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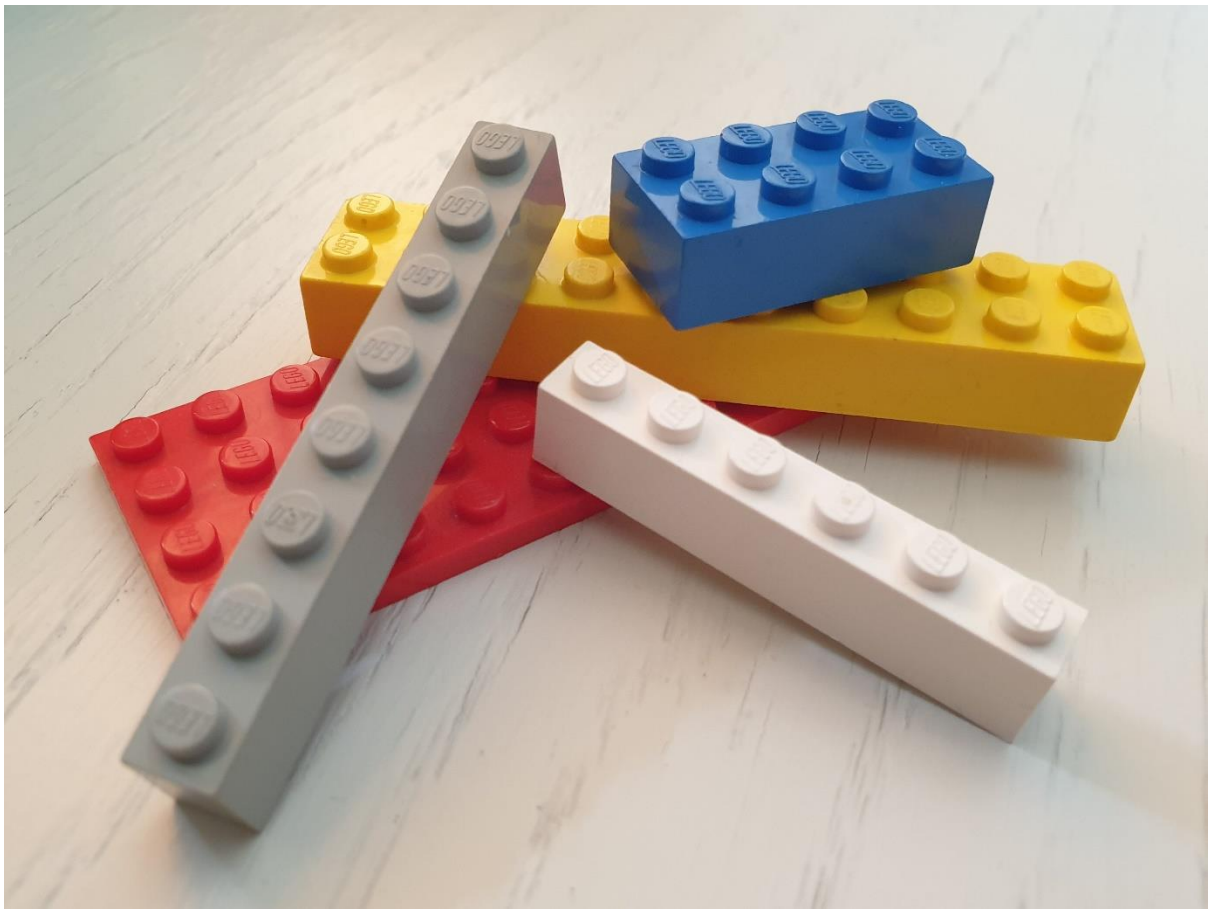
EVALUATING FORENSIC DNA EVIDENCE: CONNECTING THE DOTS



ABSTRACT

Technological developments within the field of forensic genetics have enhanced the sensitivity and specificity of DNA testing tremendously and have broadened the applications of biological evidence in criminal investigations. Evaluation and communication of the evidential findings within criminal cases have not maintained the same pace, which has largely stemmed from a failure to adopt a standardised approach within and across the various fields of forensic science. Within forensic biology, this has led to unjustified opinions on the weight of the evidence and occurrences of the association fallacy, when the weight of evidence given propositions at one level of the hierarchy of propositions is inappropriately transposed to a higher level. We further define the association fallacy to include the terms, 'source level fallacy' and 'activity level fallacy', to enable the forensic science community to better identify and address issues in biological evidence evaluation. It is important to understand these concepts and their causes, and in doing so, identify potential avenues to avoid these fallacies in forensic science casework. These avenues include training and education of forensic and legal professionals, as well as research into transfer, persistence, prevalence and recovery (TPPR) of DNA and biological evidence in general.

1. INTRODUCTION

Forensic science evidence, including DNA, is routinely interpreted and evaluated given propositions within the framework of the 'hierarchy of propositions', as proposed by Cook *et al.* (Cook, Evett, Jackson, Jones, & Lambert, 1998a). This hierarchy initially consisted of source, activity and offence levels, but in forensic genetics, the hierarchy has been extended to include further source 'sub' levels to accommodate the complexities of DNA evidence. For example, the weight of the evidence given propositions stating inclusion versus exclusion of DNA of the person of interest (POI) in a crimestain was once considered to be at the source level, but is now determined at the sub-source level, with evaluations given source level propositions now including consideration of the attribution of DNA to a specific body fluid or cellular material (Evett, Gill, Jackson, Whitaker, & Champod, 2002). For the interpretation of DNA mixtures, if the mixture as a whole is compared to a reference profile(s), then this is also interpretation given sub-source level propositions; however, if only a component of the mixture (for example, the major profile) is compared to the reference profile, then this interpretation requires sub-sub-source level propositions (Taylor, Bright, & Buckleton, 2014). For the purposes of this review, we will use the term sub-source level to encompass evaluations of DNA evidence given propositions that solely consider who the DNA, or part thereof, comes from.

To ensure that an appropriate evidential weight is provided for a particular piece of evidence, it is crucial that (a) the propositions, and therefore the level within the hierarchy, to which the evidential weight relates are specified, and (b) the evidential weight has been determined using data relevant to the evaluation of the evidence given those propositions. This allows for the provision of a different opinion and/or calculation of a different likelihood ratio (LR) for each level (Gill et al., 2018) and requires understanding, and transparency of, the limitations of evaluating DNA evidence given propositions at each level of the hierarchy. This is particularly important to ensure that the 'association fallacy' is avoided. Gill defined the association fallacy as when "*a probability is transposed from one level of the framework of propositions to a higher level*"(Gill, 2014). With respect to DNA evidence, the association fallacy can mean the transposition of an LR calculated at the sub-source level to the source level, or from the source level to the activity level, or even from the sub-source level to the activity level. Each of these transpositions potentially overlooks different, but crucial aspects in evidence evaluation. To enable the forensic science community to better identify and address issues in DNA evidence evaluation, we propose further defining the association fallacy to introduce the terms, 'source level fallacy' and 'activity level fallacy'. We define these fallacies as when an opinion (whether given as an evaluative opinion, expert opinion or LR) at the sub-source level is incorrectly transposed to the source level (source level fallacy), and when an opinion at the sub-source or source level is transposed to the activity level (activity level fallacy)[1].

In this review[2], we discuss how these fallacies can occur and consider how research, further testing, and evaluation strategies within considerations of transfer, persistence, prevalence and recovery (TPPR) of biological traces can be used to help prevent them. We also review the scientific basis of common DNA-TPPR beliefs that we have experienced within casework and during discussions with forensic professionals, and consider how best to improve the quality, range and nature of data available to inform evaluations of biological evidence given alternative propositions at the source and activity levels. Finally, we bring together recommendations made by casework scientists, researchers and advisory bodies to connect the dots among the various evidence evaluation issues

and identify a path forward to minimise the occurrence of the discussed fallacies and to direct future research.

