

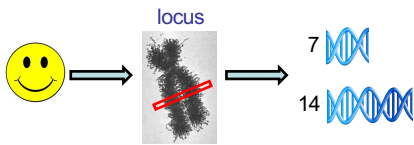
TrueAllele® validation: Computer interpretation of DNA mixture evidence

Mark W Perlin, PhD, MD, PhD
Cybergenetics, Pittsburgh, PA



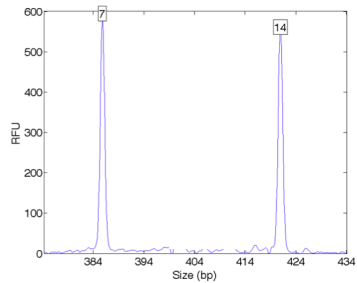
Cybergenetics © 2003-2021

One person, one genotype

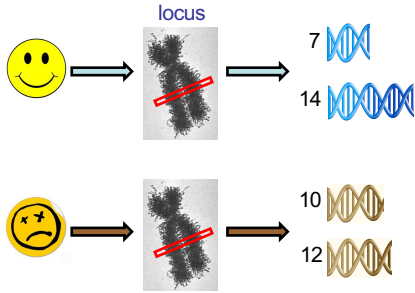


DNA data

One or two allele peaks at a locus

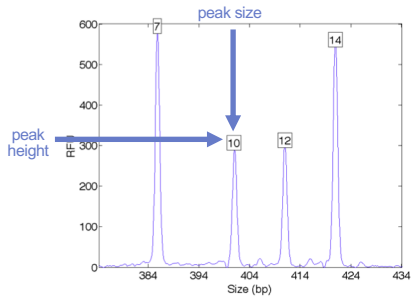


Two people, two genotypes



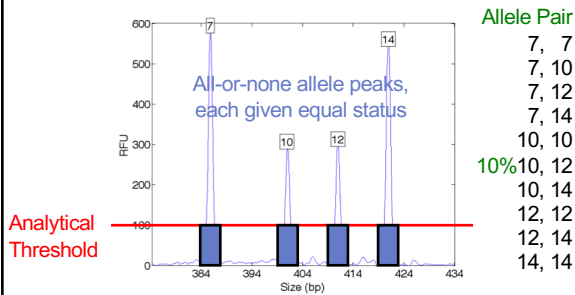
DNA mixture problem

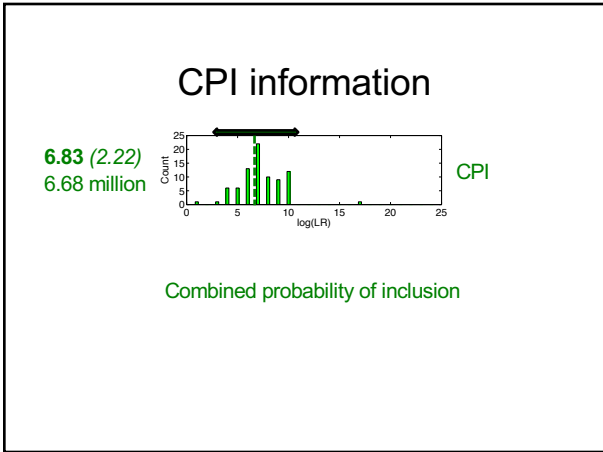
Quantitative peak heights at a locus

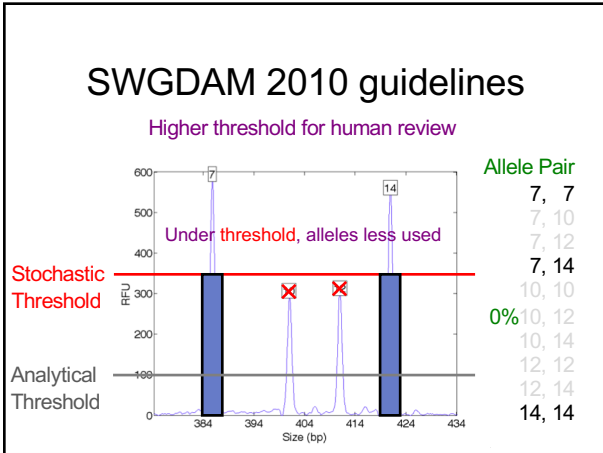


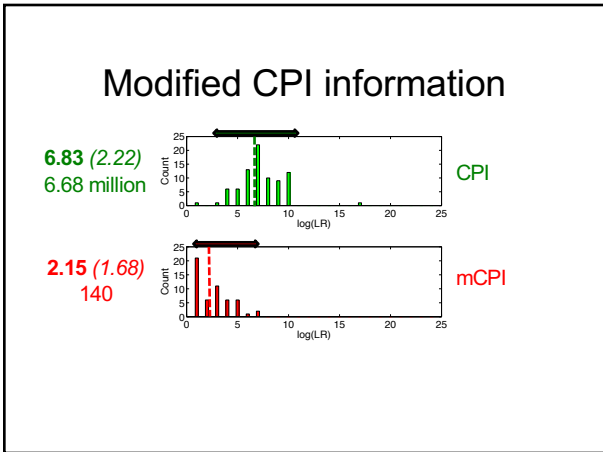
Data summary – “alleles”

Over threshold, peaks are labeled as allele events









SWGDM 2010 guidelines

3.2.2. If a stochastic threshold based on peak height is not used in the evaluation of DNA typing results, the laboratory must establish alternative criteria (e.g., quantitation values or use of a