

Public Comment Deadline: March 28, 2022

ASB Standard 081, Standard for Training in the Use of Statistics in Interpretation of Forensic DNA Evidence

#	Section	Type of Comment (E-Editorial, T-Technical)	Comments	Proposed Resolution	Final Resolution
84	all	T	We strongly suggest not moving forward on this standard before getting guidance from the OSAC's Statistics Task Group (STG). They are in a leadership transition at present but their new chair is Danica Ommen, danica.ommen@gmail.com .		Reject. This document has gone through the OSAC process and was reviewed by OSAC statisticians. No proposed resolution or reason for comment provided. Document will be recirculated and comments can be submitted at that time.
42	General	T	Concerned that CPI/CPE are included without more explicit warnings about its potential for misuse	add language about training on limitations and add NIST mixture 05 and 13 to bibliography	Reject. WG discussed and confirmed this is covered in 4.2.2.e.6
85	Title	E	Suggested title change for improved clarity and accuracy; interpretation is too limiting as should include comparison and reporting, plus stats come after interpretation (and comparison); Evidence is not the same as data; this standard seems to be limited only to STR data based on the requirements	Suggest: Standard for Training in Statistical Calculations Used for Forensic STR DNA Data	Accept
86	Scope	E	Changes suggested for accuracy and clarity - after a comparison of data is where the statistical part comes in and not at the interpretation level; data are evaluated, rather than the evidence. May also want to expand the scope or spell out more clearly if this applies to human and wildlife and what types of DNA testing (STR, Y STR, sequencing, etc.), biological relationship testing and identification testing, or if there are specific limitations. This standard does not seem to have any sections relevant to sequencing, for example.	Suggest: ...in the use of statistical calculations and values reported for forensic STR DNA data.	Accept with modifications. changed "defines" to "outlines" to match STD 78. Added "calculations and values reported for forensic autosomal and Y short tandem repeat (STR) DNA data."
4	3.1	E	hyphen use ("proposition - they")	This should be an m-dash, not a hyphen.	Accept with modification. old definition deleted
5	3.1	E	and or comma (grandparent and grandchild)	if grandparent and grandchild go together, then change to "half-siblings, and grandparent and grandchild" If not, add comma after grandparent	Accept with modification. old definition deleted
60	3.1	E	"Avuncular index" is defined as "Likelihood ratio in which the probability of a questioned person's profile is evaluated under alternate propositions - they are an uncle/aunt/niece/nephew of a known individual versus they are unrelated to the known individual." In the first proposition, "they" has no clear antecedent. A questioned person's profile are an uncle/etc. is awkward.	"Likelihood ratio in which the numerator is conditioned on the hypothesis that an uncle, aunt, niece, or nephew is the source of DNA in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source."	Accept with modification. New definition used. Definition was found in peer reviewed publication and adapted for this standard. Morris, J.W., Garber, R.A., D'Autremont, J., Brenner, C.H. (1988). The Avuncular Index and the Incest Index. In: Mayr, W.R. (eds) Advances in Forensic Haemogenetics. Advances in Forensic Haemogenetics, vol 2. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-642-73330-7_124
48	3.2	T	fix subscripts	Pj should be Pj. equation should be 1- $\prod_j (1 - P_j)$	Accept
87	3.2	E	definition from another OSAC document re: forensic DNA statistical methods is suggested that may be easier for the forensic community to read	Probability that a randomly selected individual would be excluded as a contributor to the mixture; produced by multiplying the probabilities of inclusion from each locus chosen for inclusion and subtracting the product from 1 (i.e., 1-CPI).	Accept with modification. Note: amended with input from the initial commentor.
49	3.3	T	fix subscripts	Pj should be Pj. equation should be $\prod_j (1 - P_j)$.	Accept
88	3.3	E	definition from another OSAC document is suggested that may be easier for the forensic community to read	Probability that a randomly selected individual would be included as a possible contributor to a mixture; produced by multiplying the probabilities of inclusion from each locus chosen for inclusion.	Accept with modification. Note: amended with input from the initial commentor.
6	3.4	E	second use of "sequence or haplotype" add comma	change to "sequence, or haplotype" as was done directly above	Accept
7	3.5	E	use of "e.g." not needed	remove "e.g."	Reject: WG evaluated and believes the e.g. is appropriate because there could be other possibilities
8	3.6	E	p2 and q2	superscript the 2 so it means squared	Accept
51	3.6	T	p2 and q2	should be p ² and q ²	Accept
89	3.6	E	the formulas need to be corrected to show the square of the frequency	make homozygote p squared and q squared	Accept

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61	3.7	3.9	T	In the definition of "inbreeding," "random" does not refer to a population; it refers to selection of mates within the population.	Change "random breeding population" to "randomly mating population" or "randomly breeding population."	Accept
43	3.9	3.11	T	The LR does not express the weight of the evidence.	Delete the last sentence.	Reject: Revised definition was approved by industry statistitions and has been used by the discipline. CB feels the definition as revised is appropriate for the document. Used a modified definition from the OSAC Lexicon available online as of 12/12/2023
62	3.9	3.11	T	"Likelihood ratio" is defined as "The probability of the evidence under one proposition (hypothesis), divided by the probability of the evidence under an alternative, mutually exclusive proposition (hypothesis). The magnitude of its value expresses the weight of the evidence." The ratio is not a reasonable measure of weight of evidence unless the hypotheses are simple (not composite), and even then information theory uses log-LR for weight in that situation.	Define "likelihood ratio" as "a quantity that equals the probability (or probability density) of the evidence under one simple proposition (hypothesis), divided by the probability (or probability density) of the evidence under an alternative, mutually exclusive, simple proposition (hypothesis). The logarithm of the ratio expresses the weight of the evidence."	Reject: Revised definition was approved by industry statistitions and has been used by the discipline. CB feels the definition as revised is appropriate for the document. Used a modified definition from the OSAC Lexicon available online as of 12/12/2023
90	3.9	3.11	E	definition from another OSAC document re: forensic DNA statistcal methods is suggested that may be easier for the forensic community to read	The ratio of two conditional probabilities of the same event under mutually exclusive hypotheses. The general formula is: $LR = \frac{Pr(E H_1, I)}{Pr(E H_2, I)}$. For DNA testing, a statement of comparison of the probability of the evidence (E) (i.e., the DNA profile), given two competing hypotheses, inclusionary (H_1) or exclusionary (H_2) for an individual or specific sets of individuals, and in the context of relevant information (I).	Reject: Revised definition was approved by industry statistitions and has been used by the discipline. CB feels the definition as revised is appropriate for the document. Used a modified definition from the OSAC Lexicon available online as of 12/12/2023
63	3.10	3.12	T	"Linkage equilibrium" is defined as "Two loci are in linkage equilibrium if the probability an individual jointly receives particular alleles at the loci is the product of the probabilities of receiving each of the alleles separately. If both Hardy-Weinberg and linkage equilibrium hold, then match probabilities may be multiplied over loci." The main problems with the definition are that it does refer to a population as being in uilibrium and that the term "match probabilities" is undefined. The probability of matches between what and what under what conditions?	A definition of "linkage equilibrium" is "the condition in which the probability of two alleles at different loci of a gamete occurring together in a gamete selected at random in a population equals the product of the probability of one allele being present times the probability for the other one. When Hardy-Weinberg holds in a population, the single-locus probability is simply the product of the probabilities of alleles at the locus (and a factor of two for heterozygotes). When linkage equilibrium holds, then the probability of a multilocus genotype is simply the product of the probabilities of the single-locus locus genotypes."	Accepted with modifications. Definition edited.
64	3.12	3.14	T	The paternity index is not "the likelihood ratio for observing the data in a parentage case." It is the likelihood ratio for two particular hypotheses in a parentage case--that the putative father is the biological father and that an unrelated man is the biological father. Many other likelihood ratios could be constructed in a parentage case, so the word "the" is misleading (and, by the way, the phrase "for observing the data" is unnecessary).	Replace with "the likelihood ratio computed under the hypotheses that the putative father is the biological father and that a man who is not related to the putative father is the biological father."	Accept with modification. New definition used to be consistent with all likelihood ratio-dependent definitions
65	3.12	3.14	E	The sentence, "More specifically, the probability of observing this data if the alleged father is the biological father of the child, divided by the probability of observing the data if a random, unrelated male in the population is the biological father," suggests that both randomness and unrelatedness are used in the computation. Only unrelatedness is required to compute the conventional paternity index.	Replace with "the likelihood ratio computed under the hypotheses that the putative father is the biological father and that a man who is not related to the putative father is the biological father."	Accept with modification. New definition used to be consistent with all likelihood ratio-dependent definitions
91	3.12	3.14	E	data is a plural word	change to "these" data	Accept with modification. New definition used to be consistent with all likelihood ratio-dependent definitions
9	3.13		E	(SPI)2	superscript the 2 so it means squared (and is the "S" correct?)	Reject with modification. Definition removed, not referenced in the standard
50	3.13		T	(SPI)2' the S should be a sigma sign	should be $(\Sigma PI)^2$	Reject with modification. Definition removed, not referenced in the standard

