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Formulating Propositions for Likelihood Ratios in Forensic DNA Interpretations

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DRAFT

Foreword

When DNA testing data are generated from evidence and then compared to data from known individuals, it is necessary to provide a statistical statement for any comparison for which a questioned individual cannot be excluded as a possible contributor to the DNA. One common reporting format is based upon the assignment of a likelihood ratio (LR):

$$LR = \frac{Pr(E|H_1, I)}{Pr(E|H_2, I)}$$

where:

E are the findings (e.g., DNA profile(s), presumptive test results, observations),

H_1 and H_2 are two mutually exclusive propositions, but not usually mutually exhaustive, and

I is the relevant information.

The terms H_p and H_d are often used in place of H_1 and H_2, and are assigned for the prosecution (p) and the defense (d), respectively. The arguments for the use of H_1 and H_2 in lieu of H_p and H_d, respectively, relate to avoiding any unintended assignment of propositions or scenarios to the prosecution or defense. In some jurisdictions, such as the United States, the accused has no burden to prove or disprove anything at trial; the burden of proof rests solely on the government. Assignment of a defense hypothesis may be seen as burden shifting. This weighs strongly in favor of using H_1 and H_2 in lieu of H_p and H_d. The arguments in favor of the alternative set, H_p and H_d, relate to directness of language. The exact propositions of the prosecution and defense may not be known, and in such circumstances, reasonable propositions consistent with both viewpoints should be selected for the analysis. The value of the likelihood ratio depends in part upon the choice of these propositions.

Cook et al.[6] and Evett et al.[8] classified propositions into three levels: from top to bottom these are offense, activity and source. This was expanded to include the sub-source and the sub-sub-source levels and is explained in detail in Buckleton et al.[3], pp. 46-48. This document is limited to propositions at the sub-source and sub-sub-source levels.

The propositions in any given case depend on the knowledge of the case circumstances at the time the interpretation is carried out. Relevant information (I) may include, but is not limited to, the following elements.

a) The alleged location, direction, and time of transfer.

b) The location and time that the sample was taken.

c) The genotypes of the person of interest (POI), the complainant, and proposed consensual partners, any persons who admit activity that could deposit DNA or have legitimate access to the sample, and any elimination samples such as scene of crime staff or lab staff.

d) Evidence of opportunity for alternate donors may be relevant. In particular, the genotypes, population groups (i.e., ascriptive identity[1]), or relationships[2] of persons who could reasonably be alternative donors are relevant[16]. Also relevant is information of those who could not reasonably be considered possible donors because of lack of opportunity.

e) Information of the results of other forensic analyses that suggest the presence at the scene of an alternate donor.

Information regarding case circumstances is not always numerically expressed in the calculation of the *LR*. Instead, this information informs the choice of propositions, which in turn determines the value of the *LR*.

When talking about the case information, it needs to be emphasized that one does not consider information such as prior conviction, motive, or a confession of the POI as relevant forensic information for the evaluation of the DNA results.

It is important that laboratories are aware of the limitations of the propositions that can be accommodated by their selected software.

This document was revised, prepared, and finalized as a standard by the DNA Consensus Body of the AAFS Standards Board. The draft of this standard was developed by the Biology Subcommittee of the Organization of Scientific Area Committees (OSAC) for Forensic Science.

The AAFS Standards Board (ASB) is an ANSI-accredited Standards Developing Organization with the purpose of providing accessible, high quality science-based consensus forensic standards. The ASB is a wholly owned subsidiary of the American Academy of Forensic Sciences (AAFS), established in 2015 and accredited by the American National Standards Institute (ANSI) in 2016. The ASB consists of Consensus Bodies (CB), which are open to all materially interested and affected individuals, companies, and organizations; a Board of Directors; and Staff.

All hyperlinks and web addresses shown in this document are current as of the publication date of this standard.

Keywords: *DNA profile, DNA mixture validation, mixture interpretation protocols, likelihood ratios, propositions*

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[1] Ascriptive identity (ascribed racial or ethnic background) may be correlated with population genetic background and/or genetic ancestry.

[2] There is a misperception that the likelihood ratio approach is unsuitable if any individuals within the pair of propositions are related. This is not true. Likelihood ratios for kinship evaluations account for this relatedness and have been used for decades for paternity cases and missing persons. They are also suitable if, for example:

a) the known individuals are related and have been genotyped; or
b) one, or more, of the postulated unknown individuals is related to the genotyped individuals.

Failure to account for pedigree information may lead to a misleading likelihood ratio.

