

Delivering Computer Automation in Forensic DNA Science

Legal Medicine & Forensic Science
Duquesne University Law School
March, 2022
Pittsburgh, PA

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



Cybergenetics

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JUSTICE
THROUGH
SCIENCE

The power of DNA testing

Nice try but no potato for New Zealand



News: Fails to make the Guinness World Records (March 2022)

Florida v. Lajayvian Daniels

In May of 2014

A Palm Beach County gas station was robbed at gunpoint.
Clerk Shihab Mahmud (22) was shot and killed.

Charred clothing, a charred hat, and a pair of sneakers
were found within a mile of the crime scene.

The Palm Beach County Sheriff's Office crime lab developed
DNA mixture data from the clothing, hat, and sneakers.

Due to the degraded nature of the data,
the lab was unable to fully interpret some mixtures.

TrueAllele® computer solution

- Accurate. 42 validation studies, 8 published
- Objective. Workflow removes human bias
- Accepted. Reported in 45 states, used by 10 labs
- Transparent. Give math, software (4GB DVD)
- Neutral. Can statistically include or exclude

Computer Interpretation of Quantitative DNA Evidence

State of Florida v. Lajayvian Daniels
May, 2018
West Palm Beach, FL

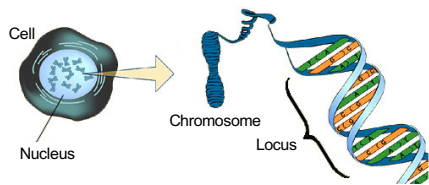
William P. Allan, MS
Cybergenetics, Pittsburgh, PA




Cybergenetics

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DNA biology



Short tandem repeat



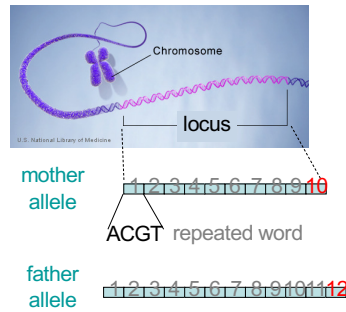
23 volumes in cell's DNA encyclopedia

DNA locus paragraph

Take me out to the ball game
take me out with the crowd
buy me some peanuts and Cracker Jack
I don't care if I never get back
let me
root root root root root root root root root
for the home team,
if they don't win, it's a shame for it's one, two,
three strikes, you're out
at the old ball game

"root" repeated 10 times, so allele length is 10 repeats

DNA genotype



Chromosome

locus

mother allele
1 2 3 4 5 6 7 8 9 10
ACGT repeated word

father allele
1 2 3 4 5 6 7 8 9 10 11 12

A genetic locus has two DNA sentences, one from each parent.

An allele is the number of repeated words.

A genotype at a locus is a pair of alleles.


10, 12

Many alleles allow for many many allele pairs. A person's genotype is relatively unique.