probabilistic genotype approach) for addressing potential stochastic amplification. The criteria must be supported by empirical data and internal validation and must be documented in the standard operating procedures.

Use TrueAllele® Casework for DNA mixture statistics

TrueAllele® computer solution

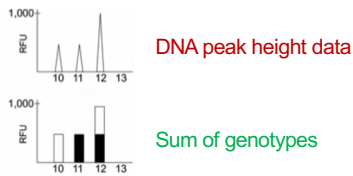
- Accurate. 41 validation studies, 8 published
- Objective. Workflow removes human bias
- Accepted. Reported in 44 states, used by labs
- Transparent. Give math, software (4GB DVD)
- Neutral. Can statistically include or exclude

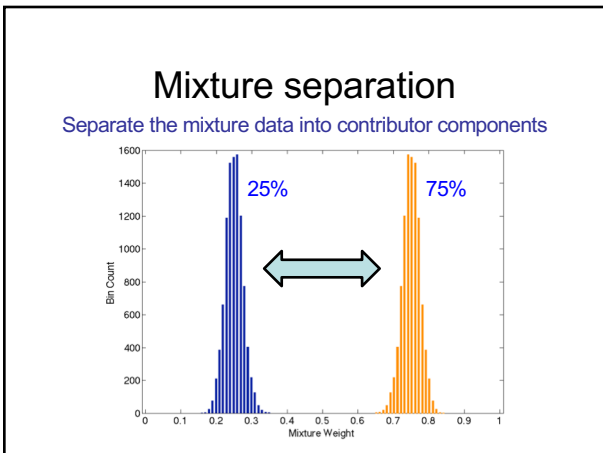
Explaining DNA mixtures

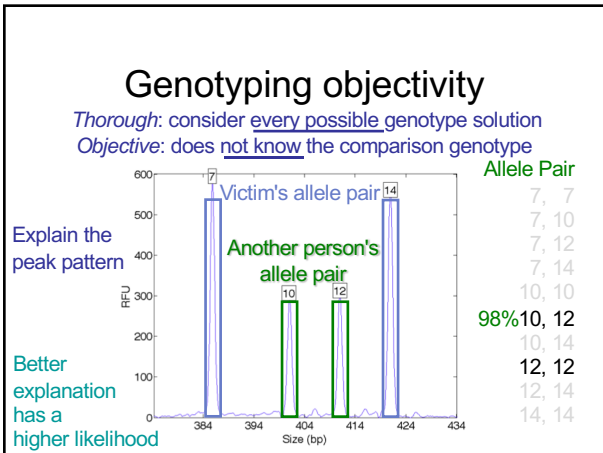


Mark W. Perlin,¹ Ph.D., M.D., Ph.D. and Beata Szabady,¹ Ph.D. 2001

Linear Mixture Analysis: A Mathematical Approach to Resolving Mixed DNA Samples







Peer-reviewed validation studies

Perlin MW, Sineelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE*. 2009;4(12):e8327.

Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information. *Science & Justice*. 2013;53(2):103-114.

Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences*. 2015;60(4):857-868.

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276.

Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors. *Journal of Forensic Sciences*. 2020; 65(2):380-398.

Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences*. 2011;56(6):1430-1447.


Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-1466.

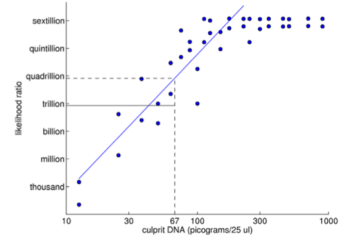
Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLoS ONE*. 2014;9(3):e92837.

TrueAllele predictability

An Information Gap in DNA Evidence Interpretation

Mark W. Perlin^{1*}, Alexander Sinehnikov²

 2009




TrueAllele reliability

TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases

Mark W. Perlin^{1*}, Kiersten Dormer¹, Jennifer Hornyak¹, Lisa Schliermeier-Wood², Susan Greenspoon²

¹ Cybergeneics, Pittsburgh, Pennsylvania, United States of America, ² Department of Forensic Science, Richmond, Virginia, United States of America

 2014

Validation axes

- sensitive
- specific
- reproducible

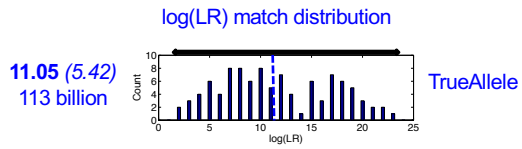
Sensitivity

The extent to which interpretation identifies the correct person

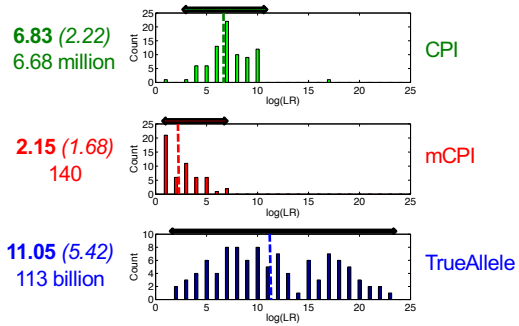
True DNA mixture inclusions

101 reported genotype matches
82 with DNA statistic over a million

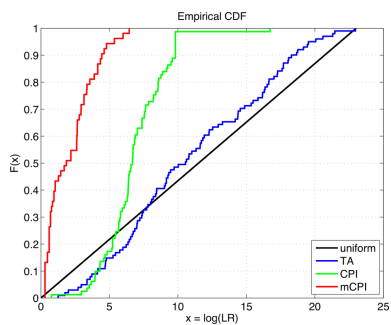
TrueAllele sensitivity



Comparison



TrueAllele accuracy



Specificity

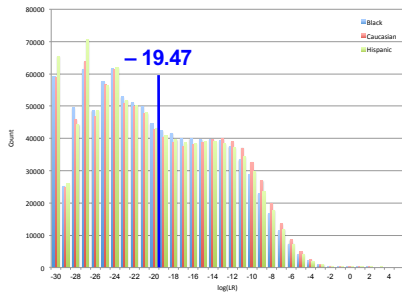
The extent to which interpretation does not misidentify the wrong person

True exclusions, without false inclusions

101 matching genotypes x 10,000 random references
x 3 ethnic populations,
for over 1,000,000 nonmatching comparisons

TrueAllele specificity

log(LR) nonmatch distribution



False positives

in over 1,000,000 comparisons per group

Tail distribution	Black	Caucasian	Hispanic
0	39	32	29
1	8	11	9
2	2	1	1
3	0	0	1
log(LR) > 0	49	44	40

false positive rate is under 1 in 20,000 (0.005%)
for LR > 100, rate is 1 in 1,000,000 (0.0001)%

Higher human error rate

TrueAllele specificity (million samples)
From noncontributor distribution, for LR > 100:
Error rate = 1 in 1,000,000 (**0.0001**)%