2. "SOURCE LEVEL FALLACY" AVOIDANCE: MAINTAINING A DISTINCTION BETWEEN SOURCE AND SUB-SOURCE LEVELS

The weight of evidence given propositions stating inclusion versus exclusion of DNA of the POI in a crimestain, represented by an LR, is determined at the sub-source level and calculated, in part, using frequencies of the observed alleles within the relevant population. When such a sub-source level LR is incorrectly transposed to the source level, we suggest that this is termed a source level fallacy. Of note here, is the use of the word 'incorrectly', as there are exceptions when it may be appropriate to transpose the sub-source level LR to the source level. An example of such an exception is when a full, single source DNA profile is recovered from a sample taken from a visible body fluid, e.g. a pool of blood near the body of a deceased. In this situation, to be able to transpose the LR given the sub-source level propositions to an LR given source level propositions, some assumptions need to be made. The first assumption is that the sample contains DNA of only a single individual; hence the probability of masking of contributors, or two individuals having the same DNA profile (e.g. identical twins), is considered to be zero. The second assumption is that the cellular material or body fluid is present in the sample; hence the probability of *human* blood being present in the sample is one. The third assumption is that this blood is the only body fluid or cellular material present in the sample. If these assumptions can reasonably be made, then the LR at sub-source level would equal that at the source level. It must be noted that these assumptions are based in part on observations made on evidentiary items (testing results), and in part on contextual information of the case that is provided to the scientist (i.e. sample taken from *a pool of visible blood near the body of a deceased*), and as such, these assumptions will always be partly dependent on case context. These assumptions may be reasonable within the context of a specific case, but must be recognised and communicated as such to facilitate full transparency of the scientific opinion and allow appropriate review by others assessing the case, such as opposing lawyers.

As described by Gill *et al.* in the ISFG DNA Commission's guidelines for evaluating DNA evidence given sub-source level propositions, these assumptions of the biological nature of the DNA can only be made in such defined circumstances, allowing the sub-source LR to be elevated to the source level (Gill et al., 2018). However, if a DNA profile, especially a low level profile, is obtained from a dilute or mixed body fluid, then the biological nature of the DNA may be disputed and therefore the sub-source LR cannot be elevated to the source level (Gill et al., 2018; Taylor, Kokshoorn, & Biedermann, 2018). Similarly, if a mixed DNA profile is obtained, even from a confirmed body fluid, it may be unclear as to which DNA profile(s) in the mixture can be confidently attributed to the body fluid. With today's highly sensitive DNA technology and the common detection of mixed profiles, it is now routine to encounter case circumstances in which the sub-source LR cannot be transposed to the source level. Case examples in which the source level fallacy has occurred and has led to miscarriages of justice have been previously described (Gill, 2014), and similarly, we have experienced occasions in casework where unsupported assumptions have led to the source level fallacy, such that the likelihood of DNA attribution to a particular biological material has been the centre of discussion between prosecution and defence (scientists).

To facilitate avoidance of this fallacy, there are a number of considerations to take into account. Firstly, it is crucial to ensure that both casework and research scientists are clear as to which level they are referring. For example, it is common to see within the published literature, the use of the term '(sub-) source' to encompass evaluations given both sub-source and source level propositions (Taylor, 2016b; Taylor, Abarno, Hicks, & Champod, 2016), and yet, there are occasions when this can be used incorrectly, particularly when referring to elements that relate solely to the sub-source level. Similarly, in casework, scientists should be transparent about the propositions used in their assignment of the LR, to ensure that they do not inadvertently elevate the sub-source LR to the source level. In the ISFG DNA Commission's further guidelines for evaluating DNA evidence, in addition to being explicit about the level of the hierarchy being considered by the propositions within a casework report, it is also recommended that casework scientists ensure that they clearly understand the aspects to be considered within the hierarchical level of the propositions in which the LR is assigned (Gill et al., 2020). When a sub-source level LR is knowingly elevated to source level, scientists should also clearly state the assumptions made about the biological nature of the DNA and the information on which those assumptions are based. In addition, a caveat should be included in such reports to state that, if these assumptions are contested, a new evaluation given activity level propositions is required.

Secondly, when evaluating DNA evidence at the source level, whether that is considering if a sub-source LR can be appropriately elevated or forming a separate source level opinion, body fluid testing may provide valuable information, but only if the results of such testing are handled appropriately and assessed probabilistically. In the published literature, such tests are frequently labelled as being either 'presumptive' or 'confirmatory' (Harbison & Fleming, 2016; Virkler & Lednev, 2009), but these labels are misleading, and it is a widely held misconception that there are so-called 'confirmatory' tests. To say that a test is a confirmatory test suggests that a positive test result unequivocally signals the presence of the tested substance, while a negative result proves the absence of said substance. However, every test that is currently used in forensic biology will display both types of errors, and no test currently has 100% sensitivity and specificity under all conditions and for all substrates. For example, the ABAcard® HemaTrace® test for blood is commonly reported as being a confirmatory test for human blood and yet it can also test positive in the presence of blood from higher primates and ferrets (Johnston *et al.* 2003). To label a test as confirmatory means that several crucial assumptions are being made by the scientist who is reporting the findings. These assumptions include that: no cross-reactivity of the test with other substances or substrates can occur, the procedures are adequately followed, no contamination of disposables or laboratory equipment has occurred, and there is no human error in the reading, logging and interpretation of the test outputs. Hence these assumptions require a leap of faith from LR to posterior probabilities of the propositions that the cell type is present or absent, and subsequently (given some probability threshold) to a decision/assumption that the cell type is present or absent. These assumptions may or may not be reasonable given the particular test performed and the case circumstances (many cases will not involve primates or ferrets, for instance), but they are assumptions nonetheless and should be recognised and documented, and reported when crucial to the evaluation of the observations. Since the case circumstances, and particularly the context in which the trace was found, needs to be taken into account when assigning the posterior probability of a cell type being present or absent, the test itself can, by definition, not be confirmatory. Additional molecular testing to standard serology is available to provide further assistance with identification of the type

of body fluid and/or tissue that gave rise to the DNA profile of interest. Such methods include various RNA-based technologies, epigenetic approaches (Sijen, 2015; Vidaki & Kayser, 2018) and microbiological analyses (Harbison & Fleming, 2016), with mRNA profiling being used in casework in some jurisdictions, such as New Zealand and the Netherlands (Lindenbergh, Maaskant, & Sijen, 2013). However, as with all body fluid or other cellular material testing, these mRNA, epigenetic or microbiological tests are not confirmatory. A probabilistic assessment of the testing results can be used to calculate the weight of evidence for results from body fluid and cellular material tests (Danaher, White, Hanson, & Ballantyne, 2015; De Wolff, Kal, Berger, & Kokshoorn, 2015; de Zoete, Curran, & Sjerps, 2016).

