isolated in lab and a bucket of urine. A buccal swab sample will generally provide only skin cells, but in a case of oral rape may include blood and semen cells. A bloody hand may have skin cells and blood under the fingernails deposited at quite different times.

Lab contamination? In *R v Hillier*,[76] doubt arose because an expert fairly revealed deficiencies in where and how the exhibits had been stored and tested. Cross exhibit contamination left the judge (sitting alone) with doubt as to whether the accused's DNA could be associated with the murder.

Investigator contamination?

> *QUESTION*: Based on your scientific training, is it the best practice to change gloves between the handling of items to prevent contamination of DNA, item to item?

[73] Goray, M, Eken, E. Mitchel, JR van Ooschott R.A., 2010 *Secondary Transfer of biological substances under varying test conditions, Forensic Science Int. Genetics. 4, 62-67.* Goray, M,. van Ooschott R.A.S, Mitchel, JR, *DNA transfer within forensic exhibit packaging; potential for DNA loss and relocation*, Forensic Science Int. Genetics. 6 158-166. And other articles cited in (Gill 2014).
[74] See also the Phantom of Heilbronn & Gill (2014) p. 32.
[75] Goray, M., Mitchell, R.J., van Oorschot, Investigation of secondary DNA transfer of skin cells under controlled test conditions. Leg.Med.12,117-120, 2010; Goray,M., Eken, E., Mitchell, R.J., van Oorschot, Secondary DNA transfer of biological substances under varying test conditions. Forensic Sci. Int Genet, 4, 62-67, 2010
[76] *R v Hillier* [2010] ACTSC 33.

ANSWER: Yes. Generally the best practice would be to use multiple sets of gloves, put on underneath the other, and then use a fresh set of gloves every time you handle a new item, or to completely change your gloves each time. That would also be the same if you were to handle a suspect. So, for example, if you were to handcuff someone, you should then change your gloves afterwards.

Put the alternatives to the expert. Press the expert on whether their opinions and answers are based in intuition, not experiments, testing or probabilistic analysis. However please note in both *Velevski*[77] and *Xie,* evidence based on general experience in the field rather than experiment and scientific method was allowed.

Cross-examination – complex profiles

All the basic limitations of DNA evidence must be explored if the prosecution expert has not already done so. Most, in fairness will have set them out in their evidence in chief or the reports served. If the expert says what in their opinion is the more or less likely, ask than what data, research or experiments underpin those conclusions. Where modelling was used, presume all models are wrong[78] (as they are simulations not real events) but also realise some models are well constructed and will provide a proper basis for an expert opinion. There will however be outliers in the result and false positives or negatives. Each application of a model produces different results, care needs to be taken, as the expert will be ready with a response that essentially 'it doesn't matter, given the high LRs that gives weight to the DNA profile matches found.

Recently in *Xie v R* the CCA were prepared to excuse use of terms that equated a match statistic with evidence of identity on the basis that mathematically the expert was correct in attributing the maximum likelihood of seeing this match statistic for a person who was not in fact a contributor as being the inverse of the match statistic:

> Q. With match statistics ranging from 10 trillion to 10 quadrillion, it would be extremely unlikely, in fact, a *chance of less than 1 in 10 trillion*, that he wouldn't be present.
>
> Q. 'He wouldn't be present'. So does that equate to being very strong statistical support for him being present?
>
> A. Yes, 1 in 10 trillion or 1 in 10 quadrillion is a very small number of a chance of a false positive." (CCA emphasis added)[79]

[77] *Velevski v The Queen* (2002) 76 ALJR 402.
[78] "All models are wrong but some are useful" "Since all models are wrong the scientist must be alert to what is importantly wrong." George Box, https://en.wikipedia.org/wiki/All_models_are_wrong.
[79] Xie CCA at [329].

I am not so forgiving. I would not put any emphasis on the pronoun “he”. I always recommend any match be referred to in these terms - very strong statistical support for a profile match.

The more common ‘binary’ models use thresholds [80] that rule information in or out. They seek to identify or otherwise exclude information that is or may not be an allele and then see if what is identified corresponds to an another’s profile.

Continuous probability models generate an enormous number of possible matching or inferred profiles. Only one propriety systems is currently used in Australia- STRmix®. TrueAllele® is not used by Australian DNA labs. To date TrueAllele® was only used in the Xie trials.

STRmix® uses some of the logic of the older binary approach in that different hypotheses are compared and the probability of one or the other calculated given different contexts, such as the number of contributors. Its inclusion v exclusion guidelines are based on probability distributions not binary thresholds. True Allele uses all available data even artefacts of testing. By modelling every piece of data TrueAllele® can present LRs for every conceivable circumstance but its maths are complex, it underlying assumptions and use of sub-population data obscure. It remains, so far as I am concerned, impenetrable.[81]

The results from the reference samples are then added to the programme and LR’s generated for matches. Given the high figures often generated, any “match’ will generally have a high LR. This is particularly so with TrueAllele®. The danger exists that this may give weight to the match that might not ultimately deserve. Close attention to the parameters used is thus required.

