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 statisitcal 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 statisitcal 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 useage 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"

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**
37		3.1	Editorial	A likelihood ratio does not evaluate a hypothesis, humans do.	Adjust the wording to reflect that the likelihod 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 cleaar 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 Pj is the probability of exclusion at locus j, then the combined probability of exclusion is 1- Πj (1 - Pj).	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 Pj is the probability of exclusion at locus j, then the combined probability of inclusion is Πj (1 - Pj).	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	Defintion 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 restrucuture 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 continuee 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.

Comment #	Text Line # (s)	Document Section	Type of Comment E-Editorial T-Technical	Current Document Wording	Proposed Revision	Revision Justification	*For Working Group and Consensus Body use only, not to be completed by commenter.* 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 / matermity 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 gramatically 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 specime…"	"….. on the hypothesis that a sibling **is** the source of the questioned profile in a specimen…"	typographical error	Accept with modification. Defintion 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. Defintion revised to be consistent with the Paternity or Maternity Index definition, based on comment # 23.

Comment #	Text Line # (s)	Document Section	Type of Comment E-Editorial T-Technical	Current Document Wording	Proposed Revision	Revision Justification	*For Working Group and Consensus Body use only, not to be completed by commenter.* Final Resolution
38		3.17	Editorial	Redlned/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. Defintion 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 sibsship index consistent with the two other likelihood ratio defininitions in this document (3.1 avuncular and 3.14 paternity/maternity)	Accept with modification. Defintion 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. Defintion 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 useage 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. Defintion 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.

Comment #	Text Line # (s)	Document Section	Type of Comment E-Editorial T-Technical	Current Document Wording	Proposed Revision	Revision Justification	*For Working Group and Consensus Body use only, not to be completed by commenter.* 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 paranthesis	Either remove "the" from the paranthesis or add "the" before law of segretation 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 approriate for statiscal 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 statisitcal 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.	Grammer/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 E-Editorial T-Technical	Current Document Wording	Proposed Revision	Revision Justification	*For Working Group and Consensus Body use only, not to be completed by commenter.* 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