Thirdly, an association needs to be made between the findings from DNA profiling and those from body fluid or cellular material testing. These associations may be exceedingly complex. For example, Peel and Gill's study showed that the ratio of DNA attributed to a body fluid and touch deposit, when sampling glass slides that had been handled before or after staining with dilute saliva or blood, were dependent on stain size and quality and the shedder status of the handler (Peel & Gill, 2004). Similar issues were also observed by Harteveld *et al.* when attempting to associate DNA and mRNA results from mixed samples (Harteveld, Lindenbergh, & Sijen, 2013). These studies illustrate the challenge of confidently attributing DNA to a body fluid under such circumstances and demonstrates the requirement for a separate evaluation given source level propositions. Examples of evaluation of findings given source level propositions are given in the following references (de Zoete et al., 2016; Oosterman, Kokshoorn, Maaskant-van Wijk, & de Zoete, 2015; Taylor, 2016b; Taylor, Abarno, Hicks, et al., 2016). With mRNA typing for body fluids and other cellular materials, progress is being made with cell type attribution to donors through mRNA sequencing (Ingold, Dørum, Hanson, Ballantyne, & Haas, 2020). With this SNP typing of mRNA markers, the current uncertainty inherent in mRNA cell typing will remain, however, and the weight of the evidence of a corresponding mRNA SNP profile of a POI to that of a mixed trace will need to be determined probabilistically as well. Nonetheless, this technique will provide valuable additional information on the potential source of a body fluid or tissue type.

Finally, background sampling, that is the sampling of areas adjacent to the area of interest, might be considered informative when considering source level propositions. Consider the example of a small bloodstain on the shoe of the suspect of a violent crime, a sample from which yields a mixed DNA profile of DNA from the suspect and victim, which is not in dispute. However, the source of the blood may be disputed; was the blood donated by the suspect or by the victim? Sampling additional, non-blood areas of the shoe might provide additional information. If the DNA of the victim is only found in the bloodstain, this might provide support for the proposition that they donated the blood over the proposition that the suspect donated the blood. However, to assign the weight of the evidence, probabilities need to be assigned to the findings given these propositions. At this point, information on the prevalence of DNA of both the suspect and the victim on the shoe needs to be taken into account. Given the proposition 'the blood in the sample was donated by the suspect', we would need to assign a probability to recovering the victim's DNA on the shoe from a non-blood material. This would require the scientist to consider probabilities of TPPR given specific activities not specified in the propositions. Hence, when considering background sampling, this is best done when considering propositions at the activity level (as discussed by (Graham Jackson, 2013)).

3. "ACTIVITY LEVEL FALLACY" AVOIDANCE: FORMALLY EVALUATING FINDINGS GIVEN ACTIVITY LEVEL PROPOSITIONS

A crucial feature of the evaluation of DNA evidence given activity level propositions is the requirement of the forensic scientist to consider a complex of factors associated with the transfer, persistence, prevalence and recovery of DNA (Gosch & Courts, 2019; G. Meakin & Jamieson, 2013). Such considerations have tended to focus on propositions concerned with activities that result in direct DNA transfer as opposed to activities resulting in indirect DNA transfer or legitimate activities that resulted in direct transfer. Since the discovery that DNA deposited on a surface through contact could be collected, transferred to another surface via a vector, and recovered from that surface (R. A. H. van Oorschot & Jones, 1997), there was a time when the prospect of indirect DNA transfer was not considered feasible (Ladd, Adamowicz, Bourke, Scherczinger, & Lee, 1999) or only possible under favourable conditions, with the belief that DNA from the vector would transfer in such large quantities that it would usually overwhelm any indirectly transferred DNA (Wickenheiser, 2002). There followed some debate in the published forensic science literature regarding the existence of indirect transfer and its relevance to forensic casework, but it was gradually accepted that issues of DNA transfer should be considered in casework (G. Meakin & Jamieson, 2013; R. A. H. van Oorschot, Ballantyne, & Mitchell, 2010) and activity level questions surrounding DNA evidence, and the factors that might have led to its transfer and subsequent recovery, are now regularly raised in casework.

Understanding the need to evaluate DNA evidence given appropriate activity level propositions with consideration of DNA-TPPR is only the first step of the process; the second step is knowing what information is required and where to find it, with the final step being how to use that information to inform such an evaluation. In addition to the debate regarding indirect DNA transfer, the last couple of decades have also seen debate within the forensic scientific community as to how best to address these questions at the activity level. This debate came to a head with the England and Wales Appeal Court case of R v Weller in 2010 ("R v Weller (2010),"), in which the Appeal Court judges chose to overlook the empirical data used to support the evaluation given activity level propositions put forward by the defence to instead rely upon the casework experience of the prosecution scientist. The scientific response to this approach of using experience to inform evaluation given activity level propositions was generally one of opposition (Champod, 2013; Jamieson & Meakin, 2010; Nic Daéid, 2010; Rudin & Inman, 2010), and whilst there has been further debate on the source of information for such evaluations of DNA evidence (Casey et al., 2016; G. E. Meakin & Jamieson, 2016), it is now generally accepted (R. A. H. van Oorschot, Szkuta, Meakin, Kokshoorn, & Goray, 2019) that the primary source of information should be experimental data where the ground truth is known, in accordance with various guidelines and recommendations on evidence evaluation from forensic science agencies and experts in the field (Association of Forensic Science Providers, 2009; Gill, 2019; Gill et al., 2020; G. Jackson, Aitken, & Roberts, 2015; Taylor et al., 2018; Willis et al., 2015). Other secondary sources of data can also be used, including unpublished empirical data, calibrated casework experience, and collated data derived from casework (Gill et al., 2020). The applications and limitations of these data sources are discussed elsewhere (e.g. (Taylor et al., 2018; R. A. H. van Oorschot et al., 2019)), however, it is important to note that casework experience must be justifiable

and demonstrable to the court, and not an arbitrary or speculative assertion (Taylor et al., 2018), nor a statement of a number of years working in forensic science (Black & Nic Daeid, 2015; G. E. Meakin & Jamieson, 2016).

In many jurisdictions, a verbal scale is used to communicate the strength of forensic evidence to the court (for examples, please see those presented by Association of Forensic Science Providers (Association of Forensic Science Providers, 2009) and European Network of Forensic Science Institutes (Willis et al., 2015))[3]. Interpretation of DNA evidence given sub-source level propositions requires the calculation of a likelihood ratio based, in part, on the frequencies of the detected alleles observed within a relevant population. Such likelihood ratios commonly reach the billions; the evidence providing 'extremely strong support' for one proposition over the other. Although there is no direct relationship between the LR for sub-source level propositions and that for activity level propositions (Gittelson et al., 2016), when evaluating the same DNA evidence, it is possible for the scientist or decision makers to incorrectly transpose the value of the LR at sub-source level to the activity level, resulting in a conclusion that there is also 'extremely strong support' for the evidence given one activity over another to explain how the DNA was deposited; if this is done without explicitly considering factors of DNA-TPPR, this is considered an activity level fallacy. When a forensic scientist relies solely on their expert belief and/or experience, there is a risk of overstatement of the strength of support of evidence at the activity level, which could be exacerbated by the activity level fallacy. In addition, not only might this be committed by the expert, but the court might also carry over the weight of evidence at the sub-source level to the activity level without sufficient guidance from the scientist (Gill et al., 2020).