DNA evidence interpretation

Evidence item → Lab → Evidence data → Infer → Evidence genotype

10, 12



DNA from one person



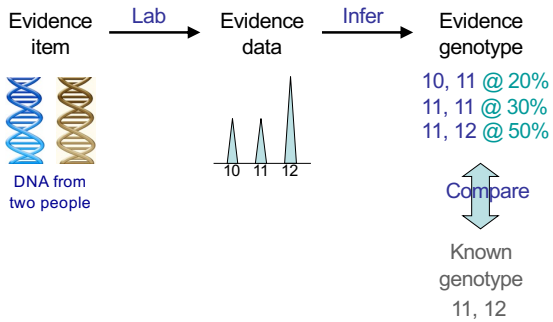
10 11 12

Compare

Known genotype

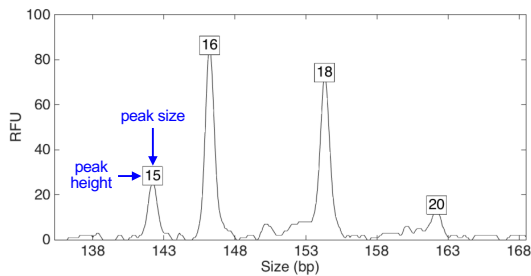
10, 12

DNA mixture interpretation



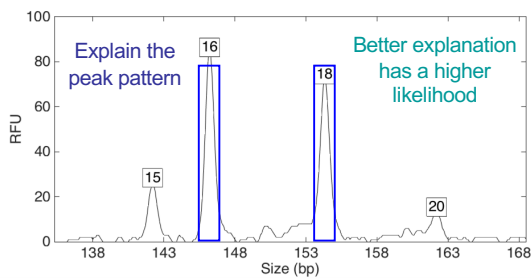
Computers can use all the data

Quantitative peak heights at locus vWA



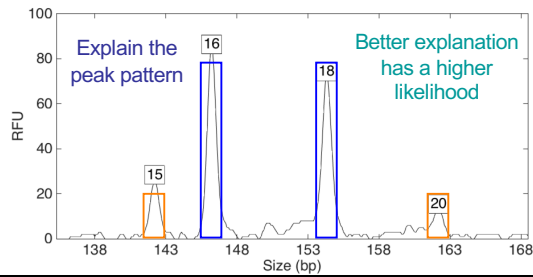
How the computer thinks

Consider every possible genotype solution



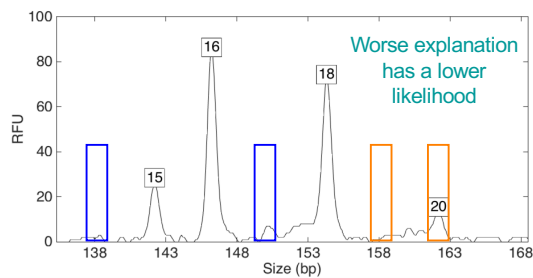
How the computer thinks

Consider every possible genotype solution



How the computer thinks

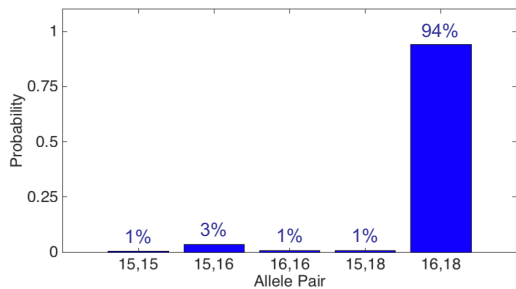
Consider every possible genotype solution



Evidence genotype

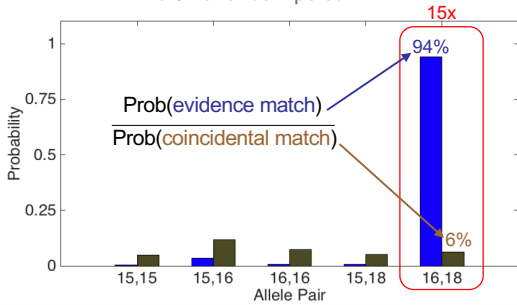
Objective genotype determined solely from the DNA data.

Never sees a comparison reference.

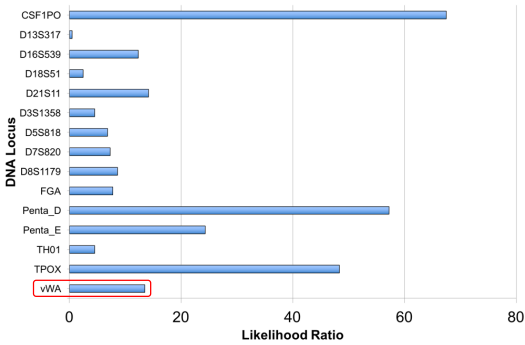


DNA match information

How much more does the **suspect** match the evidence than a **random person**?



Match information at 15 loci



Is the suspect in the evidence?