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66	3.13		T	The mixture of randomness and unrelatedness in the definition of PI is confusing: "The probability a randomly selected, unrelated individual is not excluded from being a source of DNA evidence. In human forensic DNA testing, this is often referred to as the probability a random man is not excluded (RMNE). The commonly used calculation is (SPI) ² , the square of the sum of the relative frequencies (PI) of the observed alleles at a locus. If the randomly selected individual is assumed to be related to the person of interest, this formula is inappropriate." Why would one assume that a randomly selected man is related to the source? Unless there are many related men in the population, the probability of relatedness is small. Moreover, what justifies the shift from "individual" to "man"?	Consider this definition: "The probability a randomly selected man is not excluded as a plausible source of the DNA evidence. In human forensic DNA testing, the probability of inclusion also is often referred to as the probability a random man is not excluded (RMNE)."	Reject with modification. Definition removed, not referenced in the standard
92	3.13		E	the formulae in the second sentence need to be corrected	correct formula -- a) (summation of p subscript little i) squared, and b) little i squared	Reject with modification. Definition removed, not referenced in the standard
44	3.14	3.15	E	The first sentence is incomplete.	Revise to make it a complete sentence.	Accept with modification. Revised to definition from SWGDAM and OSAC proposed standard 2021-S-0021
67	3.14	3.15	T	"Random match probability" is defined as "The probability of an unknown individual in a given population has a particular profile. More appropriately the random match probability is computed conditioned on a known individual observed to have the profile. The unconditional probability is the profile probability." The first two sentences are equivalent, and why use two if one is more appropriate? In addition, is the RMP is usually computed on the condition that at least one individual in the population has the profile in question? Isn't it computed as the unconditional probability of generating the genotype in a randomly mating population with some degree of substructure?	Define RMP as "the probability that an individual drawn at random from a population will have a given profile." Or if you prefer, "the probability of generating an individual with a given profile using some population-genetics model."	Accept with modification. New definition used from SWGDAM and OSAC proposed standard 2021-S-0021
93	3.14	3.15	E	definition from another OSAC document re: forensic DNA statistical methods is suggested that may be easier for the forensic community to read (also the grammar is incorrect in the first sentence)	Probability of randomly selecting an unrelated individual from the population who could be a potential contributor to an evidentiary profile	Accept
10	3.15	3.16	E	use of hyphen	This should be an m-dash, not a hyphen. Correct	Accept
68	3.15	3.16	E	"Reverse parentage" is a poor choice of words for a likelihood ratio. Why is it not an "index" like every other LR in the standard?	Use a more descriptive phrase, such as "parentage index when both parents are unknown."	Reject, "reverse parentage" is a commonly used term
69	3.15	3.16	E	The definition of "reverse parentage" is "Likelihood ratio in which three individuals have been profiled - the child and two questioned biological parents. More specifically, the probability of observing the data if the child is the biological child of the alleged parents, divided by the probability of observing the data if two randomly selected people are the parents of the child." The definition applies to a particular likelihood ratio. Other formulations are possible with the same data.	Define "parentage index when the parentage of both parents is questioned" as a likelihood ratio computed as the probability of the profiles for the putative mother-father-child trio given that the putative mother and father are the biological parents divided by the probability of the profiles given that a randomly selected man and woman are the biological parents.	Reject. The consensus body voted that this definition is clear as written.
11	3.16	3.17	E	use of n-dash (proposition - he)	This should be an m-dash, not an n-dash	Accept
12	3.16	3.17	E	"they are"	change to "he/she is"	Reject with modification. Definition rewritten based on comment #70.
70	3.16	3.17	E or T	"sibship index" is defined as "Likelihood ratio in which the probability of a questioned person's profile is evaluated under alternate propositions - he/she is a sibling of a known individual versus they are unrelated to the known individual." The definition has the same linguistic problems as the definition of "avuncular index," and it uses the awkward construction "he/she."	Define as "Likelihood ratio in which the numerator is conditioned on the hypothesis that a sibling of the source of the questioned profile in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source."	Accept