In recent years, several jurisdictions have started to use Bayesian Networks (BNs) to facilitate the evaluation of DNA evidence given activity level propositions (Taylor et al., 2018). There are a number of published studies in which authors have inputted data, either from their own experiments or from published empirical research, into BNs constructed from circumstances that were based on real case scenarios or on commonly encountered generic casework scenarios. For example, when applying their BN to the evaluation of DNA evidence in three different casework scenarios, Taylor *et al.* reported LRs of up to 14, depending on the specifics of the case scenario and data considered (Taylor et al., 2017). Similarly, activity level LRs of 44-150 were calculated by Szkuta *et al.* in their evaluation of aspects inspired by the "Fitzgerald case" from South Australia (Szkuta, Ballantyne, Kokshoorn, & van Oorschot, 2018), and of 0.22-5 in the evaluation of a burglary scenario by Volgin (Volgin, 2019). Even in the absence of BNs, activity level LRs can still be determined based on empirical data, as illustrated by the following two studies. Breathnach *et al*. used their research data to evaluate different DNA findings given activity level propositions considering whether an individual wore underpants as opposed to the proposition that someone else wore them and the individual touched them (M. Breathnach, Williams, McKenna, & Moore, 2016). Across the different DNA findings, LRs were determined that ranged from 0.1 to 17 (M. Breathnach et al., 2016). Similarly, Steensma *et al.* applied data from an inter-laboratory study on used cable ties to the evaluation of DNA evidence in a simplified model of a robbery in which a perpetrator tied a victim's wrists together with a cable tie (Steensma et al., 2017). The DNA finding was evaluated given the proposition that the POI tied a cable tie around the victim's wrists as opposed to the proposition that someone else tied the cable tie and the POI handled the cable tie prior to the incident.

Depending on the data used, LRs were obtained that ranged from 62 to 287.5 in support of the first proposition (Steensma et al., 2017).

There are two important observations to take from these examples. Firstly, when dealing with a single DNA finding, or a few conditionally dependent DNA findings, activity level LRs determined based on empirical data tend to be in the region of 'weak' to 'moderately strong' on the verbal scale, which is substantially different from 'extremely strong' support based on evaluations given propositions at the sub-source level. This is reflected in the recent ISFG DNA Commission guidance, in which it is noted that LRs at the activity level will commonly be many orders of magnitude lower than those at the sub-source level (Gill et al., 2020). And secondly, as Taylor *et al.* note, increasing the data available to enter into evaluations given activity level propositions may not necessarily increase the level of support obtained (Taylor et al., 2017). Caution is therefore required when evaluating DNA evidence given activity level propositions to ensure that the evidential weight is not overstated. Use of empirically-derived activity level opinions within casework will not only facilitate this and avoid the activity level fallacy, but will also provide the court with a more robust and transparent probative value of the DNA evidence (Gill et al., 2020; Szkuta et al., 2018; Taylor et al., 2018).

The need for a proper framework for evaluation of findings: An illustration

Cortellini *et al.* recently published a paper reporting the analysis and evaluation of the biological evidence in a case of an alleged sexual assault of a minor (Cortellini, Brescia, Cerri, & Verzeletti, 2020). Samples from the fingers of the accused were submitted for mRNA and DNA profiling and the paper summarises the findings as follows: "*Thanks to the use of the combined DNA profiling and RNA analysis it was possible to confirm the presence of the victim's genetic profile on the suspect's hand and to identify this biological material as vaginal secretion, confirming that the man had touched/penetrated the little child genital area. Besides, the identification of blood marker on the samples obtained from suspect's hands blotting was compatible with the presence of the lesions found on the little child's labia minora during the gynecological examination, probably due to digital penetration.*"

Apparent fallacies (aside from the transposed conditional) are made in relation to the interpretation of both the nature of the biological materials, as well as the activity that lead to their deposition:
1) It appears that the mRNA profiling results are taken as a confirmatory test for the presence of vaginal epithelial cells. However, the mRNA expression patterns presented in the paper may also be caused by cross-reactivity with other biological materials like nasal mucosa (van den Berge, Bhoelai, Harteveld, Matai, & Sijen, 2016).
2) While the association between this gender specific cell type (if present) to the female donor in the mixture may be sensible, if the samples are assumed to contain only DNA of the accused male and female victim, this is not evident for the assumed presence of blood and the implicit assumption that it derived from the victim.
3) The activity that lead to the observations is deduced from the findings, rather than considering the findings given alternative proposed activities.

We note though that this is a paper written for publication to the forensic science and legal communities, which differs from an expert report submitted for court, and therefore hope that these uncertainties were appropriately communicated to the decision maker during the case itself.

4. "ACTIVITY LEVEL FALLACY" AVOIDANCE: CONSIDERATION OF DNA-TPPR BELIEFS

Another element of DNA evidence evaluation given propositions at the activity level that might contribute to the occurrence of the activity level fallacy is reliance on unsupported assumptions about DNA transfer. It is accepted that practitioners within the range of domains that constitute forensic science are susceptible to cognitive biases, such as contextual bias and confirmation bias, in their decision making during evidence interpretation (as reviewed in (Cooper & Meterko, 2019)). When it comes to DNA evidence, it has been demonstrated that interpretation of DNA profiles given sub-source level propositions can be impacted by cognitive bias (Dror & Hampikian, 2011), and although it has been previously raised that risks from such cognitive bias are likely to be equally relevant to the evaluation of DNA evidence given activity level propositions (Taylor et al., 2018), no such research investigating this has yet been published. Nonetheless, several procedures have been proposed to minimise contextual bias in forensic casework. These include (but are not limited to) case pre-assessment given propositions at activity level by an individual who is not aware of the results of prior examinations to reduce the risk of post-hoc rationalisation (Stoel, Berger, Kerkhoff, Mattijssen, & Dror, 2014).

It is clear from the current literature that the forensic science community has come a long way in its discovery and understanding of the variables that impact DNA-TPPR and inform evaluations given activity level propositions (Burrill, Daniel, & Frascione, 2019; R. A. H. van Oorschot et al., 2019), as well as in its knowledge of the methods that can be used to conduct such an evaluation (Gill et al., 2020; Taylor et al., 2018). However, in the absence of research to consider the potential impact of cognitive bias on the evaluation of DNA findings given activity level propositions, it is vital to consider whether beliefs that are widely held about DNA-TPPR, particularly those that may get incorporated into such evaluations, are supported by the scientific research. It is therefore important to consider what we currently know, what we think we know but remains to be answered, and what we thought we knew to be true and research has proven otherwise. Here, we present a few examples to illustrate the importance of ensuring that beliefs incorporated into evaluations given activity level propositions are supported by data and are not a result of potentially biasing preconceived ideas.

"Every contact leaves a (DNA) trace"

The notion that 'every contact leaves a trace' has been adapted from Edmond Locard's exchange principle, that when two objects come into contact there is an exchange of material (Locard, 1920). When considering touched items, for the most part, DNA from an individual coming into direct contact with the item is regularly observed in the ensuing DNA profile, though this is not always the

case; on a small number of occasions, DNA from the person making contact was not observed in DNA profiles generated from surfaces following, for example, use of burglary-related tools for different periods of time and with different intensities (Pfeifer & Wiegand, 2017), using a knife in a stabbing action (Samie, Hicks, Castella, & Taroni, 2016), and a 10 second hand print on a glass plate (Szkuta, Ballantyne, & van Oorschot, 2017). These studies, in addition to many others, demonstrate that there is a low probability of not recovering DNA from the handler of an item under the observed circumstances, which incorporates the prospect that DNA has not been transferred, has not persisted, and/or, has not been recovered in quantities great enough to be profiled (Gill et al., 2020). The latter also includes the aspect of targeting, whereby areas of contact may have been overlooked during sampling and/or DNA lost to exhibit packaging (Goray, van Oorschot, & Mitchell, 2012). Thus, it is not possible to determine whether every contact does or does not leave a DNA trace, and in applying published data, the scientist can only consider the probability of recovery given the proposed activities and factors within the case, such as the time delay between the activity of interest and DNA recovery, as well as any activities performed during this delay, plus climatic conditions.