A match between the charred clothing and Lajayvian Daniels is:

872 trillion times more probable than a coincidental match to an unrelated African-American person

104 quintillion times more probable than a coincidental match to an unrelated Caucasian person

37.5 quintillion times more probable than a coincidental match to an unrelated Hispanic person

Match statistics

Item	Description	3	6	9
		Franklin Washington	Shihab Mahmud	Lajayvian Daniels
2-1	Charred hat	29.3 thousand		
3-2	Charred clothing			872 trillion
3-4	Charred clothing			77.1 million
4A-1	Pair of black Adidas sneakers, right sneaker			194 quadrillion
4B-2	Pair of black Adidas sneakers, left sneaker			789 billion

Match statistics

Item	Description	3	6	9
		Franklin Washington	Shihab Mahmud	Lajayvian Daniels
2-1	Charred hat	4.47		
3-2	Charred clothing			14.94
3-4	Charred clothing			7.89
4A-1	Pair of black Adidas sneakers, right sneaker			17.29
4B-2	Pair of black Adidas sneakers, left sneaker			11.90

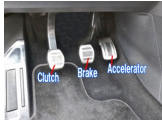
Admissibility challenge

Defendant's Motion to Exclude the Interpretation of DNA Mixtures by the TrueAllele Software Due to the Failure to Perform the Required Internal Validation

The defendant alleged that the results of the TrueAllele analysis were **not admissible** because the evidentiary requirements **under Frye** had not been met. Specifically, the defendant argued that the TrueAllele interpretation process **lacked an internal validation** mechanism, as "**required**" under **generally accepted** national standards.

Irrelevant standard

If a standard isn't relevant to a technology,
then it isn't applicable to that technology.
TrueAllele doesn't need or use calibration parameters,
because it learns that information from the data.



Manual transmission
has a clutch



Automatic transmission
has no clutch

TrueAllele® validation: Computer interpretation of DNA mixture evidence

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



Cybergenetics

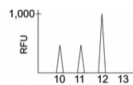
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Explaining DNA mixtures

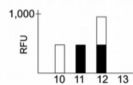
JOURNAL OF FORENSIC SCIENCES

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



DNA peak height data



Sum of genotypes

Peer-reviewed validation studies²⁵

Perlin MW, Sinelnikov 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.

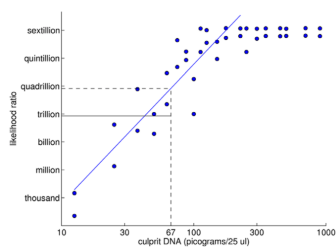
Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele[®] Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-1466.

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 Sinelnikov²



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 Schiermeier-Wood², Susan Greenspoon²

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



- Validation axes
- sensitive
 - specific
 - reproducible

Sensitivity

The extent to which interpretation identifies the correct person

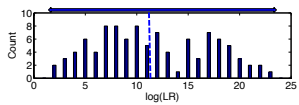
True DNA mixture inclusions

101 reported genotype matches
82 with DNA statistic over a million

TrueAllele sensitivity

log(LR) match distribution

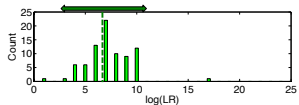
11.05 (5.42)
113 billion



TrueAllele

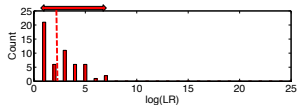
Comparison with human review

6.83 (2.22)
6.68 million



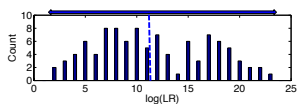
CPI

2.15 (1.68)
140



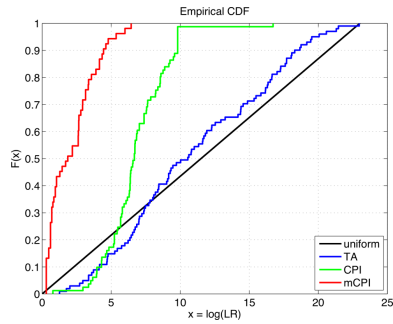
mCPI

11.05 (5.42)
113 billion



TrueAllele

TrueAllele accuracy



Specificity

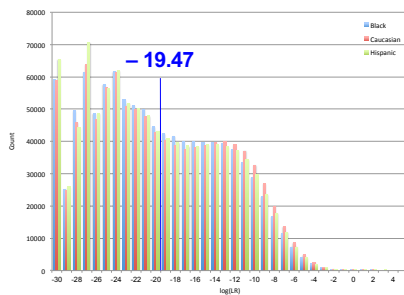
The extent to which interpretation does not misidentify the wrong person

