Research Article

Applying the Forensic DNA Likelihood Ratio to the Legal Question Regarding Whether the DNA Originated from the Person of Interest or Not

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Abstract

The forensic DNA likelihood ratio (LR) provides the primary statistical model for evaluating forensic DNA evidence, comparing the probability of the evidence if it originated from a person of interest (POI) versus someone else, which is currently calculated as a random individual from the population. In contrast, when an item of DNA evidence is tested for legal purposes, the question regarding whether the DNA on the item originated from the person of interest, or not, is being weighed by the legal system. If the hypothesis of the prosecution (Hp) is: the probability of the evidence under the condition that the person of interest (POI) is Contributor 1, then the DNA evidence that, if true, proves that the POI is not Contributor 1, is: the condition that the other potential Contributor 1s are the true contributor. When this LR equation is expressed, labeled the Factfinder LR, it produces one explanation of the direct DNA evidence v. all of the mutually exclusive alternative explanations.

Potential problem: if true, the current forensic DNA LR can be defined as: the presumption that the Hp is true, weighed against an argument where the strongest evidence that can definitively prove the POI "not true" goes unconsidered.

Keywords: forensic DNA; hypothesis of the prosecution; hypothesis of the defense, McDaniel v. Brown; Probabilistic genotyping; prosecutor's fallacy; Hd; Factfinder LR

1. Introduction

1.1 Current Forensic DNA LR

Conventionally, the LR compares two propositions: the prosecution's hypothesis (Hp), that the DNA originated from the person of interest (POI), and the defense's hypothesis (Hd), that it originated from someone else. This comparison is implemented mathematically as: LR = P(E | Hp) / P(E | Hd), and is read as the Probability of the Evidence based on the condition that the statement in the Hp or the Hd are true; where E represents the observed DNA evidence. This framework has been extensively developed in the forensic literature, can be found in most of the articles in this study, and its foundation can be found in the NRCII (National Research Council II, 1996).

In current forensic practice, Hp is modeled as the POI being the true contributor, while Hd is typically modeled using Hardy–Weinberg (HW) equilibrium population frequencies or random match (man) probabilities (RMPs). This approach is well established in the required guidelines (Scientific Working Group on DNA Analysis Methods; SWGDAM 2021), NRCII recommendations, and the literature on probabilistic genotyping (PG). This LR model calculates the probability of the evidence if the DNA originated from the POI or a ran-

domly selected individual from the population (SWGDAM 2021, NRC II 1996, Buckleton et all 2016, Dawid et al 2002).

The LR is wide-spread in and out of forensic DNA, it is recognized in the forensic literature and mathematics that the weights provided are intended for a legal setting (Biederman et al 2012) (Gill et al 2021) (Dawid et al 2002), and that the factfinder is weighing (Slooten 2022) (Bright et al 2019) whether the DNA originated from the POI or not (Gill et al 2020) (Wivell et al 2023) (Evett et al 1998). Subsequently, some laboratories are reporting the current LR weights with the statement "originated from the POI or not" (Tucson Police Department 2023) (San Diego Police Department 2021) (Federal Bureau of Investigation [FBI] 2018).

Therefore, there is recognition that the question the factfinder is weighing is whether the DNA originated from the POI or not, and the current forensic DNA LR is being presented in the literature and to the legal system as providing weight for the factfinder to deliberate that question. This question is provided weight with an LR calculating whether the DNA originated from the POI or a randomly selected individual from the population, raising the issue regarding whether the present calculation provides weight for the Hp and the Hd that the factfinder is weighing.

1.2. In-Brief and Referenced in Section 1.3.

Assume that an item of evidence is collected and tested for legal purposes, that probabilistic genotyping (PG) has been used to determine the possible genetic combinations for Contributor 1, the POI is not excluded as a possible Contributor 1, and the factfinder is weighing whether the DNA on the item originated from the POI or not. The alleles and peak heights on the item of evidence are direct facts, and the possible diplotypes that are potentially Contributor 1 are set. The cause of the peak heights is a direct result from the percentage of DNA from each donor, and the greater the difference in peak heights, the more distinguishable the pairs are individually and as a diplotype set.

The primary foundation of this article is that: if the POI is potentially Contributor 1 on a DNA sample mixed with two or more individuals, then a distribution of the probabilities for all of the potential Contributor 1s will provide statistics regarding how many DNA suspects are possible that potentially explain the evidence as well as the probability for each DNA suspect. The statistics will describe how well the evidence differentiates the suspects based on the percentages of DNA contributed, as well as how probable of a DNA suspect is the POI to produce the factual evidence, compared to the probabilities from each of the other possible DNA donors. The other potential Contributor 1s represent mutually exclusive evidence that, if true, excludes the POI as the true DNA donor for Contributor 1. These other possible Contributors 1s are calculated as the evidence that favors the accused in the hypothesis of the defense (Hd).

This same calculation is used herein for the Hp, for example, there may be multiple POIs to consider, multiple possible unknowns, or family members to consider. The POI of interest may be modelled as Contributor 1 and Contributor 2, with and without family members, and other possible diplotype combinations, and a distribution of probabilities can be provided for all of the hypotheses in the Hp, and combined for a total in the same manner as the Hd.

The LR used in this study is defined as the common probability of the evidence given the Hp v. the Hd. The LR, the Hp, and the Hd, are provided as values to augment an expert interpretation of the evidence electropherogram (EP). The statistics provide the factual evidence on the EP with contextual meaning; and along with other information such as the RMP, allows a factfinder to have the information necessary to deliberate whether the DNA originated from the POI or not.

The alleles are present as factual peak heights and the diplotypes are fixed, therefore, a uniform prior across all of the fixed data in the probability space is used to isolate which allele pairs are a better fit for the data. For example, if a DNA mixture has two rare alleles that came from the true contributor and are a reasonably distinct pair, a population frequency based prior will give weight to the true allele pair as less probable to produce the evidence, even when they are a better fit for the data; it will also provide a higher weight for an allele pair that is more common in the population; and therefore, a population frequency prior will interfere with the probability of detecting the true pair based on the peak heights that specific contributors would donate given their percentage of DNA.

Therefore, we follow the LR models using only diplotypes, and those using a uniform prior, to isolate the weight that a possible fixed genotype pair, and/or set of pairs, is responsible for the factual peak heights; this model is based on analyzing the peak heights by the amount of DNA donated by a given diplotype, relative to the other possible diplotype donors.

The Hardy-Weinberg (HW) terms are not used in the LR in this study, and retain their traditional meaning of: the frequency in the population that a random individual would be a contributor to the DNA profile, or, the probability that a randomly chosen individual is included as a potential contributor to the evidence DNA, or simply, a DNA suspect.

In this mathematical model, whether a single-source DNA profile can be identified, or not, based on alleles or peak heights, is not addressed by the RMP, however, an evidence profile calculated over 19+ loci can still be highly exclusionary regarding the population. The RMP genetic pairs identify the groups excluded/not excluded, as well as the percentage of the population in each group. If a DNA profile is among the potential contributors, and the RMP is 1 in 1 million, there are still many other DNA diplotype suspects; if the RMP is 1 in 1 octillion, it might be considered by some to be proved that the connection is not random, however, this does not eliminate the possibility of family members as donors, the evidence does not exclude other possibilities, and the RMP does not single him out for identification.

There are different DNA LR questions being weighed with different Hd's referenced herein, and all are reporting mutually exclusive evidence, for example, Hd can be the random man, a family member, or a diplotype, with each one presented as representing whether the POI is, or is not, the true contributor. This article adds to that list, and is intentionally silent regarding the definition of these other LRs. However, the different calculations have different intrinsic meaning, even if stated in the same manner. The LR in this study is presented herein as providing weights for a specific contextual definition covering the LR, the Hp, and the Hd, and is a specific version of the question regarding whether the DNA originated from the POI or not.

Postulate #1:

- Weights can be provided regarding whether the DNA originated from the POI or not; the above discussion can be calculated with current Bayesian LR mathematics as described above and shown in section 1.3. This LR, along with the traditional RMP, is the primary information necessary to weigh the question is a legal DNA evidence sample.

Postulate #2

- The weights provided in the current forensic LR regarding whether the DNA originated from the POI or a random man, is a separate and distinct question, calculated by a different LR equation, and provides different weights for the factfinder to deliberate their question.