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71	3.17	3.18	E or T	"Source attribution" is defined as "A decision made based on laboratory policy which identifies an individual as the source of the DNA that produced an evidentiary single-source or major contributor profile." Source attribution is neither more nor less than a conclusion that a named individual is the source of soje or all of the DNA in a specimen. The source attribution can involve a major contributor, a minor contributor, or a sole controibutor. It can be consistent with laboratory policy--or not.	Define "source attribution" as the inference that a particular individual is the source of or a contributor to a DNA sample.	Accept with modification. New definition used from a published SWGDAM document and the CB feels it is appropriate for this document.
94	3.17	3.18	E	grammar	change "which" to "that" or put commas around the phrase "made based on a laboratory policy"	Accept with modification. New definition used from a published SWGDAM document and the CB feels it is appropriate for this document.
13	3.18	3.19	E	"first described by Balding and Nichols" Certainly not first used by them. Maybe 'for forensic purposes" ? Also, the references says Balding et al.	Fix	Accept with modification. New definition used from a published SWGDAM document and the CB feels it is appropriate for this document.
14	3.18	3.19	E	"whole population" or whole-population" ?	make consistent	Accept with modification. New definition used from a published SWGDAM document and the CB feels it is appropriate for this document.
72	3.18	3.19	T	"Theta correction" is defined as "A method for calculating match probabilities, first described by Balding and Nichols (1994), to allow for population structure in the population for which a frequency database is constructed. It allows match probabilities for subpopulations to be calculated from whole population allele frequencies. It avoids the need to assume Hardy-Weinberg equilibrium at the whole-population level." The phrase "match probabilities" should be made more specific. Random match probabilities? Should the relationship between theta and Fst be noted? Are you sure that the correction gives the RMP in a subpopulation rather than the RMP in the strstructured population from which the random individual is drawn?	Insert "random" in front of "match probabilities." Verify that this definition is correct and correct it if it is not.	Accept with modification. New definition used from a published SWGDAM document and the CB feels it is appropriate for this document.
28	4.1		T	The statement, "Based upon the laboratory procedures, some of the requirements in this section may be omitted from the training program" is vaguely worded.	Either delete or reword to be clearer, i.e. " The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training." (I borrowed and modified that language from Standard 022 4.2.2.)	Accept
45	4.1		T	Why allow discretion to omit certain requirements?	Delete.	Accept with modification " The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training."
52	4.1		E	This section does not match 4.1 in previously published training standards.	Make all sections consistent throughout all training standards.	Accept, added wording similar to standard 023
73	4.1		T	The catch-all sentence, "Based upon the laboratory procedures, some of the requirements in this section may be omitted from the training program," could use more definition.	Identify the requirements that cannot be omitted and specify when the others can be omitted.	Accept
95	4.1		T	the training program would still need to have all of the sections included to some extent since knowledge of all of the areas should be mandatory to the analysts in the laboratory at least historically if not currently in use and for explanations to attorneys, and in cold or postconviction cases, for example; would be inappropriate to delete any of these requirements from the laboratory training program (even, if for example, the laboratory did not do YSTR testing or statistical calculations for paternity or other biological relationship testing, the analyst should still be knowledgeable about the general calculations and their meaning in the context of forensic DNA testing)	suggest: All of the requirements listed below shall be included in the laboratory training program. The extent of training on each topic is dependent upon the laboratory procedures currently or previously in use in the laboratory and the intended responsibilities of the analyst being trained.	Accept with modification " The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training."

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74	4.2.1		E or T	This section refers to laboratory protocols for "statistical applications" and the laboratory's efforts to show that it can apply a validated method properly ("the laboratory's applicable validation studies"), but it does not explicitly specify learning about validation conducted outside the laboratory prior to the laboratory's adoption of the validated method. That information may be in "literature that supports the laboratory's validation" or "literature that supports the laboratory's data analysis protocol," but the knowledge-based training should start with what is known more generally, then move to the laboratory-specific material.	Include an explicit requirement for learning about the validation of the "statistical applications" in the scientific literature. At a minimum, insert the word "scientific" in front of "literature" in the existing subsections.	Reject, scientific is implied
96	4.2.1 b)		E	This probably needs more clarity for the laboratory and any auditor such that the laboratory must define the "relevant" validation studies.	suggest changing to something like "all of the validation studies relied upon by the laboratory to support the development and use of the protocol for calculating, reporting and testifying to statistical values"	Reject, the working group feel that b. plus c. covers the same requirements succinctly
75	4.2.1(d)		E or T	The standard describes itself as presenting minimum standards, but "applicable literature as assigned by the trainer" provides no floor on what the trainer is supposed to assign.	List readings on each topic that might be assigned, linked to that topic, and require those "or comparable" readings to be assigned.	Reject, additional literature may be assigned according to laboratory needs
26	4.2.2		T	This clause lists the topics that shall be included in the training program. It does not include cognitive bias or how it may impact the use of statistics in the interpretation of forensic evidence.	Add a new part g) to 4.2.2 that states: g) The role of cognitive bias in the analysis of STRs 1) literature on cognitive bias in forensic analyses 2) examples of how cognitive bias can impact the use of statistics in the interpretation of forensic evidence 3) Strategies to insulate the examiner from cognitive bias 4) laboratory procedures that implement cognitive bias protections	Accept with modification, see 4.2.1(e).
29	4.2.2		T	Why is 5 under (a) population genetics? Isn't frequency/Bayes, etc. larger than just its application to pop gen?	Make 5) under 4.2.2. (a) its own letter and call it Statistical Foundations or something	Accept
76	4.2.2		E	The stated goal, that "the knowledge-based training component of the laboratory's training program shall provide the trainee with a basic understanding of statistics applied to autosomal and Y-STR data to include, at minimum, the following topics," is incomplete. Probability should be covered as well.	Change "statistics" to "probability and statistics."	Accept
77	4.2.2		T	The standard describes itself as presenting minimum standards. That objective would be more effectively fulfilled by advising laboratories not only to train on certain topics, but also list what the trainees are supposed to learn about these topics and to provide suggested reading on each topic, linked explicitly to the topic.	List what trainees are supposed to learn about the required topics and to provide suggested reading on each topic, linked explicitly to the topic..	Reject, this level of detail can be determined by the laboratory and/or technical leader
15	4.2.2a2		E	Equilibrium (CAP)	equilibrium	Accept
78	4.2.2(a)(5)	4.2.2(b)	T	The list of topics, "frequency, probability, odds, the laws of probability (i.e. the addition rule and product rule) and Bayes' theorem," does not belong under a section on population genetics. It belongs in a section on statistical concepts and methods that should be more extensive.	Include a new section on statistical concepts and methods that trainees need to learn about. Correct the parenthetical that might be read as equating all the laws of probability to two formulas.	Accept, see 4.2.2(b)
79	4.2.2(b)	4.2.2 (c)	T	This section is incomplete.	If this is where sampling is to be covered, the topics should include the design of sampling studies with emphasis on probability sampling and bias and the arguments for using nonrandom samples for allele - frequency estimations. Precision and statistics form expressing it need to be included.	Reject, this section is intended to cover training regarding using a pre-existing database
30	4.2.2(b)(2)	4.2.2 (c) (2)	T	Need to train on sampling uncertainty and ways to account for it	add (iv) sampling uncertainty	Accept
31	4.2.2(b)(2)(ii)	4.2.2 (c) (2) (ii)	T	This is an important requirement because it inherently acknowledges that sometimes people's "race" is ascribed to them in sample collection processes; but the term "racial origin" is problematic as race is a social construct	Explain in footnote what "racial origin" means and its purported relationship to allele frequency databases; explain relationship between "racial origin" and "population group"	Accept with modification, see 4.2.2(c)2.ii (changed racial origin to population group)