So far as TrueAlle is concerned it is important to note that no whole profile to whole profile comparisons are made,[82] as most often occurs with the usual binary systems used by FASS.[83] In my review of the Xie decisions racially based population data bases were used to estimate the rarity of profiles at a loci but it was hard to find out what if any accommodation was allowed for sub-population effects. I am aware that TrueAllele’s program can incorporate this co-ancestry coefficient (a measure that takes into account the general

[80] On peak heights or stutter proportions.
[81] See Annexure A.
[82] A point made by the defence in *R v Xie (no 18)* [2015] NSWCCA 2129 at [85].
[83] See Annexure A. NSW FASS do visual comparisons of noncomplex profiles to reference samples which is binary but other than that they now use STRmix®.

relatedness of those in a community) but that material was not tendered at trail.[84]. As I noted earlier: "[P]robabilistic genotyping is inherently different from and not directly comparable to binary interpretation."[85]

The right judicial directions

These must be discussed before addresses. No advocate wants their jury address undermined by a contrary message given by the Judge. Don't forget; Judges go last- so lock in what directions are to be given before addresses. Don't be afraid to ask for the direction you believe you need. Offer a draft. Most judges welcome such assistance. Some judicial possible directions are set out in Annexure B.

Unless your plan has been to so confuse the jurors they put the DNA evidence into a too hard basket and ignore it - they have to get it! And, you have to help the judge ensure they get it!

Addresses

DNA can provide powerful evidence of exclusion: "If the DNA don't fit – you must acquit!"

Stress anything that has uncertainty if uncertainty has been accepted by the DNA experts.

Reverse the CSI effect to the defendant's advantage. An expert's doubts can equal reasonable doubt.

Often the DNA evidence will raise more questions than provide answers. This is particularly so if multiple profiles are recovered at the crime scene and the persons associated with them cannot be excluded. While there may be a profile match between DNA found on the deceased's bra and the defendant - whose was the male DNA found on her underwear- the real killer?

Use the myths - if the defendant had have done all that he's said to have done – where is the DNA?

The defence fallacy is not always a fallacy. If the statistics say 5 more people in NSW could match the profile – there may be 5 other suspects if the other evidence at trial can't exclude the possibility that others may have the same DNA profile. This is particularly important if a low statistical weight is given to any the LR associated with a profile match.

[84] Xie CCA [348]
[85] See FN 55.

Don’t presume jurors are scientifically incompetent, but they may be common sense types, and amenable to the odd myth or two.

Conclusion

Defence lawyers must learn to be discerning consumers when it comes to DNA expert results. DNA can exclude a suspect but it can also implicate them. Any expert interpretation will always involve an opinion about the probability of certain events in comparison with other alternatives. Such evidence is rarely truly objective as assumptions have to be made. Where an expert is given too much information about a specific crime they too can suffer from CSI induced lack of objectivity or confirmation bias. The risk is always present that semi-informed guess work, untested assumptions or non-scientific analysis based on ‘experience’ not logic will be made. Unless such assessments are tested and subjective opinions or untested assumptions miscarriages can occur. Frankly, the forensic scientists are much more astute to such problems than most lawyers. And, most will volunteer their assumption and potential problems – if asked!

You are not a DNA expert, but with only a few exceptions (often where an expert is puffing their own technology or ego) the expert will give you answers that can be expected and prepared for. If you don’t have a plan, you can contribute to a miscarriage of justice. I return again, and finally, to the need for preparation.[86]

[86] The rule of the 5 P’s applies to every trial: Preparation Prevents Piss- Poor Performance. Attributed to coach Chuck Knox of the LA Rams, back in the 1970s: Thank you Justice R Button NSW SC.

Annexure A

The basics:

- DNA analysis is only useful if DNA can be obtained from a person or object associated with a crime.
- While it is often wrongly assumed that "every touch leaves a trace," we humans do tend to shed our DNA wherever we go.
- Once DNA is extracted from a crime scene sample, it is purified and 'quantified.' Increasing small quantities can now be analysed. These quantities are so small only a few cells are required.
- A technique called polymerase chain reaction (PCR) is then used to 'amplify' the sample by making exact copies of it.
- Those copies can then be separated into fragments based on their size, by a process of electrophoresis. These can be displayed on a graph, an electropherogram (EPG), and can be set out as a numerical code that can be stored as computer program.
- Those numbers provide the code or profile for a comparison with other DNA profiles- the reference samples.
- Ten years ago, the DNA sequencing machines available in Australia used as reference points 9 locations (loci) on the DNA strand and a gender distinguishing marker The FASS NSW now use a system that picks up 20 specific and highly variable loci and a gender marker.[87]
- EPG's can be interpreted by an expert and possible DNA profiles or genotypes can be deduced or inferred- the inferred genotype.
- As we inherit from both our parents, we have a maximum of two readings, or peaks, at any one locus.
- The height of the peaks, measured in Relative Fluorescence Units ("RFU"), can indicate the amount of DNA present. The position of the peaks on the graph indicates the number of repetitions of a particular combination or Short Tandem Repeats ("STR") of the four "bases" of DNA (Adenine, Thymine, Guanine and Cytosine) at that location.

[87] *PowerPlex21®*. Although there are still cases where the older *Identifiler®*(18 loci plus gender marker) and *ProfilerPlus®* (9 loci and a gender marker) are still used.

- ❖ The number of peaks at specific locus allows an assumption to be made about the number of contributors to the sample.[88]

Generally, only those peak heights that give readings above minimum mandated RFU heights are taken into account. But peak heights are very variable and can be affected by a number of factors.[89] Care must also be taken to ensure that artefacts of the testing process are not read as part of a profile.[90] While unambiguous profiles are reasonably easy to read, an expert is required to interpret EPGs and explain results for court purposes.

It is at this stage that an assessment of the rarity of the profile is made. Commonly in NSW this is expressed as a Likelihood Ratio (LR). A LR is obtained by dividing the probability of obtaining the match on the prosecution hypothesis (it is the accused's sample) by the probability of the defence hypothesis that the profile comes from another unrelated individual in a given population.