"An absence of (DNA) evidence is evidence of absence"

It is commonly inferred that a failure to recover DNA from a specific individual on an item of interest constitutes an absence of evidence and is proof that an activity did not occur. Although an absence of traces may well be evidence favouring other scenarios (Thompson & Scurich, 2018), this line of reasoning implies that evidence is only evidence if it is incriminating to an accused. As such, not finding DNA from a POI does not constitute an absence of evidence, but rather an absence of DNA (Taylor et al., 2018), and could, among other factors, be due to efficiency limitations of the targeting, collection, processing and interpretation methods applied, and/or loss during activities performed during and following the offence. Absence of biological materials where it is expected to be seen will generally support a competing proposition, as demonstrated in the evaluation of the Drummond case (Taylor, 2016a). Further, as recommended by the ISFG DNA Commission, all findings, both present and absent, relevant to a particular issue should be considered by the scientist (Gill et al., 2020). As explored by Taroni *et al.*, questions such as 'does the absence of evidence constitute evidence of absence?' are difficult to answer without the logical framework provided by Bayesian theory (Taroni, Bozza, Hicks, & Garbolino, 2019). As they demonstrate, Bayesian theory can assist the scientist in understanding the probative value of absent forensic traces.

"Shedder status does not exist"

When considering handled or worn items, the idea that some people deposit more or less DNA than others, defined as good and poor shedders respectively, was first observed by van Oorschot and Jones in 1997 and later explored by Lowe *et al.* and Wickenheiser in 2002 (Lowe, Murray, Whitaker, Tully, & Gill, 2002; R. A. H. van Oorschot & Jones, 1997; Wickenheiser, 2002). In the debate that followed, many argued that it was overly simplistic to define individuals as 'good' or 'poor' shedders, as the ability to deposit DNA could be attributable to factors including, but not limited to, skin

conditions (Kamphausen, Schadendorf, von Wurmb-Schwark, Bajanowski, & Poetsch, 2012), gender and/or personal hygiene (Lacerenza et al., 2016; Phipps & Petricevic, 2007), and the region of the skin making contact, whether due to the nature of the skin at that area (Oleiwi, Morris, Schmerer, & Sutton, 2015; Zoppis et al., 2014) or the prospect of other biological material being present (van den Berge, Ozcanhan, Zijlstra, Lindenbergh, & Sijen, 2016). It is fair to say that 'shedder status' has been a topic of interest for some time, but with a number of recent studies recognising that some people do contribute more or less DNA to a contacting surface than others (Fonneløp, Ramse, Egeland, & Gill, 2017; Goray, Fowler, Szkuta, & van Oorschot, 2016; Kanokwongnuwut, Martin, Kirkbride, & Linacre, 2018), the focus has rather drifted to how this knowledge can be integrated into casework evaluations and reporting. Recent examples of how this can be probabilistically achieved (Samie, Taroni, & Champod, 2020; Taylor et al., 2017) have demonstrated that in reality, individuals could not be defined into distinct groups (i.e. 'good' and 'poor' shedders), but rather each individual has a continuous distribution of shedding propensity, on which they will exist at different points.

"DNA deposited through touch is derived from sloughed-off skin cells"

The dangers of use of terms, such as 'touch DNA' and 'skin DNA' to describe DNA recovered from a surface that has presumed to have been handled or worn, are discussed by van Oorschot *et al.* (R. A. H. van Oorschot et al., 2019). However, it is important to note that there is still a widely held misconception, particularly by lawyers, investigators and even forensic science students, that DNA deposited through touch is derived from sloughed-off skin cells. A number of studies have shown that, although skin cells are one source of DNA deposited by touch, other sources of DNA include cellular material collected on the hands from other parts of the body, including body fluids such as saliva and nasal mucus, and cell-free DNA in sweat; for a detailed review, please see (Burrill et al., 2019).

"Increased pressure increases the amount of DNA deposited"

Whilst not a misconception, the belief that increased pressure increases DNA deposition was widely held long before it was actually scientifically supported by empirical research. It was initially shown in 2010 that the application of pressure between two contacting surfaces has the capacity to result in a greater transfer of DNA compared to passive contact (Goray, Eken, Mitchell, & van Oorschot, 2010; Goray, Mitchell, & van Oorschot, 2010). The impact of pressure on DNA transfer and recovery was then later confirmed by Hefetz *et al.* and Tobias *et al.* (Hefetz, Einot, Faerman, Horowitz, & Almog, 2019; Tobias, Jacques, Morgan, & Meakin, 2017), both of which demonstrated that increasing the deposition pressure of fingertips on a surface subsequently increased the rate of DNA recovery.

"The duration of contact does not influence how much DNA is deposited"

It seems reasonable to assume that the longer an item is in contact with the skin's surface, or an item on which DNA is deposited, the more readily DNA transfer occurs between the contacting surfaces. However, there is evidence to suggest that this is not the case. Several studies directly and indirectly assessing the impact of contact duration have found very little impact on: DNA yields from previously DNA-free polypropylene tubes held from 5 seconds to 10 minutes (R. A. H. van Oorschot & Jones, 1997); DNA yields and profiling outcomes from the palm of a hand following a paired handshake ranging from 1 to 60 seconds (Ladd et al., 1999); DNA profiling outcomes from unspecified objects and substrates held from 10 seconds to [max. unspecified] (Wickenheiser, 2002); the ability to extract amplifiable DNA from steel cables [type of contact and duration unspecified] (Saravo, Spitaleri, Piscitello, & Travali, 2004); and DNA yields and profiling outcomes from previously worn brassieres held between the thumb and index finger of another person for 2 to 60 seconds (Sessa et al., 2019). This finding is further supported by studies investigating DNA recovery from items of clothing and sweatbands worn for periods ranging from 20 minutes to 15 hours, where no correlation between the length of wearing and the ability to recover DNA (relative quantity and/or profile contribution) from the wearer was observed (Magee et al., 2018; Poetsch, Pfeifer, Konrad, Bajanowski, & Helmus, 2018; Szkuta et al., 2019). The conclusions drawn from all these studies is that a substantial transfer of material occurs during initial contact, and that other factors such as shedder status, the manner and number of contacts between the contacting surfaces, the presence of background DNA, the substrate and, specifically for clothing items, the style and fit of the garment, are likely to have a greater impact than the duration of contact as a standalone variable. Thus, it is overly simplistic to conclude that the duration of contact does not influence how much DNA is deposited, and further studies employing a more systematic approach to investigate the combined impact of these factors would be of benefit to our understanding of DNA transfer.

"DNA from the last handler, user, or wearer will be detected as the major contributor"

Early on it was proposed that when an item is used by two individuals, DNA from the first user will often be replaced by DNA from the second user, and that a recovered DNA profile is indicative of the last individual to contact the substrate (Wickenheiser, 2002). For many, this has been a prevailing assumption despite the original finding that the strongest DNA profile of samples taken from an object held by multiple individuals was not always that of the person who last held the object (R. A. H. van Oorschot & Jones, 1997). Since then, studies investigating the persistence of DNA following contact with an item or surface by two or more individuals have demonstrated that this assumption is an overly simplistic conclusion. Instead, persistence of the original user (and detection of subsequent users) is dependent on an array of factors including the duration of use by the second person (Butcher, van Oorschot, Morgan, & Meakin, 2019; Oldoni, Castella, & Hall, 2016; R. A. H. van Oorschot, Glavich, & Mitchell, 2014), the type of substrate material (Fonneløp, Egeland, & Gill, 2015; Oldoni et al., 2016), the user and their ability to deposit DNA (Boyko, Szkuta, Mitchell, & van Oorschot, 2020; Buckingham, Harvey, & van Oorschot, 2016; Fonneløp, Johannessen, & Gill, 2015; Oldoni et al., 2016), as well as differences in sampling methods, interpretation standards and/or kit/instrument sensitivities (Steensma et al., 2017). . Similar observations were recorded for scenarios involving a person's space that has subsequently been used by another person (Goray, Kokshoorn, Steensma, Szkuta, & van Oorschot, 2020) and worn sweatbands (Poetsch et al., 2018). Although studies exploring item use by multiple people commonly observe a reduction in the

proportion of the first individual's DNA, relative to the second (and further) user over time, it is not possible (nor appropriate) to infer from these outcomes (DNA quantity and/or profiling outcomes) which individual made the last contact.