1.3 Current LR models: diplotypes and a uniform prior

This study investigates the concept that a forensic DNA sample contains two fixed and defined hypotheses, which are: the Hp, "the DNA originated from the POI" (and possibly others), and the alternative Hd that "it did not," and that these will be weighed by the factfinder using the probabilities provided by the forensic calculations.

The factual DNA evidence is the alleles and their peak heights, and these are fixed and defined. The non-excluded diplotypes that are potential contributors are fixed and defined by the evidence, however this will vary based on the method used to exclude specific genetic pairs; herein the PG analysis was used to determine the acceptable genetic pairs not excluded. The alleles and peak heights contain inferences regarding the amount of DNA present for each specific allele (Steele et al 2014), and the heterozygous balance can be used to determine the probability of the different genotype combinations across all loci (Kruijver et al 2022) (Bright et al 2013). This is modelled by PG software and described in (Kelly et al 2020) (Gill et at 2021) and (Bright et al 2019). This analysis provides probabilities for every possible genotype across all loci for each potential contributor. This study attempts to isolate the fixed alleles and peak heights and analyze the distribution of probabilities from the fixed potential diplotype contributors under a uniform prior; this is accomplished by calculating all possible diplotypes separately and in the same manner, subsequently separating the possibilities into the Hp or the Hd of the fixed and defined hypotheses pair, and then adding the sum of all of probabilities they contain.

Slooten 2022 uses a uniform prior across diplotypes in the same manner as this study, and demonstrates that the alternative diplotypes can be calculated to see which ones stand out based on the distribution of diplotype probabilities, that this LR assumes that the POI did not contribute the DNA, that alternative POIs can have a higher probability to produce the DNA profile than the POI in the Hp, and if true, cause the original POI to be excluded; this is also extended to relatives, which can also be seen as analyzed as diplotypes under a uniform prior in Dawid et all 2002. Bright et al in 2013 also used a uniform prior across diplotypes when evaluating the continuous PG model for heterozygous allelic balance with respect to stutter. Balding et al 1994 used a uniform prior across all diplotypes for a kinship analysis, and compared this to DNA case work; recognized a current failure to define "not the POI;" that calculating this LR from the database populations is consistently unfair to the accused; that the diplotypes of kinfolk should be considered; and that the defense's fallacy, which is where all suspects are equally as possible, is true in the absence of other information. It is these LR models where diplotypes are considered under a uniform prior that this study follows.

Jaynes 1957 gives three primary criteria for a convincing argument in part I, and criteria b is that the model includes no uninformative assumptions, and in part II the guiding principle is that the probability of distribution that provides the most unbiased knowledge is the broadest one compatible with the factual data. Specific to the forensic DNA LR, Gill et al 2020 expresses that the available data that assists in the evaluation of DNA should be used in the LR, while Brenner 2001 states that probability, by definition, depends only on the available data. Therefore, the simple controlling feature this study uses to choose the prior is: do not add weights to the equation if they do not influence the issue being calculated.

Herein, the factual DNA evidence is the fixed alleles and peak heights, which cause the potential diplotype contributors to be fixed by the PG analysis. A uniform prior is justified because: when these weights are based on the DNA percentage from each contributor, the population frequency data provides a skewed weighting for the genotype pairs to produce the evidence; the alleles, peak heights, and diplotypes are based only on the factual data; the probabilities include no uninformative assumptions; and therefore, a uniform prior should produce the most unbiased knowledge.

1.4 McDaniel v. Brown 558 U.S. 120, 2010

This section is derived from a forensic scientist's interpretation of a legal discussion, where theoretical mathematics are applied to this interpretation. This section is illustrative of the potential to utilize specific data from forensic DNA PG analysis, presents a foundation that the literature and the law recognize that a specific legal question is being weighed with DNA evidence, and that the SCOTUS decision provides at least some guidance describing how the legal system wants to weigh an evidence DNA sample.

The Supreme Court's discussion in *McDaniel v. Brown* is a legal review of a DNA case, covering the same statistics presented in this study (SCOTUS 2010). The mathematical sections and the applied math-legal study section are separate but parallel arguments. One argument does not prove the other, but if these are parallel arguments, they necessarily must be the same. Additionally, for a mathematical study to theoretically address the same issues as a SCOTUS decision, and potentially address the weight of DNA evidence that they discuss, demonstrates that this nascent theory is a study analyzing a factor that is potentially legally important.

Assume an item of evidence is collected and tested for legal purposes. This study posits that it is the court that has a question that they themselves will be weighing, and it is their responsibility to describe it; the mathematicians do not invent the question. It is assumed by this study that after multiple legal appeals, the SCOTUS understands the legal question being weighed with DNA evidence, the meaning of the statistics presented, and is discussing what should be presented as weights for the factfinder to deliberate the legal question.

This study speculates that the legal sphere: determines their own question; that the question itself regarding a forensic DNA sample is, in fact, the Hp v. the Hd that the factfinder is weighing; if the court did not think that they understood the statistics that were presented as evidence, they would not allow them to be reported; and therefore, it is natural that the legal sphere would: define the question; understand the statistics; review whether they provide the proper weight to the question originally posed; define what information they want

presented; and have an interest in a mathematical theory that is applied directly to their words. In brief, this study posits that the SCOTUS understood what they were saying, and we applied mathematics directly to their words.

The Brown case DNA data is presented on the same tables as the mathematical model herein. The SCOTUS did not endorse any statistical model, but instead, this study demonstrates that the SCOTUS was presented with the same issues as this study regarding the weights provided for DNA evidence; for example, 1) the same question is presented regarding whether the DNA originated from the POI or not, 2) the RMP is presented as the calculation for the Hd, and 3) their discussion centers around what is, and is not, the Hd. Given that the only factor altered in this study is the Hd, and everything else that this study covers appears equivalent, we review this case and apply mathematics based on the SCOTUS direct use of these statistical terms.

Postulate #3: the SCOTUS discussion is the same two questions being weighed as our mathematical model and tables, with the same statistics as presented therein, and each produces the same result.

However, each study must stand on its own, and they do not prove each other.

This section is an applied mathematical theory on DNA statistics, in which this study claims expertise, but applied to the legal field where this study claims no expertise. There are some ambiguities in what the SCOTUS discusses, and it is a circular argument for this study to give these ambiguities specific meaning, and then later claim the consistency proves the two are the same, and therefore, this demonstrates only that it is possible that they are consistent.

2. Materials and Methods

2.1 Disclaimers and clarifications

It is reductive when this article refers to either the Hp or the Hd as one possible Contributor 1, because, neither captures the complex real-world Hp or Hd, but refers to how the base equation begins. As examples: the LR can contain a known contributor, which replaces some of the unknown variables with facts, and reduces the number of diplotypes possible for the Hd; Hp can consider whether the POI is Contributor 1 or 2; either the Hp or the Hd can consider a different number of contributors; the Hd can be reduced if family members can be factually excluded; a distribution of probabilities that supports the Hp can be calculated; and a known DNA profile will exclude any other DNA diplotype that is too similar; therefore, the Hd is every diplotype in the final non-excluded group that, if it is the true diplotype, excludes the diplotype of the POI as being the true contributor.

Herein this reductive language is used only for brevity, and in several instances recognizes a specific point without discussing others. The brevity recognizes that one possible contributor, or all other contributors, are only the starting point in the base equations, where a much more complex Hp can be presented, and the complex Hd is the diplotypes that are not excluded after a thorough examination of the Hp for each hypothesis it contains.

The RMP in this study is not calculated in an LR, and the Hp/RMP comparison has a different meaning in this study with a uniform prior than the current forensic DNA LR. The tables and mathematics herein address the definition of the comparison from this study's model, without regard for any other LRs under other conditions unless stated.

This study's definitions on the tables does not reflect the meaning of the current DNA LR model, the definition of its Hd, what it is calculating, whether it is mutually exclusive, or its full definition. However, the tables demonstrate: 1) that a HW-based LR has a distinct calculation and meaning from a diplotype-based LR under equivalent conditions, and 2) the distinct real-life contextual meaning of the weights for this study's LR are fixed, and are provided by the diplotypes under a uniform prior.