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

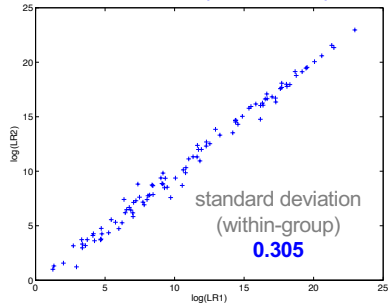
The extent to which interpretation gives
the same answer to the same question

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*[†]

A bar chart with 'Case Identifier' on the x-axis (BA, BC, BH, BD, BF, BG, BE) and 'log(LR)' on the y-axis (0 to 25). For each case, there are three bars: a tall green bar, a medium blue bar, and a shorter orange bar. The green bars are consistently the tallest, followed by blue, then orange. The values generally decrease from left to right across the case identifiers.

JOURNAL OF FORENSIC SCIENCES

J Forensic Sci. November 2013, Vol. 58, No. 6
doi: 10.1111/j.1556-4029.12223
Available online at: onlinelibrary.wiley.com

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*

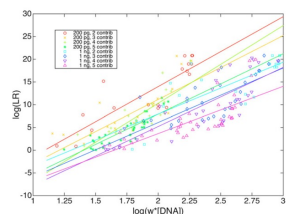
A bar chart with 'Evidence Items' on the x-axis and 'log(LR)' on the y-axis (0 to 25). The chart shows a distribution of log(LR) values for various evidence items. There are green bars and orange bars. A light blue shaded area is overlaid on the bars, showing a decreasing trend from left to right, representing a threshold or distribution curve.

PAPER

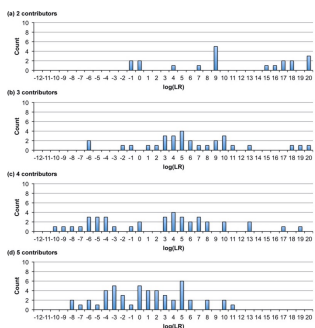
CRIMINALISTICS

Mark W. Perlin,¹ Ph.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*

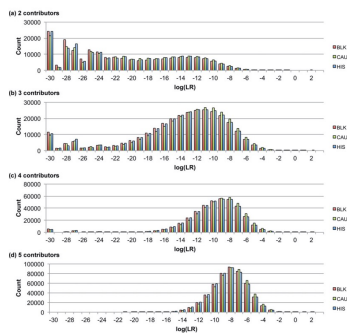


TrueAllele sensitivity



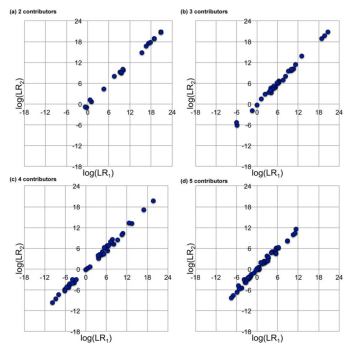
200 pg

TrueAllele specificity



200 pg

TrueAllele reproducibility



200 pg



PAPER

CRIMINALISTICS

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

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	
	Cybergnetics	CCRFSL
Genotypes	78	78
Minimum	-5.16	-9.14
Mean	8.36	8.48
Median	5.98	5.61
Maximum	29.03	29.12
SD	8.37	8.54
σ_{α}	0.70	