The LR thus indicates the chance or probability of observing the DNA profile - if it had originated from the profile in the reference sample; *against*, the chance or probability of observing the DNA profile - if the profile had originated from a random unrelated person.

In the simplest terms: once a result is obtained at one locus the relative rarity of that genome (pair of alleles) at that locus can be assessed. The rarity of the profile at each different locus is presumed to be independent of the others. The match statistics at each locus are then multiplied by one another to give a final statistic – applying a process known as the "product rule." Once the figures derived from each locus are so multiplied enormous match statistics – often in the trillions can be generated.

If the results are in the trillions or quintillions they are rarely reported at that number. The NSW FASS uses a cut off figure of a 100 billion

The chance of such a profile match is assessed after the program takes into account the rarity or the relative frequency of alleles occurring at the specific locus used. In Australia a population frequency database, broken down into Caucasian, Asian and Aboriginal databases is used. A co-ancestry coefficient is also used to put another "conservative"

[88] For example as we inherit one allele from each parent- 2 peaks at each loci indicate one contributor -6 peaks at least 3 and so on- divide the total peaks by 2 but take care. Some people have one peak at locus (indicating both parents supplied identical alleles) and others may not have been recorded (dropped out) of the EPG.
[89] Steele C. D., Greenhalgh M. and Balding D. J.; Evaluation of low-template DNA profiles using peak heights, Stat. Appl. Genet. Mol. Biol. 2016; 15(5): 431–445
[90] You'll need to become familiar with terms like stochastic variation, stochastic threshold, stutters, false peaks, drop in, drop out, and pull ups.

reduction on any results to allow for the possibility of interrelatedness. Given the figures now derived when 20 or more loci are examined, these conservative reductions only become relevant if the LR is very low.

If there is no match a person can be “excluded” as contributing to the sample. If they are “not excluded” the chance that any match occurred randomly must be determined. If this is not done a report that a person’s DNA profile was “not excluded” has no evidentiary weight and little relevance.

Any crime scene DNA profiles obtained needs a comparator – a reference sample - a DNA profile obtained from a suspect or victim, or both. A link may then be made between a known person’s profile and the crime scene sample.

The weight given to DNA evidence derives:

1. First, from the apparent objectivity of obtaining and recording the details of a DNA profile or profiles from the crime scene; and then comparing that recording with a reference profile from the offender or victim. And;
2. Secondly, from the expression in statistical form of the rarity of that profile match.

It is critical to note that the comparison is not between individuals, but between DNA profiles. The profile relates to only a small (although highly discriminatory) portion of an individual’s DNA.

EPG results can be uncertain because the product is below or over certain limits (measured in RFUs). If so, it is accepted that artefacts of testing might be confused with genuine profile results. Those readings are not added to the comparison sample. At times, no results can be reported as at certain locus they have ‘dropped out.’ If a full profile can’t be obtained due to ‘drop out’, the result at that particular location cannot be used for comparison purposes. When the end result is then compared to the reference sample, any inferences draw from that profile comparison will result in a lower LR being generated.

A skilled analyst can, by comparing relative peak heights, discern and discriminate between major and minor contributors to a crime scene sample from which a mixture of DNA profiles is obtained. The sex of contributors can also be determined by reference to the gender marker incorporated in each system used.

Where there is a known contributor in the sample (such as a complainant of a sexual assault) their sample can be used to isolate others from other results derived from a mixed sample.

A standard FASS report will thus read:

> "The DNA recovered is a mixture of two individuals. [The accused (barcode xxx)] cannot be excluded as a contributor to this mixture. Assuming there are two contributors, it is greater than 100 billion times more likely to obtain this mixed profile if it originates from [the accused] and an unknown unrelated individual, rather than if it originates from two unknown individuals in the Australian population. Assuming there are two contributors [Ms Y] is excluded as a contributor to the mixture.

Care needs to be taken in expressing a profile match. Match statistics do not, and cannot, give the probability that the person associated with the profile is the same as the person in the crime scene sample[91] - the "prosecutor's fallacy." The prosecutors' fallacy confuses the probability of finding the evidence on an innocent person with the probability that a person on whom the evidence is found is innocent.[92]

As the strength of DNA evidence is generally expressed in the form of a Likelihood Ratio (LR). The fallacy, and consequent danger from its applcaition, arises if the jury transpose that ratio into the odds of the defendant's guilt. For example:

> "The chance that the defendant is not there in the crime scene sample is less than one in a trillion"

The probability of a DNA match with a suspect's profile is not the same as the probability the suspect is guilty. For example: A woman wins Lotto but is charged with doing so by hacking the lottery computer. Her chance of winning by choosing the winning combination is 1 in 20 million. The chance she is guilty is *not* 1 in 20 million! [93]

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[91] As Simon Walsh, now with the AFP, said *"It's a scientific conclusion that has statistical validity… Not a statistical conclusion" Wash S,* To Infinity and Beyond: *A Critical Look at DNA as the "Gold Standard" of Forensic Evidence Interpretation,* AAFS Symposium on Evidence Interpretation
3-4 December 2011, Sydney, Australia.

[92] Statisticians call it 'reversing the conditional.' There is also a 'defence fallacy': "If there is a chance 10 other people in the community may share my DNA profile- there is a nine in ten chance I'm not guilty" The fallacy here is not on the math but in ignoring other evidence that might point to guilt.

[93]Statistics and probability for advocates: Understanding the use of statistical evidence in courts and tribunals, Royal Statistical Society 2017 at 26

I am firmly of the opinion that is quite wrong to ask: could the profile found in the crime scene sample come from the defendant? Rather, the question must be expressed by reference to the exclusionary power of DNA evidence:

> Can the DNA profile found be excluded as coming from the offender? And, if not, what is the likelihood that some other person might be the source of the profile?