2.2 Expert Hand Interpretation

Taylor et al 2013 discusses an expert hand interpretation of a comparison between an evidence electropherogram and POIs, and that it is highly intuitive to assess how well given diplotypes fit the evidence data. The data in the Factfinder LR provides meaningful statistics for this intuitive assessment regarding the Hp and the Hd, and this can be seen on the EP graph. For example:

- If no peak height data is used, or if mixture data consists of identical peak heights, the Factfinder LR shown in the next section is undefined, and becomes a diplotype count. This can be shown on the EP where there are many possibilities, but there is no difference among them without a differentiation based on the peak heights.
- If peak height data is used, the greater in relative difference in DNA contribution among the contributors, the more likely it will be to be identify the true pairs and partial or full diplotype sets. This can be seen on an EP, and a distribution of probabilities for the contributors can be provided (Gill et al 2021, Kelly et al 2020, Bright et al 2013, Slooten 2022).
- The RMP provides the probability of excluding random non-related individuals from the population.

Therefore, this analysis assists the factfinder to understand what the expert sees, explains the factual evidence in a meaningful manner, and supports that the factfinder would benefit from having this data.

2.3 The Likelihood Ratio with a Uniform Prior over the Fixed Alleles and Non-Excluded Diplotypes

Formalized Factfinder LR under a Bayesian framework with a uniform prior.

Let:

- E = the observed DNA evidence; alleles fixed by observation
- Ω = the set of all diplotype combinations compatible with E; alleles fixed by E
- d_{POI} = the diplotype of the person of interest; alleles fixed and known
- $|\Omega|$ = the total number of compatible diplotype combinations; alleles fixed by Ω
- Hp: The true source is d_{POI}; alleles fixed in d_{POI} and E
- Hd: The true source is some d not equal to d_{POI}; alleles fixed in $(|\Omega| - 1)$
- An Hd of $(|\Omega| - 1)$ assumes a sufficient number of loci to accept identification

2.4 Prior Distribution (Uniform)

Under a uniform prior across all compatible diplotypes:

$P(d) = 1 / |\Omega|$ for all d in Ω

This gives prior probabilities for the hypotheses:

$P(Hp) = 1 / |\Omega|$

$P(Hd) = (|\Omega| - 1) / |\Omega|$

2.5 PG-weighted likelihoods

When probabilistic genotyping provides weights W_d representing how well each diplotype explains the peak-height patterns:

$P(E \mid d) = W_d$

where the sum of W_d over all d in Ω equals 1 (normalized across compatible diplotypes).

$LR = P(E \mid d_{POI}) / P(E \mid Hd)$

Under Hd, we average over all non-POI diplotypes. With a uniform prior within Hd:

$P(E \mid Hd)$ = sum over all d not equal to d_{POI} of $[P(E \mid d) \times P(d \mid Hd)]$

$P(E \mid Hd)$ = sum over all d not equal to d_{POI} of $[W_d (1 / (|\Omega| - 1)]$

$P(E \mid Hd) = [1 / (|\Omega| - 1)] \times$ (sum over all d not equal to d_{POI} of W_d)

$P(E \mid Hd) = (1 - W_{POI}) / (|\Omega| - 1)$

Therefore:

$LR = W_{POI} / [(1 - W_{POI}) / (|\Omega| - 1)]$

$LR = [W_{POI} (|\Omega| - 1)] / (1 - W_{POI})$

This LR has two components:

1. $W_{POI} / (1 - W_{POI})$ — the odds ratio based on how well the POI's diplotype explains the evidence relative to all alternatives combined
2. $(|\Omega| - 1)$ — a multiplier reflecting the number of alternative diplotypes

The formula shows that under a uniform prior, the LR favors Hp when:

- W_{POI} is large (the POI's diplotype explains the evidence well)
- When $|\Omega|$ is large (there are many alternatives, each receiving only $1/(|\Omega|-1)$ of the total under Hd)

The formula is undefined when $W_{POI} = 1$, which occurs only when all compatible diplotypes are equally likely (pDC = 1 for all). In that case, the LR collapses to a count, not a likelihood, because the evidence offers no discriminatory weight among alternatives.

- E: the observed DNA evidence alleles are fixed
- Ω: the set of all diplotype combinations compatible with E are fixed by E
- d_{POI}: the diplotype of the person of interest is fixed
- $|\Omega|$: the total number of compatible diplotype combinations is fixed by Ω
- Hp (the true source is d_{POI}); and Hd (the true source is some d not equal to d_{POI}).

2.6 Definitions of Hp and Hd

2.6.1 Forensic Hp and Hd (Conventional LR)

Following NRCII, the conventional forensic LR is defined as:

Hp: The DNA sample came from the suspect

Hd: The DNA came from an unknown person.

Hp (forensic): The POI is a contributor to the DNA profile. This compares his diplotype to the evidence, and is calculated as a pDC, and shown below. Additional contributors are calculated consistent with unknown contributors modeled in the Hd (forensic) below.

pDC: The pDC can be binary and not utilize the peak heights; in this case it is reduced to a diplotype comparison probability equal to 1 when an allele pair is consistent with the evidence and 0 when excluded. With PG data and peak heights considered, allele pairs can be a weighted probability (e.g., PG outputs Section 2.4).

The POI is a pDC comparison, and all similar comparisons will be labelled as pDC for the probability generated by any diplotype comparison to the evidence alleles, with or without and peak heights. The specific allele pair that generates the pDC of 1 (or PG weight), such as p(8,9), is designated as 8,9pDC for specificity and are red on the tables, to distinguish the comparison probability from the RMP calculations. Other terms are also used, such as single-source probability, or the probability of a given contributor.

Hd (forensic): A randomly selected individual(s) from the population is/are the contributor(s).

2.6.2. Allele pair enumeration and diplotype count

For a locus with n distinct alleles, possible unordered diplotypes are: with homozygotes allowed: $n(n+1)/2$; with homozygotes excluded (e.g., fixed heterozygous mixture tables): $n(n-1)/2$; these counts structure the tables used to evaluate the non-excluded genetic pairs.

Based on the Caucasian database, across the 21 GlobalFiler autosomal loci in the case study herein, with homozygotes allowed, the sum of the possible alleles is 233, the sum of the possible allele pairs is 1818, and multiplied across all loci, the number of diplotype sets are on the order of 10∧35.

2.6.3. RMP Terms in the unknown contributor(s)

Table 1 below is the current forensic DNA LR table. The RMP values follow the standard HW formulas: Heterozygote: 2p1p2 and Homozygote: p1∧2; these represent population- genetic frequencies for random individuals. The calculations are standard in forensic DNA mathematics [Balding et al 1994, NRCII 1996, Buckleton et al 2016).

The Hd terms and unknown contributors in the Hp are traditionally computed using HW based RMP terms. On the tables below are alleles 7, 8, 9, and 10, at equal heights; when these are generically calculated as examples in this study, the allele frequency equals the STR repeat number, or 7%, 8%, 9% and 10%, respectively, for these four alleles.

Table 1. Current forensic DNA LR table with alleles (7, 8, 9, 10) at equal heights, assuming two contributors, with the POI's diplotype as alleles (8, 9) (NRCII 1996, p.130). This is the binary calculation where peak heights are not considered.

	Contributor 1	Contributor 2	Hp Calculation	Hd Calculation
A	7, 8	9, 10		2p7p8 x 2p9p10 = 4p7p8p9p10
B	7, 9	8, 10		2p7p8 x 2p9p10 = 4p7p8p9p10
C	7, 10	8, 9		2p7p8 x 2p9p10 = 4p7p8p9p10
D	8, 9	7, 10	1(8,9pDC) x 2p7p10	2p7p8 x 2p9p10 = 4p7p8p9p10
E	8, 10	7, 9		2p7p8 x 2p9p10 = 4p7p8p9p10
F	9, 10	7, 8		2p7p8 x 2p9p10 = 4p7p8p9p10
		Sum Total	2p7p10(8,9pDC)	24p7p8p9p10

Table 1. Current forensic LR: 1/12p1p2 = (2p7p10)(8,9pDC) / 24p7p8p9p10 = (8,9pDC) / 6(2p8p9)

The current forensic DNA LR = P(E | POI and an unknown individual are the true contributors) / P(E | random individuals are the true contributors).

In this model, the RMP is a calculation of the alleles on the evidence and not a potential cause; the genetic pairs from the evidence did not leave behind a detectable diplotype pattern of alleles and peak heights on the evidence. Regardless of the description, the LR used by this study is calculating single diplotypes by the product rule across all loci, in contrast, the RMP does not single out a diplotype to be measured as a true contributor in this model.