Mixture weight (%)	Peeling Round						
	0	1	2	3	4	5	6
13	7	K	K	K	K	K	K
22	6	7	K	K	K	K	K
12	5	4	5	K	K	K	K
16	4	4	5	6	K	K	K
13	4	3	2	1	6	K	K
15	3	3	4	1	6	8	K
2	1	1	1	1	3	3	4
2	0	2	2	3	2	3	4
4	0	1	1	1	2	0	2
1	0	0	0	0	-1	-1	0

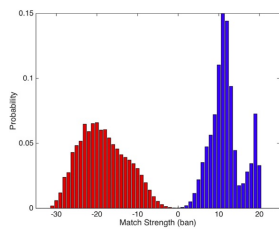
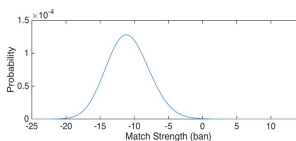


Received: 6 July 2018
Revised: 24 September 2018
Accepted: 24 September 2018
Published online: 24 September 2018

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

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.

Mark W. Perlin¹
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*Corresponding author.
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Background Reading

Background Reading binder exhibit

- Is there background reading that can help the court understand the method?
- Does the reading include a glossary?
- Are there magazine articles and book chapters for lawyers?

Validation Paper

Validation Paper binder exhibit

- What is peer-review?
- How many peer-reviewed TrueAllele validation studies have been published?
- Were the validations conducted independently of the current case?
- Do these studies test TrueAllele and establish error rates?

Validation Study

Validation Study binder exhibit

- How many other validation studies have been conducted?
- Who has conducted these studies?
- How are these studies related to the current case?
- Do these additional studies test TrueAllele and establish error rates?

Forensic Application

Forensic Application binder exhibit

- Has TrueAllele only been used by prosecutors?
- Was it used to help identify victim remains in the World Trade Center disaster?
- Has the federal government used TrueAllele to help establish DNA standards?

DNA Exoneration

DNA Exoneration binder exhibit

- Has TrueAllele helped exonerate the innocent?
- How many innocent men has TrueAllele helped free from prison?
- Has Cybergenetics sometimes done these exonerations *pro bono*?

Regulatory Approval

Regulatory Approval binder exhibit

- Do regulatory bodies oversee TrueAllele or related systems?
- What state regulators have assessed and approved TrueAllele?

Standards Compliance

Standards Compliance binder exhibit

- Are there accepted validation standards and guidelines for probabilistic genotyping?
- What is the FBI's SWGDAM (Scientific Working Group on DNA Analysis Methods)? What is ANSI (American National Standards Institute)?
- What is ASB (American Academy of Forensic Sciences Standards Board)?
- Do these organizations issue standards for validating probabilistic genotyping?
- Does TrueAllele validation comply with all of these standards and guidelines?

National Standards

Validating probabilistic genotyping

- **SWGDAM 2010** (§ 3.2.2) (January, 2010) – probabilistic genotype computer interpretation
- **SWGDAM 2015** (June 15, 2015) – probabilistic genotyping validation guidelines
- **ANSI/ASB Standard 020** (September 2018) – mixture validation and interpretation standards
- **ANSI/ASB Standard 040** (September 2019) – DNA interpretation and comparison standards
- **ANSI/ASB Standard 018** (July 2020) – probabilistic genotyping validation standards
- **FBI QAS 2020 (Section 8)** (July 1, 2020) – DNA quality assurance validation standards

Complying with Standards

Based on **empirical testing** of software on DNA data

Developmental & internal validation

Internal validation: The acquisition of test data within the laboratory to verify the functionality of the system, the accuracy of statistical parameters, **the appropriateness of analytical and statistical parameters**, and the determination of limitations of the system.