"High quantities of DNA are derived from body fluids"

There is a belief that observing a "high" quantity of DNA means that the DNA is more likely to have originated from a body fluid, rather than from DNA-containing material deposited via touch. However, it is not clear from such a belief as to what amount is required to be considered sufficiently high as to conclude that a body fluid is the biological source of the DNA. Whilst it is true that body fluids can yield quantities of DNA in the ng to µg range from just a few microlitres, whereas touch deposits can yield lower DNA amounts down into the pg range, numerous research studies have shown that DNA amounts deposited via handling or wearing can range widely and up as high as hundreds of ng. In their review articles, Meakin and Jamieson and Burrill *et al.* present table summaries of relevant research data illustrating this for touched items, with a maximum quantity of 160 ng being recorded (Burrill et al., 2019; G. Meakin & Jamieson, 2013). Similarly, in a study involving worn items of upper clothing, DNA quantities have been recovered up to 302 ng (Szkuta et al., 2019). However, we do note that the type of biological material is generally not tested in these studies and may be a variable influencing the quantity of DNA recovered. As reviewed by van Oorschot *et al.*, variation in the quantities of DNA recovered from touched items is dependent on several other variables, including the substrate, shedder status of the individual, history of use of the item, the areas targeted for sampling, and the methodologies applied to collect and extract the DNA (R. A. H. van Oorschot et al., 2019). As such, it is not as simple as concluding that the DNA came from a body fluid when the amount of DNA is "high" and casework scientists should exercise caution when considering this approach to evaluations given source level propositions.

5. THE PATH FORWARD

It is clear that evaluation of DNA evidence by forensic scientists given propositions at the sub-source, source and activity levels should be informed by empirical data to help avoid misinterpretations and miscommunications, and miscarriages of justice that might result from the source and activity level fallacies. Appropriate education on issues of evidence evaluation of all stakeholders within the forensic science process, including the judiciary, casework scientists and researchers, is essential to avoiding these fallacies. The importance of such education, and accreditation where appropriate, are discussed by, for example, Hicks *et al.* and van Oorschot *et al*. (Hicks, Biedermann, Taroni, & Champod, 2019; Roland A. H. van Oorschot, Szkuta, Ballantyne, & Goray, 2017). In addition, there are a number of avenues to consider in order to facilitate DNA evidence evaluation going forward; these include considerations of: types of data to use, appropriate generation and sharing of data, use of supplementary knowledge from casework, and the need for relevant expertise.

5.1 Types of data available for use

Whilst intrinsic characteristics of a DNA profile, i.e. the alleles observed, their peak heights, etc, are included in the evaluation of the evidence given sub-source level propositions, consideration of the applicability of extrinsic characteristics of the evidence is required for evaluations given both source and activity level propositions. Such extrinsic characteristics include the quantity of DNA recovered, the quality of DNA profile obtained (full versus partial profile), the relative proportion of DNA contributed to the profile (major/minor) and the location from which the DNA was recovered (Gittelson et al., 2016; G. Meakin & Jamieson, 2013; Samie et al., 2016).

In our casework experience, DNA quantity has been included in the findings being assessed given propositions considering different activities, but concerns have been raised as to its suitability for this purpose. Such concerns were raised by Meakin and Jamieson, who reviewed available literature on the topic up to 2012 and concluded that both the quantity of DNA and profile quality varied widely given different activities and individuals (G. Meakin & Jamieson, 2013). Although this review sparked some debate (Casey et al., 2016; Champod, 2013; G. E. Meakin & Jamieson, 2016), all parties agreed that more research and data are needed to progress our understanding of these issues. Subsequent research studies have also highlighted limitations regarding the use of total DNA quantities to inform evaluations given activity level propositions. Firstly, high intra- and inter-person variability in DNA quantities, for example, recovered from knives (Butcher et al., 2019; G. E. Meakin, Butcher, van Oorschot, & Morgan, 2017; Samie et al., 2016), guns (Gosch & Courts, 2019) and clothing (Szkuta et al., 2019, 2020) used in different scenarios, limits the reproducibility of DNA quantities for similar activities. Secondly, such variation, specifically differences in the shedder status of individuals, has been shown to impact the probabilities of DNA transfer to worn T-shirts in a simulated attack scenario (Fonnelløp et al., 2017). These limitations therefore suggest that DNA quantity alone may not be sufficiently informative to be relied upon for evaluations given activity level propositions, though it may be useful to consider alongside other case specific details (Bouzga et al., 2020; Samie et al., 2020; Taylor et al., 2017). However, it has been proposed that the relative proportions within mixed DNA profiles may be more informative, for example, with respect to distinguishing handlers of an item (Butcher et al., 2019). It would be useful to see further research consider combining DNA quantity and profile composition as the input data for evaluations given activity level propositions. Furthermore, it has been noted that the comparative information from collating contributor proportions to DNA profiles in relation to specific activities has a lower dependency upon the specific suite of methodologies employed to recover and process the DNA samples (Gill et al., 2020).

It has been shown that variations in DNA processing methods, especially those prior to the introduction of more sensitive methods (in 2012-2017, depending on jurisdiction), can also influence the quantity of DNA recovered and composition of profiles generated (for example, as illustrated by environmental DNA monitoring programmes (Ballantyne, Poy, & Van Oorschot, 2013) and inter-laboratory studies on cable ties (Steensma et al., 2017) and worn clothing (Szkuta et al., 2019, 2020)). Few studies have investigated the impact of inter-laboratory differences in the methods applied on DNA profiling outcomes, and fewer still have assessed the consequences of downstream use of such data for evaluations given activity level propositions. One such study demonstrated near negligible differences in the range of LRs generated by four laboratories following evaluations given activity level propositions, despite each using a different suite of methodologies (Steensma et al., 2017). Likewise, this was also the case in an exemplar using previously published research data (Kokshoorn et al., 2018). With both studies only representing a portion of the combination of

different methods, from sample recovery through to DNA profile interpretation, documented in the literature, further research on their impact is needed. Additionally, as recommended by Gill *et al.* (Gill et al., 2020), laboratories are encouraged to carry out comparative studies to parallel their results with others. So while it could be considered misleading to use data from different sources and varied experimental designs without considering the methods applied (Gill et al., 2020), as described by Taylor *et al.* (Taylor et al., 2018), when assigning probabilities for key factors at the activity level, with the exception of performing time consuming and costly experiments that mimic case circumstances, it is preferable to use literature values from studies where the types of biological material, object, substrate, manner of contact, and methodologies applied from sample recovery to profile generation and interpretation, most closely align with the case circumstances under consideration. The current, and likely ongoing, scarcity of available data dictates sourcing data where various alignments differ to varying degrees. The impact of any aspects of the data used, which vary from the circumstances of the case under investigation, should be considered before use. The sources of data used, justification of their use, and the limitations of the data, along with any assumptions made, should then be made transparent to the users of the guidance/opinion offered.