The RMP equation in this model has the traditional HW definition, which is, the probability that a random individual is potential contributor to the evidence, and is calculated as 2p7p8 + 2p7p9 + 2p7p10 + 2p8p9 + 2p8p10 + 2p9p10 = 0.018. Therefore, approximately 1.8% of the population is likely not to be excluded from the DNA evidence at this locus. Using the product rule across 21 equivalent loci is on the order of 10^-36; even if the RMP is does not identify an individual, matching 2 of 4 alleles across 21 loci is highly exclusionary in the population, even when there are many possibilities.

In order to support the foundation that there is a difference in the definition and general magnitude of weight provided for whether the DNA originated from the POI or not rather than from the POI or a random man, we provide the calculations for Table 1 above, based on this study's LR model, and under the given conditions only.

There is one (8,9) diplotype of the POI; the equation is 1/ 12(0.08 x 0.09) = 12. If the POI were alleles (7,9), the equation would equal 13. As the POI alleles that match evidence alleles become rarer, the ratio favors the Hp.

The result at an individual locus favors the Hp regardless of the POI without more information, and across 21 equivalent loci, if the POI were alleles (8,9), is on the order of favoring Hp by 10^22, where the Hp remains at 100%; [1/12(0.08 x 0.09)]^21. The probability for the Hd to produce the evidence is strongly reduced when the POI's genetic pairs match; the prosecution's hypothesis in the LR reduces the strength of the Hd hypothesis at each locus, but the Hd has no effect on the strength of the Hp.

The calculations show that the genetic pairs on the DNA evidence are more probable if the DNA originated from a pair matching an individual, rather than that same genetic pair matching as a random member of the population. Without additional information, this will be true for every genetic pair not excluded as a potential contributor. This also demonstrates that the pDC term is inherently larger than the RMP term for the same allele pair, and across 21 loci, has a measureable effect on the magnitude of the result. This calculation demonstrates the Balding et al 1993 statement that random selection from the population is consistently unfair to innocent suspects.

2.6.4 The alternatively stated Hd: The Factfinder LR

Hp : The DNA originated from the POI.

Hd (diplotype): The DNA did not originate from the POI.

The LR structure on Table 2 below demonstrates the diplotypes under a uniform prior, which can be used to calculate and present the data from the Factfinder LR, and = P(E | POI diplotype and unknown diplotypes are the true contributors) / P(E | one of the mutually exclusive non-excluded diplotypes is the true contributor(s)).

Table 2. Calculation of the Hd and Hp of the DNA LR, where all of the terms are pDC.

	Contributor 1	Contributor 2	Hp Calculation	Hd Calculation
A	7, 8	9, 10		1 (7,8pDC) x 1 (9,10pDC)
B	7, 9	8, 10		1 (7,9pDC) x 1 (8,10pDC)
C	7, 10	8, 9		1 (7,10pDC) x 1 (8,9pDC)
D	8, 9	7, 10	1 (8,9pDC) x 1 (7,10pDC)	1 (8,9pDC) x 1 (7,10pDC)
E	8, 10	7, 9		1 (8,10pDC) x 1 (7,9pDC)
F	9, 10	7, 8		1 (9,10pDC) x 1 (7,8pDC)
G		Sum Total	(8,9pDC)(7,10pDC) 1 pDC combination	(7,8pDC)(9,10pDC) + (7,9pDC)(8,10pDC) + (7,10pDC)(8,9pDC) + (8,9pDC)(7,10pDC) + (8,10pDC)(7,9pDC) + (9,10pDC)(7,8pDC) 6 different pDCs combinations: 1 for each diplotype pair

Table 2 LR = (8,9pDC)1(7,10pDC) / 6 pDCs combinations

Without any peak height data, or if all of the alleles are identical in height, there is a probability of 1 for each compatible diplotype, or P(E| the POI's combination) / P(E| all other combinations), LR = 1/6.

Table 2 maintains the LR framework and the pDC calculation from the POI from Table 1, but replaces the population frequency terms in the unknown contributors of the Hp and the Hd with diplotype-based alternatives.

Using the product rule across all 21 loci, assuming an equivalent value, this would result in a Factfinder LR = 1 Diplotype POI/ 10∧16 diplotypes. This is the probability of the evidence if the diplotypes of the POI and an unknown person are the true contributors versus the probability that the diplotypes of two unknown individuals are the true contributors. Every diplotype on the table, if it is the true DNA donor, excludes the other diplotypes as true contributors.

This data can be demonstrated on the evidence EP, and the statistics reflect the hand expert analysis, because the statistics from this LR directly reflect the probabilities of the factual evidence. This contextual information can be provided as the Hp and the Hd for the factfinder to weigh. For example, on Table 2 it could be shown that the alleles do not identify the POI any more than any other diplotype, because the data does not differentiate between them, and over a probability space with 10∧16 diplotypes, the probability of 100% total will be diluted and be very small for the POI or any other possibility. However, combined with the RMP, it is also true that matching 2 of 4 alleles across an EP is not likely to be random (10∧-36). It is also true that the POI is not identified, and for example, other family members are a valid consideration, but if they are a true contributor, it still would not exclude the POI.

Mutually exclusive evidence in the Hd is reasonably exhaustive and should include any relevant data; the data presented above is valid information many magnitudes higher than the Hd derived from the HW terms on Table 1 under equivalent conditions, which demonstrates its strength to provide evidence in favor of the Hd.

2.6.5 Integration of Probabilistic Genotyping (PG) Component Weights

Probabilistic genotyping (e.g., STRmix™) assigns probabilities for allele pairs proportional to how well they explain observed peak height patterns on the evidence (Taylor et al 2013, Gill et al 2021, Thompson et al 2017, Aitken et al, 2025, and NIST Reference 2024) For a contributor, PG outputs provide:

- A distribution over allele pairs for each locus, for each contributor
- Summing to 100%
- Representing the probability that each allele pair can produce the observed peaks.
- Based on the PG values, these already function as weighted pDC terms in the Hp for the POI, refining the probability for allele pairs at each locus.

If PG assigns weights to the allele pairs, they can be incorporated onto the tables with each weight replacing the binary 1, and a defined LR can be calculated from these weights. Table 3 below incorporates hypothetical PG weights onto Table 1 from the current forensic LR.

Table 3. The forensic DNA LR table with hypothetical PG weighted terms. The pDC terms and PG weights are in red. The locus has 4 alleles (7, 8, 9, and 10) at unequal heights, assuming two contributors, where the POI's diplotype is alleles 8, 9.

	Contributor 1	Contributor 2	Hp Calculation	Hd Calculation
A	(0.06) 7, 8	9, 10		(0.06)2p7p8 x 2p9p10 = 4p7p8p9p10
B	(0.01) 7, 9	8, 10		(0.01)2p7p9 x 2p8p10

C	(0.02) 7, 10	8, 9		(0.02)2p7p10 x 2p8p9
D	(0.84) 8, 9	7, 10	0.84(8,9pDC) x 2p7p10	(0.84)2p8p9 x 2p7p10
E	(0.04) 8, 10	7, 9		(0.04)2p8p10 x 2p7p9
F	(0.03) 9, 10	7, 8		(0.02)2p9p10 x 2p7p8
	1.00	Sum Total	0.84(8,9pDC) 2p7p10	(1)4p7p8p9p10

Table 3 LR = 0.84(8,9pDC) / 2p8p9.

The PG weight for each genetic pair does not reduce the number of potential genetic pairs, it does not alter the number of diplotypes that can be considered, nor the percentage of individuals in the population that likely possess any allelic combination. In the Factfinder LR model, the RMP calculated for Table 1 is unchanged, and the weights from the PG analysis are not incorporated into the RMP calculations.

Like Table 1, the RMP terms are derived from the evidence alleles, and in this model, and under these specific conditions, is not potentially the person who left a diplotype, is not a cause of the evidence, and does not present a single-source diplotype to measure for the probability to produce a specific pattern of peak heights on the evidence.

In effect, the PG weights reduce the Hp on Table 1 by the weight given to the genetic pair for the POI, and reduce the Hd from 6 total possibilities to a summation to 1 from the 6 possibilities. This will significantly decrease the magnitude of the Hp and the Hd across all loci, with the advantage being much more pronounced in the Hd, and a final LR that will be strongly affected by the PG weights.

In Table 4 below, the same hypothetical PG weights from Table 3 are incorporated onto Table 2 (pDC terms). The forensic LR totals from Table 3 incorporate the hypothetical PG weights for a POI with alleles (8,9), and at the bottom in row H, is the totals for a POI with alleles (7,9).