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53	4.2.2.b.3	4.2.2 (c) (3)	E	Population group seems to belong under 4.2.2.b	Move to 4.2.2.b.iiii	Accept with modification, moved to 4.2.2(c)2.ii
16	4.2.2b, 4.2.2b3, etc.	4.2.2 (c) etc.	T	use of the word "Population" (throughout)	"Population" has a biological meaning, and it is not being used correctly here. Also, what is a 'population group'?	Reject, no proposed resolution provided
46	4.2.2(b)(4)	4.2.2 (c) (4)	E	Alleles should be allele	Delete the "s" from "alleles"	Accept
17	4,2,2c1 and actually throughout	4.2.2 (d) (1)	E	using "and" before the last in a list	This is done in most of the document (but not all, so very uneven) Make consistent (best is to drop all such "ands" in the penultimate lines)	Accept
97	4.2.2 c) 1)	4.2.2.(d) (1)	T	additional part of the requirement suggested - the analyst needs to know when to use each calculation if options are available in the laboratory, as well as understand the basics of all types of calculations for biological relationship and identity testing whether currently in use in the laboratory or not	add to the end of the statement: and which statistical calculation available for use in the laboratory to apply for the type of data obtained and comparison performed	Accept with modification, added "and which statistical calculation is validated for the type of data obtained and comparison performed"
18	4.2.2c2	4.2.2.(d) (2)	E	"to included" and "to include" (awkward	term used twice; not sure of meaning And throughout consider "including" instead of "to include"	Accept, sentence rewritten
32	4.2.2©(2) (ii)	4.2.2.(d) (2) (ii)	T	I am unclear what © (2) (ii) means. When do you exclude an allele with partial allelic data? (is this CPI related?). Risks of excluding loci in statistical calculations should be stated.	Clarify what this means; add risks of excluding data (ignoring exclusionary data)/effect on resulting statistical analysis	Reject, the requirement is to instruct on which data is included in the statistics, depending on lab thresholds, etc.
98	4.2.2 c) 2)	4.2.2.(d) (2)	T	missing important concepts - allele drop in, possible stutter and other artifacts	add terms to the list	Accept with modification. Added "STR artifacts" as item iv)
19	4.2.2c2iii	4.2.2.(d) (2) (iii)	E	comma needed after "null alleles,"	add comma	Accept
19	4.2.2.2	4.2.2	T	Sources of error, including false positives and false negatives should be part of knowledge based training. Additionally, effect of different assumptions (i.e. what if you misspecify NOC; what if you are off on mixture ratio) on interpretation and comparison should be emphasized.	Add wording to 4.2.2.2(d): how assumptions affect interpretation and conclusions. Add e) to 4.2.2.2: sources of false positives and false negatives	Reject, For the comment about how assumptions affect interpretation - that is covered in 4.2.2.e6 "limitations and assumptions of statistical method(s) in use by the laboratory." The comment about sources of false positives and false negatives - if the false positive and false negatives are due to statistical methods, it is covered under 4.2.b.6 "2)6)Sources of uncertainty (e.g. modelling uncertainty and sampling variability)." If it is due to non-statistical sources of error, it is outside of the scope of this standard.
37	4.2.2(d)		T	relatedness is a critical limitation and deserves to be delineated in the standard	add "relatedness and its effect on statistical analysis"	Accept
40	4.2.2(d)	4.2.2. b) 6	T	critical to understand sources of uncertainty and how the method accounts for them	add sources of uncertainty in calculations and how the method accounts for them (or doesn't)	Accept with modification. Added new section 4.2.2. b) 6
80	4.2.2(d)		T	This section is incomplete.	Should statistical tests for Hardy-Weinberg and linkage disequilibrium be a required topic in this section? The effect of database trawls on the value of matches?	Reject, this is covered in 4.2.2 a)
20	4.2.2d, e, f		E	Analysis (CAP)	change to analysis	Accept
54	4.2.2.d.1	4.2.2 e) 1	T	General principles of autosomal STR statistical methods' is too vague. Language removed from OSAC draft should be considered.	Add "how to perform statistical calculations to include derivation and use of applicable equations" to requirements.	Partial accept, reworded in section 4.2.2 e) 1
99	4.2.2 d) 1) & 2)		E	clarify language	insert "calculation" between "statistical" and "methods"	Accept
1	4.2.2d3iii		E	If the lab uses a conditional math probability rather than random match probability, can this be added	random math probability or conditional match probability as applicable. On January 25, 2024, the commentor provided an updated recommendation of "random match probability (or modification)"	Accept with modification. Sentence modified with input from original commenter.
55	4.2.2.d.4		T	the software programs in use by the laboratory' is too vague.	Include "how to use the program, what equations are being used by the software and how to review output data" in requirements	Accept
57	4.2.2.d.5	4.2.2. e)5	T	source attribution statements, if applicable' is too vague.	Add "how this threshold was determined for your laboratory"	Reject, covered under 4.2.1 the laboratory's applicable protocols and validation studies

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38	4.2.2(d)(5)		T	Source attribution --is this a thing anymore? I thought rejected as stating the posterior probability/transposing the conditional/eliminating uncertainty....	?	Reject, "if applicable" included in sentence
39	4.2.2(d)(6)			need to add assumptions	add assumptions, i.e. "limitations and assumptions"	Accept
56	4.2.2.e.2		T	the software programs in use by the laboratory' is too vague.	Include "how to use the program, what equations are being used by the software and how to review output data" in requirements.	Accept
2	4.2.2f1 and 4.2.2f1i		E	concern if the lab does not have a IBD or IBS calculation	add in as applicable for both lines	Accept
21	4.2.2F1i	3.7 and 3.8	E	IBS and IBD	Consider adding both to section 3 (definitions)	Accept, added as 3.7 and 3.8
33	4.2.2.-add requirement	4.2.2 b) 6	T	understanding effects of choice of statistical methods/modelling choices critical	Add requirement "Effect of choice of statistical method; effect of choice of modelling decisions"	Accept with modification, covered in 4.2.2 b) 6
34	4.2.2.-add requirement		T	understanding what calibration is and how applies to forensic dna critical	add calibration	Reject, covered in 4.2.1 b) Validation
35	4.2.2.-add requirement	4.2.1 a) and c)	T	concept of conservativeness is critical in forensic dna (see NRC I)	add training on concept of conservativeness	Reject, covered in 4.2.1 a) and c)
36	4.2.2.-add requirement	4.2.1 c) and 4.2.2 e) 3)	T	how/when/why/by how much one statistical method produces different results from others is critically important to understand	add requirement how/when/why/by how much one statistical method produces different result from others or extent and cause (if known) of variance of results produced by different methods	Reject, covered under 4.2.1 c) and 4.2.2 e) 3)
100	4.3.1		E	word correction for clarity	change "DNA evidence" to "DNA data"	Accept
101	4.3.1		T	incorrect language - interpretation must occur before statistical values are calculated; the statistical calculations are NOT a part of interpretation	change to "...the skills for calculating statistical values for DNA data used by the laboratory to include, ..."	Accept
102	4.3.2		E	It's unclear how a protocol can be observed and this requirement monitored in an audit	Suggest changing to "the use of the protocol..." or "the application of the protocol to DNA data..." or some similar language	Accept
22	4.3.3		E	missing colon	"include the following:" (make consistent)	Accept
103	4.3.3		E	need to include DNA data	insert "and DNA data" after "samples"	Accept
23	4.3.3a, b, c		E	End with periods	Change to ";" to be consistent?	Accept
3	4.3.3b		E/T	If labs do not allow for manual calculations, would this be required as part of the training still. Additionally, modify line to include CMP	random math probability or conditional match probability as applicable On January 25, 2024, the commentor provided an updated recommendation of "RMP (or modification)"	Accept with modification, Yes, it would still be a requirement to understand how to do a manual calculation. "CMP" removed, "(or modification)" added after "RMP"
27	4.4		T	The Competency Component should require the results for each analyst to be easily accessible.	Add a 4.4.4 that requires competency results to be easily accessible: "The results of competency testing for the analyst(s) involved in the case should be made available to all stakeholders."	Reject, Competencies are considered personnel records by many laboratories and are subject to agency specific policies. Competencies can be provided upon subpoena. Record retention is covered under ASB Std 022.
41	4.4		T	The competency test should be performed on sample(s) representative of the range, type, complexity encountered in casework. Standard 022, 4.3.2(a)(2) does contain a requirement that a practical test on a lab's analytical procedure be performed on samples representative of the range, type, and complexity typically analyzed by the lab but that requirement is important enough to be repeated here.	Add language: "Practical competency tests shall include samples representative of the range, type, and complexity typically analyzed by the laboratory."	Accept, with modification - language added to 4.4.3: DNA data from samples representative of the range, type, and complexity for which the trainee will be authorized to perform statistical calculations shall be included in the practical competency test.
47	4.4	4.4.1	T	This section should require that the criteria for passing a competency test be documented and established in advance.	Add a requirement that the criteria for passing should be documented and established in advance.	Accept, requirements added to 4.4.1 for all training standards
58	4.4.1		E	Missing title of document for ASB 022	Add "Standard for Forensic Training DNA Analysis Training Programs"	Accept