Recently in *Xie v R* the Court of Criminal Appeal were prepared to excuse use of terms that equated a match statistic with evidence of identity on the basis that mathematically the expert was correct in attributing the maximum likelihood of seeing this match statistic for a person who was not in fact a contributor as being the inverse of the match statistic.[94]

The absence of a person's profile from a sample is not necessarily evidence that they were not associated with a crime scene – "absence of evidence is not evidence of absence." Simply put, not every contact leaves a trace that can be found and recovered.

If the likelihood of a profile match is low, then the chance that some other person was associated with the crime scene cannot be discounted. While a low match probability can be augmented by other evidence, the possibility that the real offender is out there cannot be disproved. For example: "there are 100 people in Australia that could have left that DNA"– "the defence fallacy." Obviously, if there is no other evidence connecting the defendant to the crime scene and there are 100 people in Australia that could have left that DNA, it is not a fallacy at all![95]

Complex profiles

Most of the DNA operating systems and software available and verified for use in all Australian Forensic Labs are limited in their capacity to properly analyse and interpret complex DNA. That is; DNA that:

- Has been degraded; and/or
- Is a mixture of many possible profiles;

[94] At [317] "One of the complaints under this heading about Dr Perlin's evidence is that at various points in his evidence he proffered what the appellant identified as identification evidence in that he stated it was extremely unlikely that the DNA of the victims was not present in Stain 91. These instances are addressed below but it suffices to state that, to the extent he did, the opinions he expressed were within his expertise and he explained how that was so."

[95] If the probability of a DNA profile match is 1 in 1 million and there are 5 million in population from where the offence occurred this means there 4 other possible matches just on profile evidence alone this means there is a 4/5 or 80% chance someone else left the DNA.

- There a possibility those in the mix are close relatives and thus share DNA; and/or
- Is from a small (by DNA standards) quantity of DNA.

Results can still be obtained if the machines are pushed standard operating procedures. Such results are still valid but they carry a greater risk the results may be tainted by contamination; at the crime scene, during collection or at the lab. This risk requires careful examination of each aspect of the collection and processing of the crime scene sample and of every assumption made by the expert analyst,

There are some fundamental limitations when we are dealing with this 'trace' or 'low copy number (LCN)' DNA which, given the size of the original crime scene sample may only be a few cells. Similar problems arise when a mixed DNA sample's minor contributors make up only a very small percentage of the original.

As DNA analysis becomes increasingly able to pick up profiles from smaller and smaller quantities of DNA, the interpretation of results can be confounded by the possibility that the DNA from the crime scene was not directly associated with the crime under investigation. The DNA can get to the scene by transfer from where it was initially deposited at another location. The DNA may persist from an earlier event. And, it cannot be determined with accuracy or reliability how long DNA persists in different environments. Given these potential problems and the possibilities of both active and passive transfer of DNA between or on objects, nothing is certain or predictable. [96]

Advanced computing potential over the last decade has led to alternatives to the type DNA analysis commonly used by most DNA labs in Australia since the 1990's. In contrast with the more common or binary analysis, these 'continuous probabilistic models' use a computer programme to look at all available data, including peak heights below the thresholds set to avoid reading as DNA what may be an artefact of testing.

Probabilistic programs assess the likelihood of alternative solutions to the puzzle posed by the mixed or degraded DNA sample. They still use the EPGs of other operating system, such as the *PowerPlex21*® used by the FASS NSW, but these computer models or simulations use all of the data in the EPG, including what may be artefacts or peaks too low for other systems to use. They calculate all the possible genotypes in the crime scene sample. The probability of each genotype is calculated at each locus. The program then predicts which profiles are more likely at a certain locus. A reference sample is then added

[96] Gill, *Misleading DNA Evidence: Reasons for Miscarriages of Justice* (2014), p 67.

to the model which it compares with the genotype probability distribution from the crime scene sample - any 'fit' described is measured by a LR. The model's LR thus gives statistical weight how good the 'fit' is across each of the loci in the profile's being compared.

The continuous probability model's program takes all the data recorded and assesses the likelihood of all the potential solutions, given the presumed number of contributors and population data about the rarity of profiles at each locus used.[97] At a certain locus on a DNA strand, there may be say 100 possible base pairs and distinct pairs calculated. An enormous number of possible matching profiles will then be generated. The programmes then reduce those possibilities by comparisons with the range of readings for each allele pair within a known population or population group. This is then repeated for each of the loci produced by the genotyping machine used.

The computer program infers peak heights and asks; "How well do they explain the data?" This phase is done without knowledge of any reference samples from the defendant and/or other crime scene samples, but with an estimate of possible contributors. The results allowed for the statistically most likely inferred profile or more commonly profiles at each locus to be generated. The results from the reference samples of known DNA, say from the accused or victim or victims are then added to the programme and LR's generated for matches at each loci. Expert evidence is then given about the conclusions and inferences drawn from them and about the likelihood of the profiles matching. A LR will be calculated for the DNA profile data (genotypes) provided in the reference samples. Those LR's allow for those a comparison to be made and any 'fit" reflected by the LR.

Only one propriety systems for such profile interpretation is used in Australia - STRmix®. TrueAllele® was used in the Xie trial and some jurisdictions in the United States. STRmix®. TrueAllele® are quite different systems. STRmix® will make its computer codes available (on strict terms); TrueAllele® do not. Only STRmix® is used by NSW FASS. It has been validated for many complex mixtures.[98] Only STRmix® has been assessed by FASS for a mixed crime scene sample with 5 contributors, however such a mixture is not something that typically they would report on; and if there was a report it would include limitations and caveats.[99] STRmix® has some threshold criteria and binary features. It can create the

[97] Using a statistical process known as Markov Chain Monte Carlo (MCMC).