Table 4. The forensic LR from Table 2 incorporating pDC terms with hypothetical PG weights from Table 3. The locus has 4 alleles (7, 8, 9, and 10) at unequal heights, assuming two contributors, where rows A-G are the table for the POI with alleles (8,9), and row H is a POI with alleles (7,9), showing only the column totals.

	Contributor 1	Contributor 2	Hp Calculation	Hd Calculation
A	(0.06) 7, 8	9, 10		(0.06) (7,8pDC) x 1 (9,10pDC)
B	(0.01) 7, 9	8, 10		(0.01) (7,9pDC) x 1 (8,10pDC)
C	(0.02) 7, 10	8, 9		(0.02) (7,10pDC) x 1 (8,9pDC)

D	(0.84) 8, 9	7, 10	(0.84) (8,9pDC) x 1 (7,10pDC)	(0.84) (8,9pDC) x 1 (7,10pDC)
E	(0.04) 8, 10	7, 9		(0.04) (8,10pDC) x 1 (7,9pDC)
F	(0.03) 9, 10	7, 8		(0.03) (9,10pDC) x 1 (7,8pDC)
G		Sum Total	(0.84)(8,9pDC)(7,10pDC) 1 pDC combination	(0.06)(7,8pDC)(9,10pDC) + (0.01)(7,9pDC)(8,10pDC) + (0.02)(7,10pDC)(8,9pDC) +(0.84)(8,9pDC)(7,10pDC) + (0.04)(8,10pDC)(7,9pDC) + (0.03)(9,10pDC)(7,8pDC) 6 different pDCs combinations totaling 100%
H	POI is (7,9)		(0.01)(7,9pDC)(8,10pDC) 1 pDC combination	Same as above 6 different pDCs combinations totaling 100%

Table 4 LR from POI with the (8,9): (0.84)(8,9pDC) (7,8pDC) / 6 pDC pairs at relative weights equaling 100%; and from the POI with (7,9): (0.01)(7,9pDC)(8,10pDC) / 6 pDC pairs at relative weights.

In both examples there are 5 unequal but mutually exclusive alternatives to the Hp in the Hd, and there is one equal probability in the Hp as in the Hd that the DNA originated from the POI with an (8,9) or (7,9) allele pair, except that, there is only 1 POI diplotype, whereas the diplotype diversity in the Hd for an (8,9) or (7,9) allele pair across all loci is on the order of 10∧16, divided into an equal number for each genetic pair.

The weighted Factfinder LR is calculating the probability of the evidence regarding whether the DNA originated from the diplotype of the POI and an unknown diplotype, or from two unknown diplotypes, based on the peak heights of the evidence and the most likely allelic combinations across all loci. This is done by providing the distribution of probabilities for a given contributor, and then separating them into the Hp and the Hd of an LR.

If the evidence DNA presented a genetic pair across all loci at 84% or more, it would be similar to the major/minor DNA mixture in our true case study. A major profile can be shown to a factfinder on an EP from an evidence sample, and with these statistics, explained that these alleles are facts, that specific genetic pairs are factually true pairs, and that a sufficient number of true pairs can be proved to originate as a true set by their peak heights. This would leave no other diplotype as a possibility for that specific contributor, but would not rule out an identical twin.

The diplotypes that are most probable to produce the DNA evidence are in either the Hp or the Hd. In cases where the contributors are less certain, and on a sliding scale, the statistics will reflect whether the peak height evidence is more or less discriminating towards identification (Slooten 2022). This would provide the factfind-

er with context to weigh whether the DNA originated from the POI or not by a visual explanation of an EP, including statistical weights that describe how many possible contributors there are, how well any given contributor is distinguished by the factual evidence, how well the POI could produce the evidence compared to other contributors, and that matching the evidence DNA at every locus is highly improbable, reflected by the RMP at ~10^-36.

2.6.6 True United States Public Crime Laboratory Case Study

The true meaning of the current DNA LR and PG data is not discussed in this study, but it is recognized that the LR conditions and PG process provide complexities not discussed, and therefore, the data they present is not fully synonymous with the tables in this study. However, the values provided by the uniform prior across diplotypes are a good approximation based on the research (Buckleton et al 2021, Wivell et al 2023), are considered a good approximation by expert hand analysis herein, and are discussed herein as equivalent to our tables under these conditions. The approximation is sufficient for this study, because the primary focus is the general magnitude of Hd provided, and the contextual real-life definition of the calculation.

This study illustrates the Factfinder LR, which demonstrates the integration of PG allele pair weights with the pDC terms, compares the different outcomes provided by the two different LR questions in an equivalent environment, and compares the weights provided by the different LRs for their definitions and general magnitude. None of this section is intended as a validation of this model, but instead, is a foundation that there are two different questions, and the real-life meaning of the Factfinder LR provides contextual weight for the factfinder to deliberate the true-life legal DNA question regarding whether the DNA originated from true-life POI or not.

An anonymized case study from an accredited U.S. crime laboratory was used to illustrate the application of diplotype-based Hp/Hd formulations. The case involved:

- A three-person major/minor mixture with PG analysis generating contributor proportions of 81:16:3
- There are two suspects (POI-A and POI-B); POI-A is the major DNA donor at ~81%, and POI-B is analyzed as potentially Contributor 2 at ~16%.
- For this study, PG component probabilities were available for all contributors across all loci.
- All allele frequencies, RFUs, contributor probabilities, and PG weights are rounded and reordered to preserve ratios while preventing case identification. Non-autosomal markers (Amelogenin, Y-indel, DYS391) were excluded from calculations.

Table 5. Case Study PG weights: Contributor 2 weights for a redacted locus that detected three alleles. The PG Deconvolution Report stated: Contributors: 3; Component Interpretation of Contributor 2 (16%); Questioned Contributor. The laboratory determined that the DNA sample was a major/minor mixture, with major alleles (10,15); allele 10 is higher than allele 15, and allele 14 is the minor allele.

Locus 1	Genotype	Weight
(10,14,15)	Contributor 2 - Hd	PG Weight
A	14,14	36.35%
B	10,14	31.39%
C	14,15	24.57%
D	10,15	2.48%
E	Q,14	2.13%
F	10,10	1.26%
G	15,15	1.03%
H	Q,15	0.40%
I	Q,10	0.31%
J	Q,Q	0.07%
		100%

There is a (Q,Q) at every locus in the PG analysis of the DNA sample. The RMP calculation for an unknown contributor with no exclusions, (Q,Q) sums to 1 in this model, because it does not exclude any genetic pair from the population. The number of diplotypes in an unknown contributor with no exclusions (Q,Q) across all 21 loci [n(n+1)0.5], is on the order of 10∧35 diplotypes in the Caucasian database, based on the product rule.

The PG weights are incorporated on Table 6 below into the Conventional and Factfinder's LR calculations for the Hp and the Hd. The RMP is 1, and the pDC calculations sum to 1, the POI calculation contains 1 diplotype, and the unknown individuals present 10∧35 possible diplotypes.

The table below demonstrates the tables from this study incorporating the PG weights from a true case, and does not reflect how the laboratory calculated their forensic DNA LR by conventional methods. This table reflects the difference in the definitions of these two equations in this environment, and does not reflect the laboratory's calculations, or the meaning of their equation.

Table 6. Forensic DNA LR two-person minor mixture of Contributors 2 and 3. The data is from a public laboratory case study, including Locus 1 presented below. Comparison of calculations from a conventional forensic DNA LR with the Factfinder LR.

Contrib 2			Conventional Forensic LR		Factfinder LR	
Possible Allelic Pairs		PG Weight	Hp Calculation (10,14pDC x RMP)	Hd Calc RMP x RMP	Hp Calculation pDC x pDC	Hd Calculation pDC x pDC

A	14,14	36.35%		1x1		0.3635(14,14pDC) x 1
B	10,14	31.39%	0.3139(10,14pDC) x 1	1x1	0.3139(10,14pDC) x 1	0.3139(10,14pDC) x 1
C	14,15	24.57%		1x1		0.2457(14,15pDC) x 1
D	10,15	2.48%		1x1		0.0248(10,15pDC) x 1
E	Q,14	2.13%		1x1		0.0213(Q,15pDC) x 1
F	10,10	1.26%		1x1		0.0126(10,10pDC) x 1
G	15,15	1.03%		1x1		0.0103(15,15pDC) x 1
H	Q,15	0.40%		1x1		0.0040(Q,15pDC) x 1
I	Q,10	0.31%		1x1		0.0031(Q,10pDC) x 1
J	Q,Q	0.07%		1x1		0.0007(Q,QpDC) x 1
		100%	0.3139(10,14pDC) x 1 x 1 diplotype	1 x 1	0.3139(10,14pDC) x 1	1 x 1 x 10^35 diplotypes across all options

Under these specific conditions, the magnitude and definition for the conventional forensic DNA LR = 0.3139(10,14pDC); or the probability of the evidence if: the POI and an unknown random individual are the true contributors v. the probability that a random person in the population is a potential contributor.