#	Section		Type of Comment (E-Editorial, T-Technical)	Comments	Proposed Resolution	Final Resolution
59	4.4.2		E	This section does not match previously published training standards.	Make all sections consistent throughout all training standards.	Accept
104	4.4.2		E	typo	change to 4.2 rather than 4.1	Accept
47	4.4.3		T	If the trainee is going to testify about statistics, he/she needs to demonstrate that he/she actually has a background in statistics.	Add that the trainee also has an educational background in statistics to proffer to the court.	Reject, The requirements for analyst include education in statistics
81	Appendix A		T	The bibliography is not explicitly linked to the specific topics for which each of the 45 references apply.	Provide specific readings for each topic.	Reject, the bibliography meets ASB standards
82	Appendix A		T	The bibliography omits standard statistical texts, texts written for forensic analysts generally, texts written for DNA analysts in particular, and educational materials from statistical societies and other organizations or groups. If it has not already occurred, experts in statistical pedagogy should be enlisted to select an appropriate set of readings and AV materials.	Develop a bibliography that is selective and truly useful for training DNA analysts in the logic of probability and statistics in general and as it applies to the interpretation of DNA evidence.	Reject, the bibliography meets ASB standards
83	Appendix A		T	The bibliographic includes a couple of references on the database trawl issue. Why, when that is not a required or even recommended topic?	Include the implications of database trawls on the value of a match among the required topics and note the best writing for instructional purposes in the section that does so.	Reject, a specific reference and proposed resolution was not provided
25	Bibliography		E	Hyphen (-) between page numbers	These should be n-dashes (–), not hyphens	Accept
24	References		E	Likely way too many.		Reject, proposed resolution of specific references to delete not provided
42	General	4.2.2 d) 6	T	Concerned that CPI/CPE are included without more explicit warnings about its potential for misuse	add language about training on limitations and add NIST mixture 05 and 13 to bibliography	Reject with modification, covered under 4.2.2 d) 6 "limitations of statistical methods..." - The OSAC 2021-S-0021 proposed standard covers this information. Once it is approved as an ANSI Standard, the CB can address adding it to this document as an errata or addendum.

Deadline of Submission of Comments: 18-Apr-24

Document Number: ANSI/ASB Std 081

Document Title: Standard for Training in Statistical Calculations Used for Forensic Short Tandem Repeat (STR) DNA Data

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Final Resolution
		Forward	Editorial	This standard defines the minimum requirements for a forensic DNA analyst training program in...	This standard defines the minimum requirements to be met in a forensic DNA analyst training program for ..."	consistency across training standards	accept
		Forward	Editorial	Forward	E	This standard defines the minimum requirements for a forensic DNA analyst training program for...	Accept: This standard defines the minimum requirements to be met in a forensic DNA analyst training program for ..."
2	Overall		Technical	Sometimes the oxford comma is used sometimes it is not - seems to not be used most often	Choose one method for comma usage and remain consistent throughout	Consistency purposes	Accept. ASB Staff will review document for editorial consistency throughout the document.
15		Title	T	Standard for Training in Statistical Calculations Used for Forensic Short Tandem Repeat (STR) DNA Data	Standard for Training in Statistical Calculations Used for the Interpretation of Forensic Short Tandem Repeat (STR) DNA Data	This document only addresses statistical calculations used in the interpretation of STR data. It does not cover other statistical calculations (i.e., calculations not part of the interpretation of STR DNA data, such as statistical calculations for population genetics not related forensic DNA interpretation).	Reject. Interpretation and statistical calculations, and interpretation is covered in ANSI/ASB Std 078
		Scope	Editorial	This standard outlines the minimum requirements for a training program in the use of ...	This standard outlines the minimum requirements to be met in a training program in ...	consistency across training standards	Accept.
16		Scope	T	"...statistical calculations and values reported for forensic autosomal..."	"...statistical calculations and values reported for the interpretation of forensic autosomal..."	This document only addresses statistical calculations used in the interpretation of STR data. It does not cover other statistical calculations (i.e., calculations not part of the interpretation of STR DNA data, such as statistical calculations for population genetics not related forensic DNA interpretation).	Reject. Interpretation and statistical calculations, and interpretation is covered in ANSI/ASB Std 078
17		3.1 (avuncular index)	T	"The likelihood ratio that evaluates the hypothesis that the tested individual is the biological uncle (or aunt or niece or nephew) of the profile donor versus the hypothesis that the tested individual is unrelated to the profile donor."	"Likelihood ratio in which the numerator is the probability of the DNA data given the proposition that the tested individual is the biological uncle (or aunt or niece or nephew) of the profile donor, and the denominator is the probability of the DNA data given the proposition that the tested individual is unrelated to the profile donor."	There are two major errors in the current wording: 1) The definition is an incorrect definition because the avuncular index is not a ratio of the probabilities of the two propositions as the current wording states. The current wording is a Prosecutor's Fallacy or Transposed Conditional. 2) The word "hypothesis" is incorrect terminology for the interpretation of forensic STR data. The correct terminology is "proposition".	Reject with modification. Definition was deleted, use of "avuncular" in the text was revised to "aunt or uncle"
30	14	3.1	T	avuncular index The likelihood ratio that evaluates the hypothesis that the tested individual is the biological uncle (or aunt or niece or nephew) of the profile donor versus the hypothesis that the tested individual is unrelated to the profile donor.	avuncular index The likelihood ratio that evaluates the hypothesis that the tested individuals are related as biological uncle/aunt and niece/nephew versus the hypothesis that the tested individuals are unrelated.	The coined name avuncular index comes from the from Morris et al., The Avuncular Index and the Incest Index, Advances in Forensic Haemogenetics 2. It is a calculation that combines a Paternity Index with expectations of shared alleles between relatives to address the assertion, "I'm not the father. My brother [or other relative] is the father." The usage currently in this document addresses the assertion, "I'm not the donor of that evidence DNA. My nephew is." That is the premise behind the NRC II equations 4.8a and 4.8b. Please either come up with a new coined phrase for that, or even better, don't try to increase the number of coined phrases. Note: Line 206 has the avuncular index used in terms of kinship testing, not in the manner of the current definition.	Reject with modification. Definition was deleted, use of "avuncular" in the text was revised to "aunt or uncle"