[98] Personal Communication with Sharon Neville FASS (19.03.2021). NSW FASS is NATA accredited. "Validation can include testing the models in the software programmed by checking the calculations produced by hand calculations, to make sure they were the same. Having the code checked by a professional IT company; by comparing the results of STRMix® to other lab's interpretations of the same profiles. By having it tested by a number of independent forensic labs and testing against a number of artificially produced mixtures with a known source:" see R v Fuller [2013] SADC 130.

[99] Personal Communication with Sharon Neville FASS (19.03.2021).

probabilities for all the possible interpretations of the data. Those interpretations are then compared to the reference sample profiles, as either a full set – all persons thought to be in the sample or one at a time. Its program can assess different hypothesis in different contexts after making assumptions as to the number of contributors.

TrueAllele® remains, in my view more problematic; but was it was accepted as "validated" by the CCA in *R v Xie*. TrueAllele® takes every possible piece of data including all artefacts of the testing process. No thresholds are applied. It has been described to me as an 'elastic probability model.' Few, if any, other than its inventor Dr Perlin, can explain the maths, which to me, and many others, remain impenetrable. But I note: the CCA in *Xie* were not ultimately concerned that TrueAllele® had been not validated for such a complex profile as found in stain 91. Rather; "By the time of the 2016 trial any dispute over the validity of the general methodology of TrueAllele in producing a match statistic was in the distant past."[100]

My major concern with the use of probabilistic models is confined to the results derived from complex mixed profiles (exemplified by the Xie trials). That is; where more than four contributors and or relatives are said to be in the crime scene sample. For example; no Australian DNA lab would comment on Xie's stain 91. Even today while they may have the capacity to produce results for a Xie type stain, NSW FASS would not typically report the results and if they did, they would include limitations and caveats.[101]

I have no problem with using advanced computing power and probabilistic statistical modelling. The older binary models could not produce reliable, let alone reportable results when confronted with such crime scene mixtures mix but the new models do produce results previously unobtainable. The results that are now generated by probabilistic models for other less complex mixed samples appear to be more robust and informative than those generated by the older binary system, as more information is available to be utilised.

Similarly I have no problems with using advanced techniques for investigative purposes, but as my 2021(above) and 2012 papers set out not every technological advance should be put before a jury until it has been thoroughly and robustly validated and it is demonstrated reliable results can be obtained for the sort of crime scene sample the model is used on. Section 79 Evidence Act as applied in Xie appears to allow for an expert to put before a jury results that stretch beyond the outer limits of what has been validated as reliable and reproducible. That way injustice lies.

[100] Xie CCA at [206]
[101] Personal Communication Sharon Neville FASS 19.03.2021

When the mixed crime scene sample is deconvoluted (modelled) the probabilistic models look at each loci. They calculate the probability for every genotype (pair of alleles) at each loci found in the data from the crime scene sample; and, make a genotype probability distribution. For a simple two contributor sample that might show that it is 100% likely that there are two separate profiles in the mix. In such case it is relatively easy to distinguish up to full 20 loci profiles. The number positive results may depending on how much DNA is recovered and whether or not it has been degraded. These full or partial profiles can be compared reference samples or run through a data base.

In a complex mixture however there might be a number of highly probable alternatives at each loci. The models don't (unless programmed to do so) simply infer a 20 loci (or less) profile from the most probable results at each loci. This means that when the comparison with the reference sample is made it occurs at each loci. The loci ultimately used, that is the one that bests fits the data used and the models parameters, might not be the most probable genome at a loci that matches the reference sample.

A calculation of the LR for this particular match might still give a very high figure and an intuitive analysis may conclude it is the 'best fit' overall but that conclusion comes with a loss of objectivity. Further, the the 'best fit' approach means an element of uncertainty is introduced to any calculation of LR for each individual loci. When the overall LR is calculated using the product rule enormous figures can still be generated by multiplying the probabilities at up to 20 loci. If the most probable genome at a loci is not used, the one that is may give a lesser probability and thus a smaller LR overall but that LR can still be impressively high. It is this LR that give evidentiary weight to any profile match asserted.

If that LR is generated by multiplying certain and independent probabilities it will have considerable weight.[102] If however the items multiplied are not independent of the other, for example if there is a genetic link between the loci examined; and, there is no certainty that the probability generated is as accurate as it could be, any figure given for the LR will not have the same probative force as the gold standard now associated with by the older DNA analysis systems.

The need to incorporate the reference sample into the model before any 'match' can be made; and the fact the matches are made at each loci (and not necessarily to the most probable genome generated), not the whole genotype, I argue diminishes the apparent objectivity and thus probative value of this technique when presented as evidence in court.

[102] A common example is asks; what is the probability of drawing an ace of spades, tossing a coin to heads and rolling a six on a dice = (1x52) x (1x2) a (1x 6)= 1/624

For example: The TrueAllele® probabilistic model used in Xie did make whole profile to whole profile comparisons between the profiles generated and the reference samples,[103] as occurs with the more common binary system used by FASS when they review less complex crime scene samples. The initial decovolution was objective, although subject to assumptions based on the number of contributors but once the reference sample was added to the modelling, the results at a loci with a higher LR were ignored. No whole 20 loci profiles for each inferred contributor were produced before the comparison with the reference sample. Those comparisons then required subjective evaluation and thus a reliance placed on the expertise of the operator; in Xie, as expert with a professional and proprietary interest in TrueAllele®.