Table of Contents

Formulating Propositions for Likelihood Ratios in Forensic DNA Interpretations

1 Scope

This standard provides the requirements for the formulation and assignment of propositions for the interpretation of DNA profiling evidence using likelihood ratios. It includes requirements regarding practical issues such as case file documentation, conditioning on profiles of assumed contributors, evaluating the weight of evidence for multiple individuals of interest, and assigning the number of contributors.

2 Normative References

There are no normative reference documents. Annex A, Bibliography, contains informative references.

3 Terms and Definitions

For purposes of this document, the following definitions apply.

3.1
analysis
An interpretation and/or likelihood ratio calculation.

3.2
conditioning
The act of assuming one or more pieces of information when assigning a conditional probability. The information might be the profile of an individual, or profiles of a set of individuals, that are assumed to have contributed DNA to the evidentiary item under a particular proposition, or it might simply be the assumption that a particular proposition is true. Any events (or information) that have been used for conditioning are placed to the right of the conditioning bar in a conditional probability expression.

3.3
conditioning profile
The DNA profile of an individual assumed to be a contributor to the DNA (or DNA profile) obtained from an evidentiary item in both propositions, H_1 and H_2, of a pair of propositions.

3.4
evaluative analysis
An analysis using propositions that are used with the intent of producing an *LR* for reporting.

3.5
hierarchy of propositions
An organizational structure for propositions. Proposition pairs are classified by the level of information required to assist the trier of fact: offense (e.g., “Mr. X raped V”), activity (e.g., “Mr. X had intercourse with V”), source (e.g., “The semen came from Mr. X”), sub-source (e.g., “Mr. X is a contributor to this DNA”), and sub-sub-source (e.g., “Mr. X is the minor contributor to this DNA mixture”). (Buckleton et al.[3], pp. 46-48.)

3.5.1
sub-source level proposition
A proposition that specifies a defined set of one or more assumed contributors (known or not) to the questioned DNA (evidentiary) sample.

3.5.2
sub-sub-source level proposition
A proposition that specifies an assumed contributor (known or not) to one contribution of a questioned DNA (evidentiary) mixture (e.g., the major contributor of a two-person mixture).

3.6
intimate contributor
An individual from whose body a biological evidentiary item has been directly obtained.

3.7
investigative analysis
An analysis using propositions that are used to determine the best pair(s) to use for an evaluative analysis.

3.8
person of interest
POI
An individual whose contribution to the biological evidence sample is in question. Depending upon the case circumstances this could be the complainant, the accused, or a third party individual.

3.9
probabilistic genotyping
The use of biological modeling (i.e., statistical modeling informed by biological data), statistical theory, computer algorithms, and/or probability distributions, to infer genotypes and/or calculate likelihood ratios.

3.10
probabilistic genotyping system
Software, or software and hardware, which utilizes a probabilistic genotyping approach to infer genotypes and/or calculate likelihood ratios.

3.11
proposition
A statement that is true or false, associated with the standpoint, known or assumed, of one of the parties on a disputed issue of interest.

3.11.1
simple proposition pair
A pair of propositions where no more than one POI in H_1 is replaced with an unknown (U) donor in H_2 or vice versa.

3.11.2
compound proposition pair
A pair of propositions where more than one POI in H_1 is replaced with unknown donors in H_2 or vice versa.

4 Requirements

4.1 The laboratory shall have a documented policy that outlines the difference between relevant and irrelevant information with respect to formulating propositions.

4.2 The laboratory shall have a documented policy on the reporting of results within the hierarchy of propositions. The policy shall define the level within the hierarchy of propositions (i.e., sub-source or sub-sub-source) that the laboratory reports.

Within the capabilities of the analysis approach used, the laboratory should report results for a pair of propositions that addresses the issue of interest. This level is the highest level in the hierarchy for which the forensic scientist can provide information. Hence, the laboratory should report results given sub-source level rather than sub-sub-source level propositions.

If a single source profile is deduced from the mixture, even where sub-source propositions for mixtures are possible, then a sub-sub-source proposition pair may be used. However it is permissible, and may be advisable, to continue to operate at the sub-source level.

4.3 Propositions shall be set and then documented in the case file prior to comparison to any individuals who are not intimate or reasonably assumed (e.g., consensual partners) contributors.

Laboratory's reports should contain statements that:

a) likelihood ratio results depend in part upon the choice of propositions, and

b) the propositions chosen do not reflect every possibility and may not even reflect the positions of the parties in the case.