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			E-Editorial T-Technical				Final Resolution
37		3.1	Editorial	A likelihood ratio does not evaluate a hypothesis, humans do.	Adjust the wording to reflect that the likelihood ratio can be used to inform either the acceptance or the rejection of a hypothesis by a decision-maker. For example, change wording to "The likelihood ratio is interpreted by the DNA analyst to determine how much support there is in the results for each hypothesis" or something similar that makes it clear the LR is interpreted by a person to inform their opinion about each hypothesis.		Reject with modification. Definition was deleted, use of "avuncular" in the text was revised to "aunt or uncle"
31	19	3.2	T	Combined Probability of Exclusion CPE The probability that a randomly selected individual would be excluded as a contributor to the DNA mixture. If the single-locus exclusion probabilities are independent, and if P_j is the probability of exclusion at locus j , then the combined probability of exclusion is $1 - \prod_j (1 - P_j)$.	delete	Including this concept here is tacit approval. It should be deleted.	Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied.
32	25	3.3	T	Combined Probability of Inclusion CPI The probability that a randomly selected individual would not be excluded (i.e., is included) as a contributor to the DNA mixture. If the single-locus exclusion probabilities are independent, and if P_j is the probability of exclusion at locus j , then the combined probability of inclusion is $\prod_j (1 - P_j)$.	delete	Including this concept here is tacit approval. It should be deleted.	Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied.
3	27	3.3	T	First sentence is bolded. Is there a reason for this?	Unbold if appropriate.	Consistency purposes	Accept.
4	36	3.4	Technical	add hyphen to " Y STR" to remain consistent with other occurrences in the document	Y-STR	Consistency purposes	Accept.
5	41	3.5	Editorial	Definition of haplotype includes that the combination of alleles/SNPs "found on the same chromosome." Is this statement coming directly from another source, otherwise, it would be more appropriate to include mention of linkage. Since we do have loci on the same chromosome that we do not consider haplotypes (D5 STRs).	"A haplotype can refer to a combination of alleles or to a set of single nucleotide polymorphisms (SNPs) found along a single chromosome that tend to be inherited together". Definition modified from NIH website.	Clarification	Accept.
6	49	3.6	Editorial	"Use of the theta correction removes the need to assume Hardy-Weinberg equilibrium in the population for which a frequency database is constructed." I would argue that the theta correction allows us to assume Hardy-Weinberg equilibrium, instead of not needing to assume. One assumption of a population in HWE is that there is random breeding - which inbreeding violates. The theta value takes possible inbreeding/substructuring of a population into consideration in the genotype frequencies.	"Use of the theta correction allows the assumption of Hardy-Weinberg equilibrium in the population for which a frequency database is constructed"	Statement accuracy	Accept.
7	49	3.6	Technical	The 2nd part of the 2nd sentence is a bit hard to follow the way it is currently written (lots of p's and q's). It would be better to separate this part as it's own sentence and restructure for clarity.	Period after HW principle. "For a locus with 2 alleles, p and q, the genotype frequencies can be calculated as follows:" ...and then continue as written.	Clarity	Reject. The recommended modification would remove the difference between the alleles and the frequencies.
18		3.11 (Likelihood Ratio)	T	"In forensic science applications, the likelihood ratio is used as an expression for the meaning of scientific evidence and as measure for its value."	"In forensic science applications, the likelihood ratio expresses the value of the scientific evidence with regard to a pair of competing propositions by measuring the support this evidence provides for one or the other of these two propositions."	The second sentence in this definition is currently incomplete/ambiguous. A likelihood ratio only gives the value of scientific evidence with regard to a pair of competing propositions, and it measures this evidence's support for one or the other of these two propositions.	Accept with modification. The second sentence has been removed.

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			E-Editorial T-Technical				Final Resolution
19		3.12 (linkage equilibrium)	T	"Linkage equilibrium describes the situation in which the haplotype frequencies in a population have the same value that they would have if the alleles at each locus were combined at random."	"The situation in which the match probability for a combination of alleles in a population has the same value as it would have if the alleles at each locus were combined at random."	The current wording makes it sound like linkage equilibrium is only for haplotypes. According to this document's definition for 'haplotype', a haplotype is "a set of linked DNA variations, or polymorphisms, that tend to be inherited together (e.g., commonly used for human Y-chromosome or mitochondrial analysis)". It is incorrect to say that linkage equilibrium is only for 'haplotypes' for the haplotype definition given in this document. Linkage equilibrium is for any two loci. In addition, from a statistics point of view, the correct term is 'match probability', not 'frequency'.	Accept with modification. The definition has been updated from a NIJ glossary with a modification to define disequilibrium. https://nij.ojp.gov/nij-hosted-online-training-courses/population-genetics-and-statistics-forensic-analysts/glossary#l
20		3.12 (linkage equilibrium)	T	"...random match probabilities..."	"...match probabilities..."	The current wording is incorrect. Here the referred to probabilities are 'match probabilities', not 'random match probabilities'.	Accept with modification. The definition has been updated from a NIJ glossary with a modification to define disequilibrium. https://nij.ojp.gov/nij-hosted-online-training-courses/population-genetics-and-statistics-forensic-analysts/glossary#l
21		Paternity or Maternity Index PI/MI	T	"The likelihood ratio that evaluates the hypothesis that the tested individual is the biological mother or biological father of the profile donor versus the hypothesis that the tested individual is unrelated to the profile donor."	"Likelihood ratio in which the numerator is the probability of the DNA data given the proposition that the tested individual is the biological father (or the biological mother) of the profile donor, and the denominator is the probability of the DNA data given the proposition that the tested individual is unrelated to the profile donor."	There are two major errors in the current wording: 1) The definition is an incorrect definition because the paternity / maternity index is not a probability of a proposition as the current wording states. The current wording is a Prosecutor's Fallacy or Transposed Conditional. 2) The word "hypothesis" is incorrect terminology for the interpretation of forensic STR data. The correct terminology is "proposition".	Accept with modification. Modified to "biological parent"
22		3.15 Random Match Probability RMP	T	"The probability of randomly selecting an unrelated individual from the population who could be a potential contributor to an evidentiary profile."	"The probability an unknown individual in a given population has a particular profile. More appropriately, the random match probability is computed conditioned on a known individual observed to have the profile. The unconditional probability is the profile probability."	The current wording is incorrect. The RMP is not the probability that an individual "could be a potential contributor to an evidentiary profile". It is the probability of an individual having a particular profile. In addition, it is important to explain the difference between the conditioned RMP and the unconditioned RMP (which is not a match probability, but a profile probability) to avoid misunderstandings that can lead to calculation errors and the reporting of incorrect statistics.	Reject. The definition as written is appropriate for this document and consistent with other ASB documents.
23		3.17 sibship index	T	"Likelihood ratio in which the numerator is conditioned on the hypothesis that a sibling of the source of the questioned profile in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source."	"Likelihood ratio in which the numerator is the probability of the DNA data given the proposition that the tested individual is the biological sibling of the profile donor, and the denominator is the probability of the DNA data given the proposition that the tested individual is unrelated to the profile donor."	1) The current definition is incomplete (and grammatically incorrect). It doesn't explain what the numerator and denominator probabilities are probabilities of. 2) The word "hypothesis" is incorrect terminology for the interpretation of forensic STR data. The correct terminology is "proposition".	Accept with modification. Revised to read "is a biological sibling"
29	108	3	E	".....on the hypothesis that a sibling of the source of the questioned profile in a specimen..."	"..... on the hypothesis that a sibling is the source of the questioned profile in a specimen..."	typographical error	Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.
8	108	3.17	Technical	"that a sibling of the source of the question profile of a specimen" Should the first "of" be "is"?	If yes: "that a sibling is the source of the question profile of a specimen". If no, the first hypothesis statement is confusing.	Statement accuracy	Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.