Since Xie's pre-trial hearings and trials STRmix®; the continuous probability model now universally used in Australia and New Zealand has been evaluated and verified by robust experiment. Unless a person is assumed to be a contributor to a mixture, such as when modelling a DNA mixture generated from an intimate swab of a female in a sexual assault case, the initial modelling (or deconvolution) makes no presumptions. The program simply calculates the probability for each and every possible genotype at a locus. The probabilities generated will range from very low to very high. This is an objective process.

When that deconvolution from the crime scene is compared to the reference sample it can generate an LR that is less than 1: i.e. in favour of the defence hypothesis, or, a LR greater than 1 in favour to the prosecution hypothesis. It can also generate a zero, which then results in exclusion.[104]

The LR then generated is dependent on how well the reference sample fits the genotypes at each loci produced by the modelling (the deconvolution) by comparison with the all the probabilities across the profile. The reference sample is compared to the genotype probability distribution at each loci, with 'fit' described or measured by the calculated LR. For complex mixtures it is less likely this will always be the genome with the highest overall probability at every loci. But, if the reference sample is a good fit, the LRs are typically very high.[105] The current version of STRmix® used by FASS also has the capacity to upload a single profile extrapolated from the deconvolution (modelling); that single profile can then be compared with the reference sample or compared with profiles stored on a DNA data base. It also has the capability to do mixture to mixture searching

[103] A point made by the defence in *R v Xie (no 18)* [2015] NSWSC 2129 at [85].
[104] Personal communication Sharon Neville NSW FASS 19.03.2012.
[105] FASS do not typically report low LRs. As a low LR can indicate higher levels of uncertainty and the risks of adventitious matching.

In my view a danger exists that advanced probabilistic systems may give weight to the profile match that they might not ultimately deserve. Close attention to the parameters including, number of presumed contributors, sub-population effects and other assumption used, is thus required. Further, the weight of evidence generated by use of the two binary and continuous probability models is based on different assumptions, thresholds and formulae. As probabilistic genotyping is inherently different from a binary interpretation, the results obtained are not directly comparable.[106]

As probabilistic models are commonly used where low quantities of DNA recovered or where in mixture there may be low quantities from some of the contributors, any DNA found could have been left or put at a crime scene because of contamination (deliberate or inadvertent) In addition, the possibility there was contamination of equipment or contamination during collection or contamination at the lab can never be ruled out. A DNA profile analysis may be confounded by relatives being in the mix or by the complexity of the mix because of the number of contributors and the possibilities of differing amounts of DNA being deposited by different contributors, some of whom may not be detected or masked by others who have similar profiles.

ANNEXURE B:
DNA Directions

DNA Evidence - No contest:

After the crime scene sample was taken from the complainant and analysed, two DNA profiles were found in it. Semen was also found. The complainant cannot be excluded as a contributor to the sample. Later the defendant provided a sample of his DNA and a profile was obtained from it. He cannot be excluded as being part of the mixture. There is a high statistical probability that both the accused and the complainant's DNA profiles are in the mixture, as compared to a mixture with the complainant's DNA and that of some unknown individual unrelated to the defendant.

There is no real contest about the DNA evidence. You can use the evidence/chart/summary when you come to determine whether the prosecution has proved the offence beyond reasonable doubt.

[106] See US- Scientific Working Group on DNA Analysis Methods (SWGDAM) Guidelines for Validation of Probabilistic Genotyping Systems– FINAL APPROVED 06/15/2015. Available at: www.swgdam.org/publications

You can consider the DNA and statistical evidence, and weigh it along with the other evidence. Do not, however, allow it to displace or overwhelm your consideration of *all* material evidence - give it such weight as you think proper.

If the prosecution says that it is powerful evidence proving the alleged events took place, then:

> The defence should accept the DNA results, but say this evidence shows nothing as to how the events took place. Ask: "Can you be satisfied beyond reasonable doubt it took place as the complainant told you it did?"

That question cannot be answered by reference to the DNA evidence, which on this point, remains entirely neutral.

DNA Evidence - more complex:

The DNA expert's evidence including the statistics – like the rarity of some other person having that profile - may help you consider the significance of what they say is a match between the DNA profile found in the crime scene sample, and the defendant's DNA profile. It is not evidence of the probability that the defendant was the source of the incriminating DNA. To regard the evidence as such would be to make miscarriage of justice.

The statistical evidence interpreting the DNA profile 'match' is expert evidence, which you can to decide whether you are satisfied beyond reasonable doubt that the defendant was the source of the incriminating DNA, but is not the direct evidence of that fact. It must be considered in the light of *all* the other evidence in the case, the challenges to it, and the other aspects of the prosecution case.

It is for you to decide what significance and weight should be attached to the evidence of the DNA profile's 'match', the statistical evidence, and the challenges made to it.

The prosecution may say that the presence of DNA matching the defendant's profile supports the version of events given by the complainant - that he did touch her where and how she said he did. But an expert can freely conceded that even if it was the defendant's DNA, it could have got there quite innocently by secondary transfer.[107]

[107] Goray M., Van Oorschott RA., *The complexities of DNA transfer during a social setting*, Leg Med (Tokyo). 2015 Mar; 17(2):82-91. doi: 10.1016/j.legalmed.2014.10.003. Epub 2014 Oct 13

For the defence it is said that as there is a reasonable explanation consistent with innocent transfer - and as such, the DNA evidence adds nothing to the prosecution case. Again, I caution you not to give the DNA evidence more weight or value than it deserves.