4.4 The laboratory shall have a documented procedure defining when a conditioning profile will be used. Support for the assumption of non-intimate conditioning contributors shall be documented in the case file.

A profile should be assigned as a conditioning profile to a mixture when an individual is identified as an intimate contributor, or when it is reasonable to assume the individual's presence based on case specific information, and the associated data supports the assumption. The conditioning profile could be from the complainant, POI, or other individual depending on the case scenario.

When conditioning on individuals in non-intimate samples, propositions that do not condition upon that individual's profile may also be examined. A positive log (LR) value for an individual may be used as evidence of support for calculations that condition upon them.

4.5 Where multiple POIs have *LRs* that support an association to a DNA mixture, within the capabilities of the approach used, an analysis shall be performed using proposition pairs that test whether the multiple POIs can be included together in the observed DNA profile.

The analysis should separate the propositions into their simplified constituents (i.e., simple proposition pairs) when an LR favoring H_1 has resulted from a compound proposition pair in order to establish the weighting and the consequent probative value of the evidence per contributor under H_1.

The results of the analyses using the simple proposition pairs should be included in the report.

a) A simple proposition pair may include conditioning upon each POI separately in H_1, where all other contributors are treated as unknowns. This could, however, contradict the assertions of the party represented by that proposition.

b) A simple proposition pair may include conditioning upon multiple POIs in H_1 and one or a subset of POIs in H_2 with the goal of isolating the weight attributable to the POI not conditioned upon in H_2. In the case of non-intimate samples, if a POI's profile is assumed in both H_1 and H_2, then an *LR* shall also be calculated for a simple proposition pair with the POI not assumed in H_2. For example, if the compound proposition pair has H_1 = POI1 + POI2 and H_2 = U + U, and an associated simplified proposition pair has H_1 = POI1 + POI2 and H_2= POI1 + U, then the simplified proposition pair with H_1 = POI1 + POI2 and H_2 = POI2 + U would also be required.

4.6 If an analysis requires the number of contributors to be declared for each proposition or pair of propositions tested, then the laboratory shall have a documented procedure regarding the assignment of the number of contributors for each proposition or pair of propositions.

While the number of contributors to an evidentiary sample is strictly unknown, assessments of the number of contributors should involve profile traits such as:

a) the number of alleles;

b) the relative intensities of the results (e.g., relative peak heights);

c) the relative proportions of peaks in expected artifact positions (e.g., STR stutters);

d) the known observed heterozygosity of each locus in comparison to the number of detected alleles (e.g., seeing 4 alleles at TPOX is rarer in a 2-person mixture than seeing 4 alleles at SE33 in a 2-person mixture);

e) any assumptions regarding the contribution of a conditioning profile's alleles; and

f) any assumptions regarding rare genetic traits (e.g., tri-allelic genotypes).

Probabilistic methods may be used to provide estimated probabilities for the number of contributors.

4.6.1 A number of alternatives for the number of contributors may be used.

4.6.2 The number of contributors may be the same or different for H_1 and H_2.

4.6.3 For approaches that utilize probabilities, as opposed to probability densities, the number of contributors may be assigned values that maximize the probability of the evidence separately under *H1* and H_2 [5]. In such cases, the number of contributors under each proposition need not be the same within a given likelihood ratio.

4.6.4 Assigning the number of contributors may involve assessing possible drop-in events and also assessing or specifying the number of drop-in events allowed. Typically, if more than two drop-in events would be required, the assumed number of contributors should be increased [10].

4.7 If an analysis requires a predefined number of contributors, then an assessment of the number of contributors shall be documented in the case file prior to comparison to any individuals who are not intimate or reasonably assumed (e.g., consensual partners) contributors.

4.8 If the approach used to calculate the *LR* cannot accommodate different numbers of contributors in H_1 and H_2, then the profile of the POI shall not be used in the initial assignment of the number of contributors. If the approach can accommodate different numbers of contributors in H_1 and H_2, then the profile of the POI shall not be used in the initial assignment of the number of contributors for the proposition that does not assume their presence.

4.9 Use of conditioning profiles in the contributor number assessment shall be documented in the case file.

4.10 Biological relationships between contributors in the propositions shall be documented in a case file and/or case report.

4.11 If the laboratory allows for drop-in events in their probabilistic genotyping procedures, the laboratory shall have a documented procedure regarding contributor number assumptions that require drop-in events.