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			E-Editorial T-Technical				Final Resolution
38		3.17	Editorial	Redlined/proposed new wording appears to be missing a part of a sentence or, at a minimum, lacks clarity.	Revise the wording so that the intended meaning is clear - the HFTG had trouble determining what the SC intended to convey and, as a result, couldn't think of a concrete suggestion except that the wording should be revisited.		Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.
1	108-110	3.17	E	Likelihood ratio in which the numerator is conditioned on the hypothesis that a sibling of the source of the questioned profile in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source.	The likelihood ratio that evaluates the hypothesis that the tested individual is the biological sibling (or half-sibling) of the profile donor versus the hypothesis that the tested individual is unrelated to the profile donor.	Make the definition format of sibship index consistent with the two other likelihood ratio definitions in this document (3.1 avuncular and 3.14 paternity/maternity)	Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.
40	108-110	3.17	E	Likelihood ratio in which the numerator is conditioned on the hypothesis that a sibling of the source of the questioned profile in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source.	Consider restructuring the definition in a similar manner as avuncular index (section 3.1) and paternity or maternity index (section 3.14) definitions.	Cohesive and consistency between definitions within a document.	Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.
33	107	3.17	T	sibship index Likelihood ratio in which the numerator is conditioned on the hypothesis that a sibling of the source of the questioned profile in a specimen, and the denominator is conditioned on the hypothesis that an unrelated individual is the source.	sibship index The likelihood ratio that evaluates the hypothesis that the tested individuals are biological full siblings versus the hypothesis that the tested individuals are unrelated.	This is another coined phrase used in relationship testing. It is a calculation that compares the profiles under two propositions: the two people are siblings vs. the two people are unrelated." The usage currently in this document addresses the assertion, "I'm not the donor of that evidence DNA. My brother is." That is the premise behind the NRC II equations 4.9a and 4.9b. Please either come up with a new coined phrase for that, or even better, don't try to increase the number of coined phrases. Note: Line 206 has the sibship index used in terms of kinship testing, not in the manner of the current definition.	Accept with modification. Definition revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.
34	112	3.18	T	source attribution A declaration which identifies an individual as the source of the DNA that produced an evidentiary single-source or deduced contributor profile. This statement is based on a statistical estimate that meets or exceeds a laboratory-defined threshold.	delete	Including this concept here is tacit approval. It should be deleted.	Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied.
24		3.18 source attribution	T	"A declaration..." and "This statement is..."	"A decision..." and "This decision is..."	Source attribution is not just a declaration or a statement. It is a decision (= statistical definition of source attribution), and this needs to be clearly communicated in this definition.	Reject. The recommended modification does not add any substance to the definition. Additionally this wording is consistent with other DNA standards.
25		3.19 theta correction	T	"A value used to adjust statistical calculations that rely on population databases to correct for substructures within populations."	"A method used to adjust match probabilities, allowing match probabilities to be assigned for subpopulations from whole population allele frequencies."	The current definition states that theta correction is a value. This is incorrect: "Theta" is a value. "Theta correction" is a method. In addition, the term "statistical calculations" is too vague. What statistical calculations?	Accept with modification. "value" revised to "method". Remainder of definition is appropriate for this document as "statistical calculations" is broad and intended to address multiple formulas.
26		4.2.1 e)	T	"literature on the effects of cognitive bias in decision-making processes associated with statistical calculations used for forensic STR DNA data"	explain what is meant by this point with examples or remove it	How can cognitive bias affect a statistical calculation? Without further explanations containing concrete examples, this point is not understood by the reader.	Reject. This was added based on previous input. This is consistent across the set of ASB DNA training documents. The intent of this requirement is for the user to review the literature.

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			E-Editorial T-Technical				Final Resolution
36		4.2.1 f)	Technical	This item seems too narrow in scope	Remove the second part of this item (i.e., "associated with analysis used for forensic STR DNA data").		[Correct section is 4.2.1 e]) Reject. It is important that the bias training be specific to the scope of this document.
9	139	4.2.2	Technical	"and Y-STR data to include, at minimum, the following topics." Change period to a colon since a list is next.	"and Y-STR data to include, at minimum, the following topics:"	Appropriate punctuation	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.
		4.2.2			replaced "basic understanding" with "basic instruction" for consistency with the other training documents.	Consistency purposes	accept
10	141	4.2.2 a. i.	Technical	"laws of Mendelian genetics (law of segregation and the law of independent assortment);" add or delete "the" for the 2 laws in parenthesis	Either remove "the" from the parenthesis or add "the" before law of segregation for consistency purposes.	Consistency purposes	Accept.
11	142	4.2.2.a.2	Editorial	Including the understanding of evolutionary factors like mutation, gene flow, random mating, etc., and their affects on HWE will allow the trainee to recognize why certain genes/loci are not appropriate for statistical analysis involving population databases.	"Hardy-Weinberg equilibrium, assumptions, and related evolutionary forces"	Additional knowledge to round-out the training on this topic.	Accept.
12	150/151	4.2.2 b. 5./6.	Technical	Change the period after Bayes thm to a semi colon and add period after 6.	"Bayes' theorem;" and "Sources of uncertainty (e.g. modelling uncertainty and sampling variability)."	Appropriate punctuation	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.
35	183	4.2.2e5	T	source attribution statements, if applicable;	delete	Including this concept here is tacit approval. It should be deleted.	Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied.
13	200	4.2.2. g. ii.	Technical	Change the semi colon to a comma at the end of the statement	"how to set-up competing propositions for kinship calculations,"	Appropriate punctuation	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.
27		4.3.1	T	"...statistical values for DNA data used by the laboratory to include..."	"...statistical values used by the laboratory for the interpretation of forensic DNA data to include..."	This document only addresses statistical calculations used in the interpretation of STR data. It does not cover other statistical calculations (i.e., calculations not part of the interpretation of STR DNA data, such as statistical calculations for population genetics not related forensic DNA interpretation).	Reject. Part of the sentence was deleted.
		4.3.2					"at least once or until clearly understood" moved to the end of the paragraph in response to a comment in standard 079 and for consistency across all training documents.
		4.4.2 and 4.4.3					(as defined by the laboratory's policy) added to 4.4.2 and 4.4.3 in all training documents for consistency in response to a comment in standard 078 and 080. sentence structure edited for consistency across all training standards.
28		Annex A	T	none	Add the following reference: "Buckleton et al. NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis, Forensic Science International: Genetics 37 (2018) 172-179."	If the NIST MIX 13 study is going to be cited in this Bibliography, then this article must also be cited in order to not present a biased perspective.	Accept.
14	255	Annex	Technical	Period at the end of the reference	"2023."	Consistency purposes	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.
39	268	References	E	A. Bright	J.-A. Bright	Author's first name is hyphenated as in refs 15, 31, 34, 41	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.
41	255	Bibliography	E	AABB. Standards for Relationship Testing Laboratories (16th ed.). 2023	AABB. Standards for Relationship Testing Laboratories (16th ed.). 2023.	Grammar/consistency. Add a period at the end of the referenced citation.	Accept with modification. Punctuation cleaned up through the section to be consistent with the ASB Style.