I also caution you: Do not let any expert opinion be used as a substitute for your own satisfaction of a matter required to be proved as part of the prosecution case. This is another way of saying that you are not obliged to act on the evidence or accept any interpretation of only one part of the evidence. In approaching the issue of whether the incriminating DNA came from the defendant, and the issue of his guilt of the crime charged, you are to treat the DNA and statistical evidence as evidence to be considered and weighed along with the other evidence, *not* allowing it to displace or to overwhelm the consideration of *all* material evidence, but at the same time giving it such weight as you think proper.

DNA Evidence – even more complex:

First, some important cautions:

1. Expert evidence may match a profile from the crime scene sample and the defendant's DNA profile. This is of itself not proof the defendant committed the crime. It would be an error to conclude that the statistics said to support what the expert say is a match between the DNA profile found at the crime scene and the defendant's DNA profile, is evidence of the probability that the defendant committed the offence alleged, or even that he is the source of the incriminating DNA.
2. The probabilities associated with DNA matching are not the probabilities linking a person to committing the crime or not.
3. The statistical evidence interpreting the significance of what the expert says is a match between the DNA profiles found at the crime scene and an defendant's DNA profile is not evidence of the probability that the defendant was the source of the incriminating DNA.

However, the statistical evidence interpreting the DNA profile 'match' is expert evidence, which you can use in deciding whether you are satisfied beyond reasonable doubt that the defendant was the source of the incriminating DNA.

Statistical evidence is undeniably strong evidence pointing to a conclusion that the defendant was the source of the incriminating DNA, but is not direct evidence of that fact. It must be considered in the light of *all* the other evidence, challenges to it, and the other aspects of the prosecution case. It is for you to decide what significance and weight should be attached to it.

[Note in summary form the prosecution DNA and statistics evidence]

[Note in summary form the defence challenges to the DNA and statistics evidence]

I caution you not to allow any expert opinion put before you to be used as a substitute for your own satisfaction, to the appropriate degree of proof, of a matter required to be proved as part of the prosecution case. This is another way of saying that you are not obliged to act on the evidence but must form your own opinion.

In approaching the issue of whether the incriminating DNA came from the defendant, and the issue of his/her guilt of the crime charged, you are to treat the DNA and statistical evidence as evidence to be considered and weighed along with the other evidence,. Do *not* allow it to displace or to overwhelm the consideration of *all* material evidence, but at the same time give it such weight as you think is proper.

Here, the Crown must prove that [the semen and the DNA within it found on the complainant's underwear] was deposited there by this defendant. To do so the Crown must exclude, as a reasonable possibility, that the DNA:

a) came there by chance;
b) came there by way of contamination either:

    i. deliberately, or
    ii. accidentally;

c) came there by some indirect or secondary transfer, such as the underwear coming into contact with another source of the defendant's DNA; or,
d) came there by direct but not criminal contact.

I reiterate; it is not for the defendant to prove any of these things. The onus is on the Crown to exclude them as reasonable *possibilities*.

Further, the DNA evidence is only one part of the prosecution's circumstantial case against the defendant, and you already have my directions on how circumstantial evidence is to be evaluated. Where the DNA, as part of a circumstantial case, has a reasonable hypothesis consistent with innocence this would require a not guilty verdict.

DNA Direction - State of Western Australia v Edwards No 7 [2020] WASC 339; Hall J at [184] –[190]

“It was not seriously in dispute that the DNA of the accused was in the mixed sample – the real issue was how it got there.

Deoxyribonucleic acid (DNA) is a molecule which is one of the basic building blocks of humans. It contains the information that determines the personal characteristics of each person. Because DNA is highly variable as between different people it has come to be used as a means of proving the identity of a suspected offender. DNA evidence is now widely accepted for use in investigations and court proceedings. However, it is important to understand the nature and limitations of such evidence.

DNA evidence involves the comparison of a questioned sample of DNA from a crime scene with a known sample of the DNA of the accused. This is done by analysing both samples using a kit that identifies the alleles that are present at a number of loci on the DNA molecule. At each locus an individual will have two alleles, one inherited from each parent. Loci are chosen that are known to be highly variable in the population. By comparing the results to see whether alleles present in the sample from the accused are also present in the questioned sample it is possible to determine whether there is a likelihood that the accused is a contributor to the questioned sample or whether the accused can be excluded as a possible contributor. If there is a reasonable possibility that the questioned DNA is that of the accused, or that he has contributed to a mixed sample, any conclusion is expressed in the form of a likelihood ratio. That is the case here.

The production of DNA profiles is the end result of an analysis of samples that involves a number of discrete steps. The validity and reliability of the profile depends upon each of those steps being carried out with care and in accordance with recognised scientific methods. It is relevant, therefore, to consider the procedure followed in a particular case in determining whether the evidence is reliable. It is not simply a matter of referring to the end results.

Before making a comparison the reporting scientist may examine the profile and discount or exclude some features, for example because they do not reach reportable limits or because they are recognised artefacts of the kits used to analyse the sample. The reliability of the final conclusions may depend on whether these judgement calls are sound, so any evidence in this regard must be considered before turning to the likelihood ratio.

A likelihood ratio compares two competing hypotheses, that the accused is the contributor to the questioned sample or that some other unknown and unrelated person is the contributor. The ratio is expressed in statistical terms that may, as here, involve very large numbers. It is important not to be overawed by these numbers and to bear in mind that, however high they may be, the question of whether it is the accused's DNA in the sample is ultimately one for me to answer. That question must take into account all of the relevant evidence. The identity question does not involve a mechanical application of probabilities, nor is it one capable of being reduced to a mathematical computation.