4.12 Any reassessment of the number of contributors based upon a probabilistic genotyping system's diagnostic calculations, or subsequent interpretations or *LR* calculations, shall be documented in the case file. This documentation shall include the reason for the change.

4.13 The laboratory shall have a documented procedure on when and how propositions will include within the set of unknowns a relative of an individual who is assumed under one or more of propositions.

4.14 Reporting only one, or a subset, of the *LRs* for evaluative analyses that have been conducted for multiple proposition pairs, differing by the conditioning profiles and/or the number of contributors, shall require documentation in the case file providing the reason the selected proposition pairs were chosen. The existence of additional *LRs* in the case file shall be noted in the report.

Investigative analyses need not be reported, but should be retained in the case file. The report may include a comment that investigative analyses have been undertaken.

4.15 Lacking any direction from either party, the laboratory shall formulate one or more reasonable proposition pairs that address each party's assumed interests.

4.16 The laboratory shall reassess the data under a new pair of propositions if presented with a reasonable request (i.e., supported by the associated data, and presented in a timely manner) from either party regarding an alternate proposition pair.

Annex A
(informative)

Bibliography

This is not meant to be an all-inclusive list as the group recognizes other publications on this subject may exist. At the time this standard was drafted, these were the publications available for reference. Additionally, any mention of a particular software tool or vendor as part of this bibliography is purely incidental, and any inclusion does not imply endorsement.

1] Buckleton et al. “The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity.” *Journal of Forensic Science*, vol. 64(2), 2019, pp. 393-405.

2] Buckleton, J., J. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J. Curran. “Helping formulate propositions in forensic DNA analysis.” *Science and Justice*, vol. 54, 2014, pp. 258-61.

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

4] Buckleton, J. and J. Curran. “A discussion of the merits of random man not excluded and likelihood ratios.” *Forensic Science International: Genetics*, vol. 2, 2008, pp. 343-348.

5] Buckleton, J., J. Curran, and P. Gill. “Towards understanding the effect of uncertainty in the number of contributors to DNA stains.” *Forensic Science International: Genetics*, vol. 1, 2007, pp. 20-28.

6] Cook, R., I. Evett, G. Jackson, P. Jones, and J. Lambert. “A hierarchy of propositions: deciding which level to address in casework.” *Science and Justice*, Vol. 38(4), 1998, 231-239.

7] European Network of Forensic Science Institutes, *ENFSI guideline for evaluative reporting in forensic science*, version 3.0, 2015.

8] Evett, I., G. Jackson, and J. Lambert. “More on the hierarchy of propositions: exploring the distinction between explanations and propositions.” *Science and Justice,* vol. 40(1), 2000, pp. 3-10.

9] Gill, P. and H. Haned. “A new methodological framework to interpret complex DNA profiles using likelihood ratios.” *Forensic Science International: Genetics*, vol.7(2), 2013, pp. 251-63.

10] Gill, P. et. al., “DNA commission of the International Society for forensic genetics: Assessing the value of forensic biological evidence-Guidelines highlighting the importance of propositions, Part I: evaluation of DNA Profiling comparisons given (sub-) source propositions.” *Forensic Science International: Genetics*, vol. 36, 2018, pp. 189-202.

11] Gill, P., A. Kirkham, and J. Curran. “LoComatioN: A software tool for the analysis of low copy number DNA profiles.” *Forensic Science International*, vol. 166, 2007, pp. 128-138.

12] Gittelson, S., T. Kalafut, S. Myers, D. Taylor, T. Hicks, F. Taroni, I. Evett, J. Bright, and J. Buckleton. “A practical guide for the formulation of propositions in the Bayesian approach to DNA evidence interpretation in an adversarial environment." *Journal of Forensic Science*, vol. 61(1), 2016, pp. 186-195.

13] Haned, H., K. Slooten, and P. Gill. "Exploratory data analysis for the interpretation of low template DNA mixtures." *Forensic Science International: Genetics*, vol. 6(6), 2012, pp. 762-74.

14] Hicks, T., A. Biedermann, I. de Koeijer, F. Taroni, C. Champod, and I. Evett. "The importance of distinguishing information from evidence/observations when formulating propositions." *Science and Justice*, vol. 55(6), 2015, pp. 520-525.

15] Federal Bureau of Investigation, *Quality Assurance Standards for Forensic DNA Testing Laboratories*, available at www.fbi.gov and www.swgdam.org .

16] Kaye, D.H. "Logical relevance: problems with the reference population and DNA mixtures in People v. Pizarro" *Law, Probability and Risk*, vol 3, 2004, pp 211-220.

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