5.2 Generation and sharing of suitable data

As discussed by van Oorschot *et al*. ((R. A. H. van Oorschot et al., 2019) and references therein), although data collated from relevant casework can be informative under certain circumstances, empirical studies where the ground truth is known are the ideal source of data to inform evaluations given activity level propositions, particularly published data, such that the data have undergone peer-review and can be shared amongst the various stakeholders within the forensic science process. However, a number of issues with the currently available published empirical data on DNA-TPPR have been raised recently, which include a paucity of data, insufficient study design, and inconsistencies in the manner and detail of reporting the methods employed and results obtained (Gosch & Courts, 2019; Kokshoorn et al., 2018; Taylor et al., 2017).

Although there is an increasing trend in the number of DNA-TPPR studies published in the last couple of decades (Kokshoorn et al., 2018; Taylor et al., 2018), demonstrating a growing body of data in this field in general, there are aspects of DNA-TPPR that are under researched. These include, for example, DNA persistence within casework-relevant scenarios, effect of inter-individual differences in handling an item, and the relative impact of different factors affecting DNA-TPPR (Gosch & Courts, 2019; Taylor et al., 2017; R. A. H. van Oorschot et al., 2019). Studies within these areas, and other under-researched DNA-TPPR topics, are therefore required to increase data provision for evaluations given activity level propositions. To facilitate the conducting of research that focuses on understudied areas, it is recommended that researchers conduct a thorough literature search to identify areas that have been understudied prior to conducting further research (Gosch & Courts, 2019). This includes identifying studies that may need to be replicated with up-to-date methodologies and those that can be expanded by exploring the impact of further variations of the same TPPR variables or impact of different variables. Taylor *et al.* have also demonstrated that construction of an appropriate BN can also help in identifying gaps in the published research (Taylor et al., 2017). Similarly, surveying stakeholders within the forensic science process, including forensic

science practitioners and lawyers, could also provide an additional means for identifying areas of research that require attention.

When it comes to experimental design for DNA-TPPR research, it is important to note that studying DNA-TPPR has two key purposes: (1) to better understand DNA-TPPR and the impacting variables and (2) to generate the required data to inform probabilities of DNA transfer and persistence within particular scenarios. To date, there are many studies that try to accommodate both of these purposes and have failed to do either satisfactorily due to insufficient study design (Gosch & Courts, 2019) or resource limitations, such as small sample sizes, inclusion of too many variables, and use of unrealistic manipulation of impacting factors. To try to overcome this, it is important to be clear as to which of the two purposes the experimental design of the study addresses, and it is recommended that meticulous planning be conducted to form an experimental design that appropriately answers the question being asked, whilst being sensitive to limitations that researchers might encounter, such as, restricted budget, availability of volunteers, and various ethical and legal requirements.

In addition, studies designed to better understand DNA-TPPR and the impacting variables should have a different experimental design from studies designed to inform probabilities of DNA-TPPR, and vice versa. In particular, Gosch and Courts (Gosch & Courts, 2019) recommend that highly controlled and potentially unrealistic scenarios can be used in the study of DNA transfer mechanisms (to address purpose 1), whereas more realistic conditions with measurement and documentation of uncontrolled variables should be used for studies to generate DNA transfer probabilities (to address purpose 2). We would like to expand on this by recommending that consideration is given to the different type of repeats that should be employed within each of these two categories of study. To address purpose 1, *repetitions* of the experiments are required, that is, a single volunteer performing the same action multiple times or use of the same amount of DNA exposed to the same conditions multiple times; for example, to assess the impact of different substrate matrices on DNA recovery, the substrate will vary, but the volunteer of the biological material, as well as the recovery method and other variables, should remain constant. To address purpose 2, *iterations* are required, that is, multiple volunteers performing the same action once; for example, to obtain data on the prospects of DNA transfer to a knife handle within the general population, the volunteer will be different for each iteration, while other variables remain constant. To be clear, repetitions are required to better understand DNA-TPPR and identify and investigate the variables that have a significant impact on DNA-TPPR and, where possible, a large number of replicates should be performed in order to perform statistical analyses and draw conclusions, whereas iterations allow for the determination of frequencies of different DNA results (e.g. quantities, profile proportions etc) within specific scenarios. Therefore, in a comparable manner to the use of allele frequencies in the determination of sub-source LRs, these frequencies from the iterations conducted in a well-designed research study can be used to determine the probabilities required for activity level LRs. Gill *et al.* also provide further advice for designing experiments aimed at generating activity level probabilities (Gill et al., 2020).

In addition to deficiencies in experimental design, there are issues with how DNA-TPPR research has been documented in the published papers, particularly in the description of the methods used and presentation of the results obtained. Such issues include insufficient detail in the methods described to fully explain the experimental design, and inconsistences across different publications in the way

in which the results are presented. Gosch and Courts (Gosch & Courts, 2019) highlight this latter point as a particular concern, given that it is crucial for studies to be comparable to facilitate the combining of data from several publications to calculate DNA-TPPR probabilities to inform evaluations given activity level propositions. The inability to do this with many of the current DNA-TPPR publications is illustrated by the example of Dunhill and Chapman (Dunhill & Chapman, 2019), who conducted a systematic review that identified 410 articles on the indirect transfer of DNA, but were unable to conduct a meta-analysis on the data contained within those papers due to a lack of quantitative variables and inconsistencies in the format of the results. It has therefore been recommended by several authors that a standardised protocol of reporting the methods and results from DNA-TPPR research be implemented to ensure that results can be compared and combined across studies and appropriately shared among the forensic science community (Dunhill & Chapman, 2019; Gosch & Courts, 2019; Kokshoorn et al., 2018; R. A. H. van Oorschot et al., 2019).

5.3 Supplementary knowledge from casework

Applying data from published studies to casework can be challenging due, for example, to the common lack of knowledge within cases of the specific details of the scenario and impacting variables. However, it may be possible to implement practices in casework to provide supplementary case-specific information that could further assist evaluations given source and activity level propositions. Proper case assessment given relevant propositions in the case will identify (additional) examinations that may lead to results that provide support for one proposition over the other. Such examinations generally extend their scope beyond those dictated by the alleged offense scenario only, and could include cell type testing (e.g. standard serology or analysis of mRNA) and background sampling, which can be informative for evaluations given activity level propositions (as discussed in Section 2). In some cases, being able to attribute the DNA recovered to a specific cell type could assist in answering activity level questions; for example, in the investigation of sexual assaults, identification of whether the DNA in question originated from vaginal mucosa or not could help distinguish between different versions of events (Gill et al., 2020; Taylor et al., 2018). As such, associating a known body fluid to a specific donor can be highly informative when the issue is at the activity level. However cell type testing without such attribution (which may often be complex with non-gender specific cell types) can also add information that can distinguish between propositions at the activity level, as illustrated by Breathnach and Moore (M. Breathnach & Moore, 2013). Background sampling of areas adjacent to the area of interest may also assist in distinguishing between proposed activities, for instance, if DNA of a POI is only found at locations related to one of the purported activities (R. A. H. van Oorschot et al., 2019).