The likelihood ratio should also not distract attention away from a consideration of other questions, in particular, how the DNA of the accused may have got into the questioned sample and when it did so. DNA analysis cannot establish what type of cells the DNA came from, when it was deposited or how it came to be in the tested sample. Proof that the DNA of the accused is highly likely to be in the questioned sample does not in itself prove guilt. It is also necessary to be satisfied that the DNA got into the sample in a manner that implicated the accused in the alleged offence.

DNA evidence is a type of circumstantial evidence. If accepted it shows the probability of a match as compared with the chance of a random occurrence. This evidence, if accepted, may not alone prove guilt, but it can be taken into account along with all of the other accepted evidence in determining whether guilt is proved beyond reasonable doubt.”

ANNEXURE C:

A challenging DNA case – *WA v Edwards* 2020

In 1996 and 1997, 2 young women were raped and murdered in Perth. Their cases, as well as the disappearance of another young woman and an earlier rape of another, were linked by some circumstantial evidence. However, until Edwards' DNA was put on a database[108] and then linked to the 1995 rape, and one of the samples of DNA extracted from under the fingernails of one of the murder victims, the evidence to support murder charges was lacking. Justice Hall's judge-alone determination involved a careful review of how the defence sought to test and challenge the DNA evidence, and how the prosecution carefully and painstakingly engaged in predicting and then rebutting those challenges. Their efforts were ultimately successful.

The defence strategy focused on the risk that the DNA exhibits had been contaminated. They had multiple things to go on, including:

1. That the material analysed was not fingernail scrapings but clippings taken as part of the post-mortem examination procedure;
2. The collection procedure was not videorecorded;
3. There was difficulty obtaining a sample of one of the nails (AJM40) because it was close to the nail's quick;
4. One sample was initially assessed as being "debris" that was not suitable for testing;
5. Low copy number testing of other exhibits was carried out despite the laboratory not being accredited to do that type of testing;
6. When the relevant samples were sent to FSS in the UK in 2008, the samples were prepared for testing by a scientist who no longer has any memory of what he did;
7. The DNA in question is trace DNA, which was collected and stored in the 1990s when the state of knowledge and the protocols in handling such samples were much less sophisticated;
8. There was a possibility of cross-contamination with other exhibits that did have the defendant's DNA on them;
9. More examples of contamination included:
    a. Intimate swabs collected from another potential victim when analysed in 1996 produced no DNA profile. They were later analysed again in 2017 by a UK laboratory. However, the later analysis disclosed an almost complete DNA

[108] All Australian jurisdictions are linked to the National Criminal Investigation DNA database (NCIDD).

profile matching the profile of a WA scientist, who was involved earlier in preparing those swabs for DNA analysis;

b. An intimate swab collected from a victim identified yielded no results in 1997. But, when later analysed in the UK, a DNA profile was obtained in which 17 of the 19 components matched a second WA scientist. That scientist had been involved in testing the exhibit between 1997 and 2001;
c. Fingernail samples from the other victim was found, combined and analysed in 2017 or 2018. A mixed DNA profile was obtained, with the major component matching the victim's profile. The minor component was subjected to Y chromosome analysis and found to be consistent with the profile of a WA scientist although, there was no documentation that this scientist had been involved in processing these exhibits! The explanation given was that the layout of the examination area at the time of processing would have allowed for the scientist in question to be in the vicinity of the items during examination and processing, and therefore represents a possible source of contamination; and
d. A swab from a tree branch located on top of that victim was examined in 2002. It yielded a partial profile that was later found to match the profile of a victim of a completely unrelated crime.

Justice Hall convicted Edwards. His reasons are compelling given the other evidence presented, and the work done by the Crown to rebut each potential defence hypotheses.

ANNEXURE D - Further Reading:

Buckleton, J. S., Bright J., and Taylor, D. Forensic DNA Evidence Interpretation. 2nd ed. CRC Press. Boca Raton, 2016.

Butler J.M., *Forensic DNA typing*, 2nd ed. Elsivier 2005

Committee on DNA Forensic Science, National Research Council. (1996) An Update: The Evaluation of Forensic DNA Evidence. National Academy Press, Washington, DC.

Gill P, *Misleading DNA Evidence: Reasons for miscarriages of justice*, Elsivier, 2014

Gill P., Haned H. *A new methodological framework to interpret complex DNA profiles using likelihood ratios,* Forensic Science International: Genetics 7 (2013) 251–263

http://netk.net.au/DNAHome.asp

Goodman-Delahunty J. & Hewson L., *Improving jury understanding and use of expert evidence* Australian Institute of Criminology Technical Report 37, 2010.

National Research Council, *Strengthening Forensic Science in the United States: A path forward* The National Academies Press 2009

Puch-Solis R., Roberts P., Pope S., Aitken C., *Assessing the Probative Value of DNA* Evidence *Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses*

Royal Statistical Society's *Working Group on Statistics and the Law*

Science and Technology Select Committee. Forensic Science and the criminal justice system: a blue print for change, UK House of Lords; 2019. https://publications.parliament.uk/pa/ld201719/ldselect/ldsctech/333/33309.htm

Scientific Working Group on DNA Analysis Methods (SWGDAM) Guidelines for Validation of Probabilistic Genotyping Systems– FINAL APPROVED 06/15/2015. Available at: www.swgdam.org/publications

Smith M., Mann M., *Recent Developments in DNA Evidence* Trends and Issues in Crime and Criminal Justice, no 56, Canberra,

The Royal Society and the Royal Society of Edinburgh - *Science and the Law* programme 'The Use of Statistics in Legal Proceedings' https://royalsociety.org/about-us/programmes/science-and-law/.