Factfinder LR= 0.3139(10,14pDC)/ 10^43; (the diplotypes of the POI and an unknown person) / (total diplotypes from two contributors in any combination).

This is not the definition of the conventional forensic DNA LR, because the conditions have been altered, however, it demonstrates a difference in the meaning and magnitude in these two LRs, caused by weighing the two questions under the same conditions. Only the Hd is altered in these two equations.

2.6.7 Legal Case Review Methodology and Tables: *McDaniel v. Brown 558 U.S. 120, 2010*

The case was originally adjudicated in the Nevada State Court in 1994. Item 1 was an intimate item of evidence, the RMP was 1 in 3 million, and Troy Brown was a potential contributor to the DNA evidence.

The DNA analyst, Renee Romero, testified that the likelihood that the DNA on item 1 was not Brown's would be 0.000033% (1 in 3 million), and the prosecutor stated in his closing argument that there was a 99.999967% (3 million to 1) probability that the DNA belonged to Troy Brown. Brown was convicted. It was acknowledged after the trial that the statistics provided were in the form of the Prosecutor's Fallacy.

There were three appellate decisions on this case from the Nevada Supreme Court, the U.S. District Court of Nevada, and the U.S. Court of Appeals for the Ninth Circuit. Thus, the SCOTUS decision was the fourth legal court decision regarding the DNA statistics provided for this case.

Tables 7 and 8 are tabulated from the SOP's of a public crime laboratory (Phoenix Police Department Laboratory Services Bureau 2009) that are calculating a hypothetical forensic DNA LR by hand for an intimate sample of two contributors, and includes a known contributor; this calculation is based on the NRCII. This demon-

strates how a known sample can reduce the possible diplotypes in the Hd, as well as providing an example of how the LR in 2009 was calculated by hand and reported.

The DNA for the Brown case is not available, but the hypothetical tables demonstrate how a forensic DNA LR could have been calculated and reported for an intimate sample with two contributors in 2009, without PG analysis, and equivalent to binary tables in this study. It is not known if the Brown sample was a mixture, nor if the known victim's DNA was subtracted as done on these tables, however, the mathematics for a two person binary mixture is on Table 1, and could have been used as well.

TABLE 7. Possible genotypes for an unknown individual, given the genotypes of the evidence and victim from an intimate sample (Phoenix Police Department Laboratory Services Bureau 2009).

Locus	Evidence	Victim Known	Unknown Individual
1	15, 15	15, 15	15, 15
2	16, 17	16, 17	16, 16 or 16, 17 or 17, 17
3	19, 23	19, 19	19, 23 or 23, 23
4	12, 16	12, 16	12, 12 or 12, 16 or 16, 16
5	30, 31. 2, 32. 2	30, 32. 2	31. 2, 31. 2 or 30, 31. 2 or 31. 2, 32. 2

Table 8. The LR table for an intimate mixture, and calculations for illustration purposes (rows 3-9; Phoenix Police Department Laboratory Services Bureau 2009). The Hp and the Hd Calculation headings from this study's other tables (row 2), the headings for the Brown Case (row 1), and RMP total for the Brown case (row 10).

1			Hp: It is Brown's DNA	Hd: it is someone else's DNA
2			Hp Calculation	Hd Calculation
3	Locus	Suspect DNA	P(E| it is POI's DNA)	P(E| it is not POI's DNA)
4	A	15,15	1(15,15pDC)	$p^2$15
5	B	16,16	1(16,16pDC)	$p^2$16 + $p^2$17 + 2p16p17
6	C	19,23	1(19,23pDC)	$p^2$23 + 2p19p23
7	D	16,16	1(16,16pDC)	$p^2$12 + $p^2$16 + 2p12p16

8	E	31.2,31.2	1(31.2,31.2pDC)	$p^2$31.2 + 2p30p31.2 + 2p31.2p32.2
9		SOP Totals	1	0.0000011
10		Brown Case Totals	1	RMP Product across all loci 0.00000033

The laboratory's column headings are noted in the SOPs as an LR regarding whether the DNA originated from the POI or not, and the column is calculating the RMP as the "or not" in the Hd. This is consistent with the heading of the tables in this study for the current forensic LR. This is also consistent with the Brown case statements (rows 1 and 10). In 2009, the statements in the Brown case from the DNA analyst and the prosecutor were consistent with current forensic DNA LR research and calculations, except that, they stated them using the Prosecutor's Fallacy.

The Prosecutor's Fallacy is when the forensic DNA calculations are described as the probability that the DNA, in fact, originated from the POI or not, rather than the probability of the evidence, if those hypotheses are assumed in advance. Acknowledging the Prosecutor's Fallacy is mathematically equivalent to amending the given statement with the "probability of the evidence if" statement from current LR theory; and this alters the statements to be identical in meaning to the forensic laboratory SOPs. Therefore, if the analyst and prosecutor had made their statements without the Prosecutor's Fallacy, they would have been consistent with the current forensic DNA LR, and these are presented on Table 8 above.

This indicates that the laboratory and the legal sphere recognize the specific comparison as a probability of producing the evidence between the Hp and the Hd of the current forensic DNA LR, as well as how these are properly stated.

The SCOTUS was presented with the Brown case which was reported as a probability of 1 in 3 million regarding whether the DNA originated from the POI or not. They were presented with an RMP as the Hd, and 1 for the comparison of the POI in Hp, which is the same as the binary equation on the table. Therefore, the question being weighed was specified in the court case as the column headings, and forensic DNA statistics were presented as the column totals. Since this information was presented to them with these statistical terms, they naturally use them in their discussion, which allows this study to apply mathematics directly to their words, like any mathematical word problem that is sufficiently clear.

All of the references in this article agree that the true legal question is: whether the DNA originated from the POI or not. The only issue this article addresses is what should be calculated as the Hd, where the prior is chosen based on the conditions necessary to calculate the Hd used. In several instances, the SCOTUS states (what we speculate is clearly) that the RMP is not the Hd, and they define what should be presented as DNA on the defense's behalf.

No legal conclusions are asserted, and any agreement between the legal sections and the math sections does not mean that one or both are correct, or that they prove each other; instead, if the SCOTUS is stating what statistics they want presented for the Hp and the Hd in a U.S. court of law for DNA evidence, and that is provided by the Factfinder LR and what is presented herein, then these will necessarily be the same.

3. Results

3.1 Application of Diplotype-Based Likelihood Framework to Casework Data

This is a true case used as a theoretical illustration of the potential to calculate DNA evidence with PG data using the Factfinder LR, together with the RMP, to provide robust statistical information to assist the factfinder in understanding the DNA EP, and the full contextual weight of the Hp and the Hd for a case. This serves as an illustration and is not a validation-type case study.

Forensic DNA case data are highly confidential; subsequently, to prevent case recognition, only minimal data are presented. The probabilities reported by the laboratory in the true case have been altered while maintaining their relative ratio (post-rounded) and original order of magnitude.

In 2020, an accredited United States public state crime laboratory compared the DNA detected on evidence Item #1 to the known DNA diplotypes of two suspects, POI-A and POI-B. Each was suspected to be the source of some of the DNA alleles detected on Item #1, rather than the DNA originating from unrelated individuals.