CPI – analytical threshold
5 false positives in 81 comparisons
Error rate = 5 in 81 (**6%**)

mCPI – stochastic threshold
17 inconclusive results
1 false positive in 53 comparisons
Error rate = 1 in 53 (**2%**)

Reproducibility

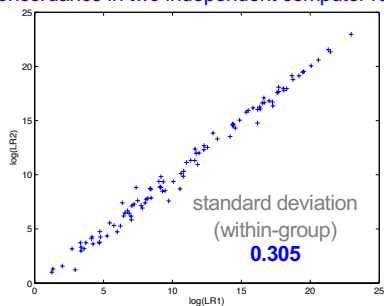
The extent to which interpretation gives
the same answer to the same question

MCMC computing has sampling variation

duplicate computer runs
on 101 matching genotypes
measure log(LR) variation

TrueAllele reproducibility

Concordance in two independent computer runs



JOURNAL OF FORENSIC SCIENCES

J Forensic Sci. November 2011, Vol. 56, No. 6
doi: 10.1111/j.1556-4029.2011.01859.x
Available online at: onlinelibrary.wiley.com

PAPER

CRIMINALISTICS

Mark W. Perlin,¹ M.D., Ph.D.; Matthew M. Legler,¹ B.S.; Cara E. Spencer,¹ M.S.; Jessica L. Smith,¹ M.S.; William P. Allan,¹ M.S.; Jamie L. Belrose,² M.S.; and Barry W. Duceman,³ Ph.D.

Validating TrueAllele[®] DNA Mixture Interpretation*[†]

JOURNAL OF FORENSIC SCIENCES

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PAPER

CRIMINALISTICS

Mark W. Perlin,¹ M.D., Ph.D.; Jamie L. Belrose,² M.S.; and Barry W. Duceman,³ Ph.D.

New York State TrueAllele[®] Casework Validation Study*

JOURNAL OF FORENSIC SCIENCES

J Forensic Sci. July 2015, Vol. 60, No. 4
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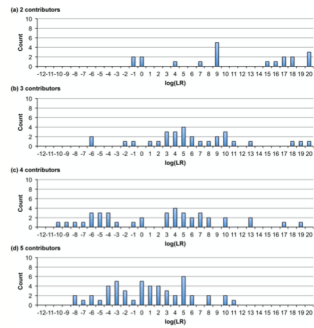
PAPER

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Mark W. Perlin,¹ Ph.D., M.D.; Jennifer M. Hornyak,¹ M.S.; Garrett Sugimoto,² M.S.; and Kevin W.P. Miller,² Ph.D.

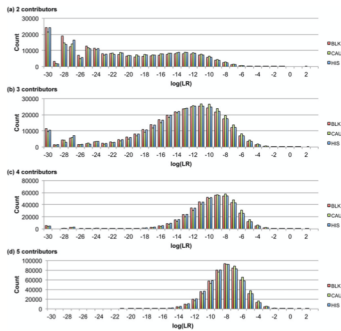
TrueAllele[®] Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors*

TrueAllele sensitivity



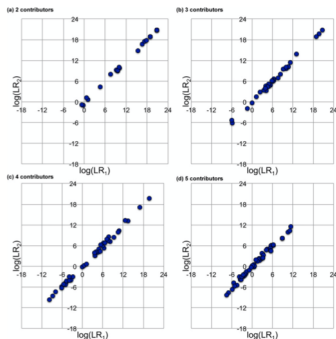
200 pg

TrueAllele specificity



200 pg

TrueAllele reproducibility



200 pg

JOURNAL OF **FORENSIC SCIENCES**

J. Forensic Sci. 2019
doi: 10.1111/1556-4029.14204
Available online at: onlinelibrary.wiley.com

PAPER

CRIMINALISTICS


David W. Bauer,¹ Ph.D.; Nasir Butt,² Ph.D.; Jennifer M. Hornyak,¹ M.S.; and Mark W. Perlin,¹ Ph.D., M.D., Ph.D.

Validating TrueAllele[®] Interpretation of DNA Mixtures Containing up to Ten Unknown Contributors*

TABLE 7—Peeling sensitivity.