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Final Resolution
42	N/A	Bibliography	E	Suggestion for references in Bibliography section.	Suggestion: Add SWGDAM autosomal STR interpretation guidelines and Y-STR interpretation guidelines as they discuss statistics (SWGDAM is also cited in other ASB documents). Also add SWGDAM footer with webpage link.	SWGDAM	Accept.
		Annex A					added reference to STRbase (26)
		Annex A #7					corrected spelling of author's name

Deadline of Submission of Comments: 13-Oct-25

Document Number: ASB Std 081

Document Title: Standard for Training in the Use of Statistics in Interpretation of Forensic DNA Evidence

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Final Resolution
1		Foreword	E	minimum requirements	delete minimum	we voted to delete minimum from the Scope; should also be deleted from the Foreword	Accept
2		1 Scope	T	This standard provides the requirements for a forensic DNA laboratory's training program for the use of statistical calculations and values reported for forensic autosomal and Y short tandem repeat (STR) DNA data.	Readd "minimum" This standard provides the minimum requirements for a forensic DNA laboratory's training program for the use of statistical calculations and values reported for forensic autosomal and Y short tandem repeat (STR) DNA data.	It is important to underscore these are minimum requirements as a lab may wish to implement even more rigorous requirements and should not be 'discouraged' from doing so	Reject: it has been decided to remove the word minimum for consistency
3		scope	E	Y short tandem repeat	Y-chromosome		Accept
4		3.2,3.2, 3.18; 4.2.2e(3) and e(4)	T	Defines CPE, CPI & source attribution; also includes requirements for training on those topics.	Add note clarifying intent is for legacy knowledge and what that means.	Public comments received expressed concerned that these concepts are outdated and unsupported and that including them indicated a tacit approval. I agree they are important to include in a training program since the lab may need to review old casework using these CPI/CPE, and source attribution statements still occur (and maybe CPI/CPE does too). However, the commenter is absolutely correct: including them IS tacit approval. Additionally, 4.2.2.(e)(3) and e(4) requirements clearly indicate this is current practice in a lab! The standard could benefit from a note that this is for legacy knowledge--in the event old cases need to be reviewed, for instance. Or some statement indicating that these methods/statements are no longer in line with current scientific knowledge. In fact, the comment resolution for comment numbers 31, 32, and 34, states "Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied. "	Reject. Since this is a training document, the intent is that the trainees should learn the concept for legacy knowledge, and it helps to distinguish different statistical methods that can be applied. There are still documents that allow the use of these statistics under certain circumstances, therefore, training is required for these statistics.
5		3.4	E	A haplotype can refer to a combination of alleles or to a set of single nucleotide polymorphisms (SNPs) found along a single chromosome that tend to be inherited together.	A haplotype can refer to a combination of alleles or to a set of single nucleotide polymorphisms (SNPs) found along a single chromosome.	Delete the repeated statement "that tend to be inherited together" as that is already in the definition. This addition does not add any clarity.	Accept
6		3.4	E	that tend to be	that tends to be		Accept
7		3.5	Ballot Comment	minor comment #1: in the definition for Hardy-Weinberg, remove the last sentence saying to "see theta correction". It is redundant since the sentence before it says that theta correction allows for the assumption.			Accept
8		3.14	E	 At the same time) and exhaustive in the context of the case (i.e., one should not consider all propositions as default, but only those that are thought to be of interest to the court.	at the same time.) Propositions are typically associated with the known or assumed standpoint of the parties on a disputed issue of interest."	the wording "exhaustive in context of the case" was interpreted many ways by the group, members of whom were concerned with misinterpretation. Replace with clearer wording from definitions in standard 041.	Accept: replaced with wording from ASB Standard 041
9		3.15	E	The probability of randomly selecting an unrelated individual from the population who could be a potential contributor to an evidentiary profile.	The probability an unknown individual in a given population has a particular profile.	group agreed with rejected comment #22, RMP is not evaluating probability someone could be a contributor (that would require prior odds)	Reject- This was not open for comment. This is the accepted definition from SWGDAM.

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Final Resolution
10		4.2.2.	T	2) statistical calculation method(s) in use by the laboratory, to address: i) population substructure, ii) mutation rates, iii) known relatedness;	iii) known and suspected relatedness.	Concerned about the modifier "known"--does that include assumed relatedness (i.e. see the calculations that STRmix does for hypothetical relatives under its Unified calculation) . Also, isn't it important to understand the issues with false positives when the true contributor is related to the noncontributing POI and other assorted issues when relatives are involved in a case?	Reject- This was not open for comment
11		4.2.2 f) 2 iii	E	(reduced...)	(e.g., reduced...)	should "e.g.," be added in the parentheses	Accept
12		4.3.2	E	... processed by the laboratory, at least once or until clearly understood.	...processed by the laboratory until clearly understood.	any observation implies at least once	Reject- This phrase was added to all training standards based on comments from round 2
13		4.4.2	T	a knowledge-based test covering the critical information obtained during the training on case record management, forensic DNA report writing, and performing technical and administrative reviews.	substitute something like: all aspects of the use of the methods for statistical calculations the trainee will be authorized to perform.	This language is from Standard 080 and does not seem appropriate for this standard.	Accept with modification, WG elected to use wording from original OSAC document
14		Bibliography #2	Ballot Comment	minor comment #2: in the bibliography for reference #2 (AABB), just use the general name for the reference without the year since this reference updated frequently...similar to how the swgdam documents are referenced			Accept with modification
15		Bibliography #6	E		the paper has 17:125	add ":125" to the reference to now be 17:125	Accept
16		Bibliography #10	E			the reference is incomplete	Accept
17		Bibliography #26	E			is this the correct format?	Reject- the citation was obtain from the NIST website
18		Bibliography #32	E			the reference is incomplete; I found the document at https://www.ojp.gov/ncjrs/virtual-library/abstracts/statistical-and-population-genetics-issues-affecting-evaluation	Accept

Deadline of Submission of Comments: 11-May-26

Document Number: ASB Std 081

Document Title: Standard for Training in the Use of Statistics in Interpretation of Forensic DNA Evidence

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Working Group Resolution
1	180		Ballot Comment	add semicolon at the end			Accept with modification. A comma was added to remain consistent with the rest of the document.
2	186-195		Ballot Comment	fix punctuation so the lists are all uniform with a comma or a semicolon			Accept with modification. Commas replaced semicolons. Also changed lines 177 and 179 to a comma
3	195		Ballot Comment	add space after the "e.g.,"			Accept
4	236		Ballot Comment	remove space after "statistics ."			Accept
5	256-257		Ballot Comment	suggestion to remove edition # and year from ASB references			Accept
6	277		Ballot Comment	remove extra period at the end			Accept
7	347		Ballot Comment	put footnote after the period			Accept