Item #1 electropherogram: In total, there are 24 loci of detection (GlobalFiler™), and all loci produced alleles. There are 21 calculable autosomal loci with 51 alleles, including 37 major and 14 minor ones; of these 21 loci, 3 detected one allele, 7 detected two, 10 detected three, and 1 detected four. The electropherogram detects more than one individual within a major-minor mixture as confirmed by a maximum of three or four alleles at 11 loci, with a PG-calculated DNA ratio of 81:19. There is a discernible single-source major profile, at 17 loci, and four loci that are ambiguous regarding the genetic pair of the major contributor, with a visually noticeable ski-slope degradation pattern. The major profile had a range of peak heights from 1,136 RFU at a locus on the far left to 127 RFU at a locus on the far right, which leaves the possibility of dropout from the major profile, with a reasonable certainty in the minor component, demonstrated by increasingly fewer or no minor alleles detected toward the longer alleles on the right of the graph. There is a minor profile of 14 alleles, with 12 loci detecting a single minor allele and one with two minor alleles, ranging from 81 to 279 RFU, with a minor peak at 6–42% of the highest heterozygous major peak at the same locus. There is no allelic evidence demonstrating a third contributor, but hypotheses with more than two minor contributors are reasonable.

- POI-A matched the major profile on the evidence electropherogram, and his genetic pair was the most likely explanation of the allelic pattern detected at all 24 loci, including the four ambiguous and the three sex based loci. Based on visual, logical, and statistical evidence, it is reasonable to conclude that the major DNA profile originated from POI-A, unless he has an identical twin.
- POI-B was consistent with 8 of 14 (57%) minor alleles, 28 of 37 (75%) major alleles, and one of two at the locus with two minor alleles. He was a possible contributor to the DNA on Item #1 only if the following conditions were met.
    - POI-A is not a true contributor. The PG analysis has determined that the DNA on the evidence could be from either POI-A or B, but not from both of them.

- The evidence DNA originated from three individuals.

POI-A is proven to be Contributor 1 and can exclude POI-B. It should be assumed that POI-B was compared to the evidence and that the 75% consistency in the major profile suggested a potential for a familial connection. Subsequently, his full sibling POI-A was tested and compared to the DNA on item 1, which excluded POI-B, and this was reported at a later time.

The two persons of interest were compared to the evidence:

POI-A: This profile visually and statistically matched the major contributor.
POI-B: This profile was evaluated as a possible contributor to the minor component, without POI-A.

PG deconvolution provided locus-specific probabilities for each allele pair that could explain the observed peak height patterns for Contributor 2 (the putative minor contributor). These PG component interpretation values allowed locus-specific probabilities to reflect both allelic compatibility and peak height evidence.

At each locus, the PG genotype weights for Contributor 2 summed to 100%, with the highest probabilities assigned to diplotypes directly consistent with the observed minor peaks. Allele dropout possibilities, represented by (Q,_) and (Q,Q), had low but non-zero probabilities at every locus.

3.1.1 The Conventional Forensic LR

The laboratory reported the conventional forensic LRs using a PG program, which incorporated a different prior as well as additional factors not addressed in the hand calculations herein, and were:

- POI-A: >900 billion
- POI-B: >25 million

These values reflect the standard LR comparing:

- Hp: POI + unknown contributor(s)
- Hd: unknown contributor(s) using (HW-based population frequencies)

Because POI-A closely matched the major profile, the LR strongly favored inclusion. POI-B's LR, while more moderate, still reflected substantial support for Hp under the conventional LR model. The values for POI-B do not account for conditioning on POI-A's established contribution, which later excludes him.

3.1.2 The Factfinder LR

The EP for this sample could be shown to the factfinder, and the statistics that describe and give context to the factual evidence could be provided with the factfinder LR and the RMP.

Once the DNA profile of POI-A was provided it could be determined by a three-prong test that he was the major profile: the three prongs were: 1) that POI-As alleles could be shown to be factually present, 2) his genetic pair could be shown to be a true pair at a sufficient number of loci, and 3) his diplotype could be shown to be a true set of true pairs that were factually present at a sufficient number of loci (17), and therefore, he was

statistically a unique and identifiable profile that could be used to resolve the 4 ambiguous loci, which then excludes POI-B. There was no other diplotype that could be considered beyond POI-A, once known.

Before the profile of POI-A was known, it could be shown that the distribution of probabilities from Contributor 1 has the potential to exclude POI-B, as well as why. POI-B is excluded from this mixture if it is a two-person mixture, because he does not account for all of the major or minor alleles. It could be shown to the factfinder that a two-person mixture is more probable than one with three contributors, because all other things being equal, a two-person mixture will match more minor alleles, and will have a much smaller probability space diluting the diplotype probabilities. However, a two-person mixture with a specific diplotype, which would almost certainly have to be a sibling, might be shown to be consistent with the minor profile, as well as a good match for the major allele pattern if masked; while this may have a low probability, if the pattern of the factual evidence supports a diplotype, this too can be explained to the factfinder to weigh.

As a three-person mixture the factfinder could be shown that the sample has very low power to discriminate between the possibilities, because there is very little information for comparison purposes, and no possible diplotypes, or genetic pairs are excluded.

When diplotype probabilities were combined across all 21 loci with the product rule, the PG-derived probabilities produced a ranked distribution of possible genotype combinations for Contributor 2:

- There are approximately 10∧35 diplotype combinations for Contributor 2.
- The POI-B diplotype combination accumulated a probability on the order of 10∧-13.
- The lowest-probability contributor combinations, primarily from dropout-(Q,Q) genetic pairs, were on the order of 10∧-38.
- The highest-probability contributor combination for any compatible (non-POI) genotype was approximately 10∧-10.

The Hd denominator sums to 1 over a large probability space.

The conventional and Factfinder LRs in this case study produced different outcomes by providing weights for different questions, and it is demonstrated here that the results have different magnitudes and definitions, based on altering the Hd.

3.2 Alignment of Diplotype-Based Hd Terms with Legal Reasoning in McDaniel v. Brown

Item 1 was an intimate item of evidence, the RMP was 1 in 3 million, and Troy Brown was a potential contributor to the DNA evidence. The SCOTUS review of this was not intended to address statistical theory, or to define the Hp and the Hd terms in a DNA LR for the mathematicians. Nevertheless, their detailed discussion describing the errors in the Brown case provides apparent descriptions and definitions regarding how to properly apply DNA statistics for a fair trial, and we applied the mathematics directly to our understanding of their words.

This section is interpretive and illustrative that some foundation exists that Postulate #3 has merit, and that the math and law sections are the same discussion regarding what is and is not the Hd for a legal DNA sample, only from a different viewpoint. This is not authoritative, and is not a validation.

[SCOTUS QUOTE #1] The "fallacy is the assumption that the random match probability is the same as the probability that the defendant was not the source of the DNA sample."

- Hd : that the defendant was not the source of the DNA sample
- Hd is not the RMP

[SCOTUS QUOTE #2] "In other words, if a juror is told the probability a member of the general population would share the same DNA is 1 in 10,000 (random match probability), and he takes that to mean there is only a 1 in 10,000 chance that someone other than the defendant is the source of the DNA found at the crime scene (source probability), then he has succumbed to the … fallacy."

Hd is:

- Someone other than the defendant
- is the source of the DNA found at the crime scene
- calculated as a "source probability"
- not the RMP.

[SCOTUS QUOTE #3] … "in a classic example of erroneously equating source probability with random match probability, whether "it [would] be fair to say ... that the chances that the DNA found in the panties - the semen in the panties -and the blood sample, the likelihood that it is not Troy Brown would be 0.000033," Romero ultimately agreed that it was "not inaccurate" to state it that way."

- Erroneously equating the "source probability of "not Brown" to the RMP
- An RMP is not a source probability
- The RMP is not the Hd of "not Troy Brown"
- "Not Troy Brown" is a source probability
- The math is a likelihood comparison between whether the DNA originated from Brown or not

[SCOTUS QUOTE #4] It is further error to equate source probability with probability of guilt, unless there is no explanation other than guilt for a person to be the source of crime-scene DNA.

- A person is a source of DNA of crime-scene DNA
- A person that could be the source of the DNA, and could be guilty, is a source probability.
- Brown's DNA is a potential source of the crime-scene DNA, and is a source probability.

[SCOTUS QUOTE #5] "In summary, the two inaccuracies upon which this case turns are testimony that equates RMP with source probability, and an underestimate of the likelihood that one of Troy's brothers would also match the DNA left at the scene."

- Using the RMP as the source of the DNA in Hd is a primary error in the Brown Case.
- Hd includes Troy's brothers.