Operator Site		Mixture weight (%)	Peeling Round							
			0	1	2	3	4	5	6	
	Cybergenetics	13	7	K	K	K	K	K	K	K
	CCRFSL	22	6	7	K	K	K	K	K	K
		12	5	4	5	K	K	K	K	K
		16	4	4	5	6	K	K	K	K
Genotypes	78	78	4	3	2	1	6	K	K	K
Minimum	-5.16	-9.14	3	3	4	1	6	8	K	K
Mean	8.36	8.48	1	1	1	1	3	3	4	
Median	5.98	5.61	0	2	2	3	2	3	4	
Maximum	29.03	29.12	0	1	1	1	2	0	2	
SD	8.37	8.54	0	0	0	0	-1	-1	0	
n _e		1								

Heliyon

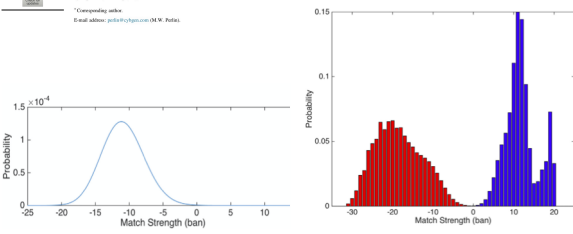
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Accepted: 21 September 2018

Efficient construction of match strength distributions for uncertain multi-locus genotypes

Mark W. Perlin, Erikson, et al.

Mark W. Perlin*
Cybergenetics, Pittsburgh, PA, USA
*Corresponding author.
Email address: perlin@cybergenetics.com (M.W. Perlin).



Over 25 admissibility rulings

- Commonwealth of Pennsylvania v Kevin Foley (admitted, 2009; appellate precedent, 2012)
- People of California v Dupree Langston (admitted, 2013)
- Commonwealth of Virginia v Matthew Brady (admitted, 2013)
- State of Ohio v Maurice Shaw (admitted, 2014)
- State of Louisiana v Chatley Chesterfield & Samuel Nicolas (admitted, 2014)
- People of New York v John Wakefield (admitted, 2015; appellate precedent, 2019)
- State of South Carolina v Jaquard Aiken (admitted, 2015)
- Commonwealth of Massachusetts v Heidi Bartlett (admitted, 2016)
- State of Indiana v Dugniqio Forest (admitted, 2016)
- State of Indiana v Malcolm Wade (admitted, 2016)
- State of Washington v Emanuel Fair (admitted, 2017)
- State of Louisiana v Harold Houston (admitted, 2017)
- State of Indiana v Randal Coalter (admitted, 2017)
- State of Nebraska v Charles Simmer (admitted, 2018; appellate precedent, 2019)
- State of Indiana v Vaylen Glazebrook (admitted, 2018)
- State of Ohio v David Mathis (admitted, 2018)
- State of Florida v Lajayvian Daniels (admitted, 2018)
- State of Tennessee v Demontez Watkins (admitted, 2018)
- State of Georgia v Thaddeus Nundra (admitted, 2019)
- State of Georgia v Monte Baugh & Thaddeus Howell (admitted, 2019)
- State of Louisiana v Kyle Russ (admitted, 2019)
- People of New York v Casey Wilson (admitted, 2019)
- State of Georgia v Alexander Battle (admitted, 2019)
- United States v Lenard Gibbs (admitted, 2019)
- State of Georgia v Guy Sewell (admitted, 2019)
- State of Georgia v Adedojah Bah (admitted, 2019)
- State of Georgia v Nathaniel Day (admitted, 2019)
- State of Tennessee v Abdullah Powell (admitted, 2021)

TrueAllele today

Invented math & algorithms	25 years
Developed computer systems	20 years
Support users and workflow	10 laboratories
Routinely used in casework	8 crime labs
Validate system reliability	42 studies
Educate the community	100 talks
Train or certify analysts	400 students
Admissibility challenges	28 rulings, 14 states
Testify about LR results	100 trials
Educate lawyers and public	1,000 people
Make the ideas understandable	975 cases, 44 states

Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLOS ONE*. 2014;(9)3:e92837.

Conclusions

TrueAllele Casework DNA mixture interpretation is:

A reliable method

- objective
- sensitive
- specific
- reproducible
- accurate

TrueAllele computer genotyping is more effective than human review
