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 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
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	Public comments received expressed concerned that these concepts are outdated and unsupported and that including them indicated a tacit approval.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 scietnific 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.

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 relatedess (i.e. see the calculations that STRmix does for hypothetical relatives under its Unified calculation) . Also, isnt it important to understand the issues with false positives when the true cntributor 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