Applying mathematics directly to this case and these quotes: this is a likelihood ratio comparison of two "probability of the evidence if" calculations, the legal question being weighed is whether the DNA originated from the POI or not; whether the DNA originated from the POI is the Hp (source probability); in that case whether the DNA did not originate from Brown is the Hd (RMP); the RMP is an erroneous Hd; and, the Hd is a source probability that properly expresses "not Browns's DNA." Based on the SCOTUS statements, everything is defined in a manner for the current forensic DNA LR mathematics to be directly applied.

It is acknowledged that quote #1 and #2 are cut off at "fallacy", and that both times the SCOTUS labels the fallacy as the Prosecutor's Fallacy, which was a known error in the original case. The error pointed out by the SCOTUS is not the Prosecutor's Fallacy, however, Quote #1 defines what they intended their words to mean, and their discussion provides examples, all discussing that the error they are focused on is specific to when the RMP replaces the "source probability" in the Hd. Their discussion of this term quotes the NRCII, p. 133, and causes them to label the term wrong, but the incorrect label does not affect the application of the math herein.

The issues that are caused by the scientific definition of the Prosecutor's Fallacy do not arise in the SCOTUS decision, and the referenced error is described, explained, and an example given, all consistent with their broader discussion referencing a source probability as the Hd, where the RMP as Hd is characterized as an error.

This is our interpretation of an important issue, is not authoritative on our part, and needs to be reviewed by others, however, if true, this definition may have an authoritative context regarding the intentions of SCOTUS to point out a specific error.

The only other potentially ambiguous issue encountered by this study in directly applying the mathematics regarded what the SCOTUS intended to be calculated as the "source probability," because the definition of the Hd is critical in this study, and the term might have alternative meaning to those provided herein. In order to apply the proper mathematics, we considered the following:

- The SCOTUS discussion as a whole.
- The issues in this study are best correlated in the SCOTUS Quote #4: "it is further error to equate source probability with probability of guilt, unless there is no explanation other than guilt for a person to be the source of crime-scene DNA." This is a direct correlation between person, source of crime-scene DNA, and source probability.
- A source probability is a reasonable label for a diplotype as the source of DNA, modelled on the calculation for Brown as a source of DNA in the Hp. We reasoned that the SCOTUS are not mathematicians, and are discussing the DNA statistical terms provided in the Hp and the Hd.
- A diplotype-derived Hd is consistent with their discussion when reviewed as a whole, and exemplified by the quotes herein.
- Brown's brothers could match the DNA at the scene.
- In forensic DNA LR, and in our limited understanding of the law, we could find no other reasonable meaning to apply to the SCOTUS words.
- This is consistent with our understanding of the legal sphere regarding one explanation of the factual evidence v. all of the other explanations, or one DNA suspect v. all of the other suspects, that if true, prove the Hp false.
- A diplotype comparison is consistent with the concept of proving that the DNA originated from the POI.

Therefore, while recognizing that other meanings may exist, we applied diplotypes to the meaning of "source probability," and the court's use of the Prosecutor's Fallacy as a labelling error. These are not proved to be the meanings, but they are consistent in all manners considered, would provide valid weight for the question asked,

would alleviate all of the issue under discussion, and we see no other reasonable meaning to ascribe to the SCOTUS words. This foundation does not make it correct, and requires review outside of our expertise.

It is recognized that this is speculative foundation, however, if true: this is a legal question being weighed in the legal sphere; and within that venue these factors may already be defined by those who have full authority to do so; therefore, if this study's speculation is true, then these definitions and calculations may not be variable or optional regarding the weights provided for legal DNA samples.

4. Discussion

4.1 The utility of the Factfinder LR

The foundation for this article is that the primary information that allows an individual to weigh whether the POI is the true Contributor 1 to a legal DNA sample, is found in an expert evaluation of the factual evidence of the alleles and peak heights on an EP, as well as their understanding of the statistics provided regarding how many contributor 1s are possible, what is the distribution of probabilities across those contributors, how probable is the POI relative to the other Contributor 1s, and the percentage of individuals in the population that are likely to be excluded from the DNA evidence. The question of whether potential family members are included can be explored, but these may or may not exclude the POI as a contributor, even if present.

This article is primarily an application of current forensic LR mathematics to that foundation, and even if this is done incorrectly herein, this information is germane and salient. This study has provided a foundation that the two separate equations under examination on the tables provided, produce different contextual meaning regardless of the statement ultimately reported. This study intentionally does not agree or disagree with whether other equations can accurately be described in this manner. Within the confines of this study, it is demonstrated that they produce different real-life meanings, and have different general magnitudes. A foundation is presented herein that the Factfinder LR is consistent with the real-life contextual legal meaning for a DNA evidence sample regarding whether the DNA originated from the POI or not.

This study provides a foundation that the following is accepted:

- It is the legal system that is weighing its own question
- The factfinder in the legal system will ultimately deliberate the question
- The question herein is whether the POI is, or is not, the true contributor to the DNA sample
- The Hp is that he is, and this must be proved
- The Hd is that he is not, and is what the Hp must be proved against

There are only two numbers to consider for an LR, the first one is the Hp and is set, and the only issue under consideration herein is what is to be calculated for the Hd. The POI can potentially be proved to the factfinder to be the best diplotype to produce the evidence for Contributor 1 (if this is assumed true in advance) against the other potential Contributor 1s (if they are assumed in advance to be the true contributor). However, without the other contributors, all that remains in the LR is the presumption that the POI is Contributor 1, and an effectively empty Hd to prove it against, because the other contributors represent the DNA evidence that has the primary data, numerical magnitude, and contextual potential to exclude the POI.

Postulate #1: Weights can be provided regarding whether the DNA originated from the POI or not, and they can be calculated with current Bayesian LR mathematics as described herein. This LR, along with the traditional RMP, is the primary information necessary to weigh a DNA evidence sample.

This study has provided a foundation that this can be calculated, how to calculate it, and that the information might be relevant in a legal setting.

Postulate #2: The weights provided in the current forensic LR regarding whether the DNA originated from the POI or a random man, is a separate and distinct question, calculated by a different LR equation, and provides different weights for the factfinder to deliberate their question.

This study has provided foundation that, within the confines of this study, these are different questions, with different contextual real-life meaning, and result in different weights being provided for the LR. Therefore, these can be different questions, but this study is silent regarding whether this is true outside of the parameters provided.

Postulate #3: the SCOTUS discussion is the same two questions being weighed as our mathematical model and tables, with the same statistics as presented therein, and both applied mathematical studies produces the same result.

This study provided a speculative foundation that this might be true, however, if it is true that their words can be taken as explaining and defining what is and is not the Hd, where every other part of the equations are identical, then this is not an optional definition for forensic science.

4.2 Limitations.

This study did not test the Factfinder LR against samples with known results; it did not run simulations; it did not explore how altering the priors with this novel LR would affect the results; it did not explore multiple PG casework samples; and therefore, the Factfinder LR is a conceptual framework for investigating the potential that additional evidence in favor of the Hd may be produced by this method, and might assist in better weighing the legal question.

However, due to the complexities and flexibility recognized in the forensic LR framework, such as altering the priors, there may be alternatives not explored herein, and this study recognizes the importance of a full validation that is not provided by this theoretical framework. Implementation would necessitate systematic evaluations of the optimal parameters to establish if this model is feasible, if it provides high quality and reproducible information, if it can be integrated into current LR mathematical framework and operational systems, and if the information is useful and acceptable to the legal system. Validation studies are needed to determine if the Factfinder LR produces useful information.

4.2.1 Proposed Validation Framework

- Ground-truth testing: Compare both LRs on mixtures with known contributors.

- Sensitivity analysis: Examine results under different priors (uniform vs. frequency-weighted).
- Simulation studies: Generate synthetic mixtures and assess discriminatory power.
- Reporting studies: Evaluate how factfinders interpret Factfinder LR values compared to conventional LR values.
- Testing on samples difficult to interpret, such as low template, degraded, or kinfolk mixtures
- Testing on both LRs to determine how they diverge, how much, and under what conditions, as well as altering the number of contributors.

4.4 Author's Note on AI modelling

Due to the confidentiality of legal samples, we do not believe that they should be entered into AI, and therefore, AI modelling is outside of the scope of this article. However, as a note to others, AI provided a very high quality and similar deconvolution to the author's interpretation without any PG data provided. This was not modelled with PG data included.

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Other

Supplementary Materials: All of the information, data, and references are publically available with the exception of the case study and laboratory reports. No identifying or confidential information on the case study is available. True laboratory reports are confidential, however, that reports from public entities given a time-frame is verifiable outside of this article.

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