Finally, when considering mixtures of DNA that are commonly recovered from regularly used items, shared items, and items used and/or stored in shared environments that are used during a criminal offence, such as tools, weapons and clothing, there are often additional profiles within the mixture labelled as coming from unknown individuals. Having an awareness of who might contribute to the 'background' DNA component of a profile can assist investigations by pinpointing the profile(s) of relevance, reducing or opening lines of enquiry, and potentially improving the LR of the POI. Studies have been conducted on the presence of background DNA from unknown individuals on surfaces and items in various public and private spaces (e.g. (van den Berge, Ozcanhan, et al., 2016)). A small

number of recent studies revealed that in private spaces, many of these unknowns appear to be close associates of the owner/user of the item, such as their partners and other house inhabitants, or work colleagues (Boyko et al., 2020; Goray et al., 2020; Reither et al., 2019; Szkuta et al., 2019, 2020; Taylor, Abarno, Rowe, & Rask-Nielsen, 2016). In addition to highlighting the frequency and relative contributions of the known and unknown associates of the person, item, and/or environment of interest in which various individuals are observed under different conditions, these studies have highlighted the importance of obtaining elimination reference samples to assist in DNA profile interpretation. More research toward understanding the prevalence and persistence of DNA from close associates, and the probability of the presence their DNA in different scenarios, would therefore be of valuable.

5.4 Different types of expertise

There have been a number of calls recently for the forensic genetics community to recognise that evaluation of DNA evidence given propositions at each of the levels of the hierarchy requires different types of expertise, and an expert in one area of evaluation is not necessarily an expert in another. In particular, evaluation of DNA evidence given activity level propositions requires specialist knowledge and an additional set of skills, training and proficiency testing compared to those reporting solely on the likelihood of the DNA findings given their biological source (Hicks et al., 2019; Taylor et al., 2018; R. A. H. van Oorschot et al., 2019). The Netherlands Register of Court Experts recognises these distinct areas of expertise and will extend competency testing for DNA scientists beyond source level, by opening up registration for experts reporting findings given activity level propositions (as well as for kinship analysis). In addition, in some jurisdictions, such as in England and Wales (Tully, 2019), cases have been noted in which prosecution scientists have been required to give oral testimony on the basis of non-evaluative DNA reports that only include sub-source level interpretations, and then been asked activity level questions by the lawyers. This is inappropriate, not only because the scientist in court may not have the appropriate expertise and training to answer activity level questions, but even if they do, they require the time and resources to conduct an evaluation of the evidence given activity level propositions. To maximise the usefulness of DNA evidence to the court, practices should therefore be in place to ensure that properly trained scientists are appropriately prepared to give expert testimony on the different issues considered at different levels in the hierarchy of propositions.

Forensic biology and beyond

While the examples of fallacies during the evaluation and communication of forensic evidence in this paper all relate to forensic biology, these fallacies are not restricted to this field. Many forensic disciplines dealing with trace evidence (i.e. fibres, glass, gunshot residue (GSR), etc) that require consideration of TPPR are susceptible to evaluation fallacies, particularly the activity level fallacy. Similar to the source and activity level fallacies in trace evidence fields, evaluation fallacies may also occur in forensic pathology, if the distinction between cause and manner of death is not recognised. The Case Assessment and Interpretation (CAI) framework was initially developed as a model for informing decisions regarding which forensic tests and analyses would be most informative in

progressing a case, based in part on informing expectations of particular findings under different propositions (Cook, Evett, Jackson, Jones, & Lambert, 1998b). The proper implementation of CAI can also assist in decision making regarding which data are appropriate to use in informing evidence evaluation given alternative propositions. Further development and implementation of this framework for evidence interpretation, as well as a solid foundation in empirical data, are therefore crucial for all fields of forensic science.

Equally relevant are issues in evidence evaluation caused by generally held beliefs that are based on experience or word-of-mouth communication only. Research in TPPR issues for trace evidence and proper documentation of the resulting data to be accessed by all parties are crucial to support or falsify such beliefs. Since different types of evidence may be crucial to address the same issues in a case, and since recovery and analysis of different trace types may affect each other (e.g. collecting from the same item both DNA and fingermarks or GSR and fibres), cross-disciplinary TPPR studies are a path forward to amend these issues and strengthen forensic science as a whole.

6. CONCLUSION

To enable the forensic science community to better identify and address issues in DNA evidence evaluation, we have proposed further defining the association fallacy to introduce the terms, 'source level fallacy' and 'activity level fallacy'. To facilitate avoidance of these fallacies, it is crucial that forensic scientists state the propositions under which the evidence is being evaluated and be explicit as to the level in the hierarchy of propositions to which these propositions refer. To avoid the source level fallacy, scientists must be explicit and transparent about the assumptions made based on test results and case context when choosing to elevate an opinion from the sub-source to source level. It is not possible to make such an elevation when there is a poor quality or mixed DNA profile, and/or a dilute or mixed body fluid is detected, and a separate source level probabilistic assessment is therefore required. To avoid the activity level fallacy, it is important to note that it is never appropriate to elevate an opinion from a lower level of the hierarchy to the activity level; a separate probabilistic evaluation is required based on DNA-TPPR data and case information that can be transparently communicated. The specific nature of the DNA results included in the evaluation, e.g. DNA quantity, relative proportions, etc, should also be transparently communicated. LRs at the activity level will commonly be many orders of magnitude lower than those at the sub-source level, especially when dealing with a single DNA finding or a few conditionally dependent DNA findings. The primary source of information to inform such an evaluation should be experimental data where the ground truth is known, although other secondary sources of data can be used, but again, transparency and communication of the information and assumptions relied upon are crucial. Evidence evaluation should not be driven by generally held beliefs that are based on experience or word-of-mouth communication only; TPPR research is essential to support or falsify such beliefs.

With respect to TPPR research for DNA, it is imperative that data are shared appropriately and in a comparable format, and that studies going forward are designed with respect to the purpose they are to address, whether to better understand DNA-TPPR and the impacting variables or to inform probabilities of DNA-TPPR. Variables affecting DNA-TPPR are numerous; improving our understanding of them, as well as our ability to measure them and to determine probabilities given a

set of circumstances, will enhance the guidance provided to the triers of fact. The appropriate implementation of this into forensic casework requires additional specific training and proficiency testing of experts involved in evaluation of forensic biology findings beyond sub-source level issues. Appropriate education of all stakeholders within the forensic science process is also required. There is therefore a need for the forensic genetics field to continue to progress not only technological enhancements, but also the appropriate interpretation and evaluation of the resulting data within a logical framework.

The issues highlighted in this review are not limited to forensic biology (Roux, Talbot-Wright, Robertson, Crispino, & Ribaux, 2015); many also hold for other fields of trace evidence (e.g. GSR, fibres, glass etc.), as well as for forensic pathology (cause of death versus manner of death). Given that the framework for evidence interpretation and evaluation is the same across fields within the overarching discipline of forensic science (Cook et al., 1998b), there is an opportunity to work collaboratively across fields to further the scientific basis of forensic evidence evaluation. Issues addressed by evaluations given activity level propositions within a case often allow for different types of evidence to be combined (e.g. fingermarks and DNA), although there is limited data available on the conditional dependencies among different types of evidence (e.g. how does observing a fingermark change the probability of observing DNA of the same and other individuals?). It would therefore be prudent for future DNA-TPPR studies to also include consideration of other types of traces.

Notes

[1] In line with these elevations between levels in the hierarchy of propositions, one could also define an 'offence level fallacy' in which an opinion at sub-source, source or activity level is unjustifiably transposed to the offence level. An example where we see this happening is when propositions at the activity level contain legal qualifiers for the activities considered, for example, 'the suspect murdered the victim with the knife' rather than 'the suspect stabbed the victim with the knife'. We suggest to avoid these legal qualifications whenever possible.

[2] The opinions presented in this paper are those of us, the authors, and do not necessarily reflect those of our host institutes. We also declare no conflicts of interest for this article.

[3] We refer the reader to Marquis *et al.* (Marquis et al., 2016) for a discussion on the implementation and communication of verbal equivalents for likelihood ratios.

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