		2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42
4.1.6	Mixture samples	4, 7, 8, 9, 11, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 39, 40, 41, 42
4.1.6.1	Various contributor ratios	4, 7, 8, 9, 11, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 39, 40, 41, 42
4.1.6.2	Various total DNA template quantities	4, 7, 8, 9, 11, 12, 15, 17, 18, 19, 20, 21, 27, 28, 32, 35, 36, 37, 40, 41
4.1.6.3	Various numbers of contributors in samples	7, 10, 11, 12, 15, 16, 17, 18, 19, 21, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42
4.1.6.4	Over- and under- estimating of number of contributors input	8, 27, 28, 30, 32, 34, 39
4.1.6.5	Allele sharing among contributors	8, 11, 12, 18, 20, 26, 29, 38, 40

Method Reports

Method Reports binder exhibit

- Is the mathematics underlying TrueAllele available?
- Are Cybergenetics TrueAllele procedures provided?
- Can TrueAllele calculate an error rate for each reported match statistic?
- Was that done in this case?

General Acceptance

General Acceptance binder exhibit

- How many TrueAllele reports has Cybergenetics issued?
 - In how many states?
- In how many trials has Cybergenetics testified?
 - In how many states?
- Has TrueAllele been used by both prosecution and defense?
- How many crime labs use TrueAllele for DNA mixture analysis?
- How many scientific papers cite TrueAllele publications?
- Is probabilistic genotyping generally accepted in the forensic community?
 - Does the FBI use probabilistic genotyping?

Related Systems

Related Systems binder exhibit

- Are there other probabilistic genotyping systems for computing match statistics?
- How many other software systems are there?
- Do crime labs use these methods to calculate match statistics for DNA mixtures?

feature

Suspect-centric Bias in DNA Mixture Interpretation

Mark W. Perlin, Ph.D., M.D.

Bias abounds in criminal justice. Predictive policing can bake bias into software, reflecting and reinforcing prior beliefs. Bail-risk computer programs may entrench pre-trial detention disparity. Human judgment pervades the process. Prosecutor and defender alike passionately argue their client's case, drawing opposite conclusions from identical facts.

Science is above the fray. Objective data suggest forensic match between crime scene and suspect. Statistical data analysis yields incontrovertible numbers for the strength of match. Cold DNA facts are presented as confirmed theories in court.

But what if DNA analysts could pick and choose their data? Or adjust software parameters to suit their theories? Changing data and parameters will alter forensic match results. Quantitatively, subjective manipulation can artificially inflate match strength. Qualitatively, some DNA evidence that excludes a suspect may be statistically twisted to include him.

Subjective computer analysis

New York v. Oral "Nick" Hillary

New Zealand probabilistic genotyping software

Calibration

Modern **Bayesian computing** derives parameter probabilities directly from the data. However, **limited DNA modeling may lack that math capability**, and instead substitute historical data for case evidence. Crime labs usually develop calibration data to tune the foreign analysis software. However, **no lab-specific calibration** was done in the Hillary case. The foreign expert had to **pick and choose calibration parameters** in order to run his software on the NYSP lab data.

Validation study shows limits

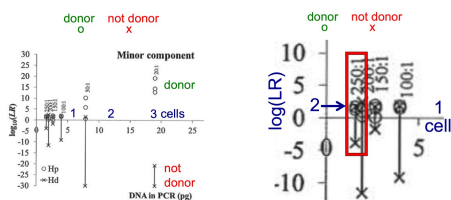


Figure 1. Validation match statistics for minor components. The x-axis gives the amount of DNA, represented in picograms (pg), number of cells (blue) and mixture ratios (major:minor). The y-axis gives the base 10 logarithm of the likelihood ratio (LR). The scatter plot shows true donors (Hp circles) and false non-donors (Hd crosses). (a) A zoomed out view to 25 pg. (b) A zoomed in view to 5 pg. One cell has 6 pg of DNA.

Picking & choosing parameters

RFU	Data choices	LR	All stutters
80	0	0	9
70	30	30	51
60	250	250	1,660
50	15,500,000	15,500,000	69,200
40	0	0	0
30	0	0	0

Table 1. Match statistic LR values on the same data are shown (blue) for computer runs using different threshold (rows) and stutter (columns) data assumptions.

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Human limitations of other PGS

Feature	Description	Human	STRmix	TrueAllele
<i>bias</i>	Cognitive bias?	yes	yes	no
<i>bias</i>	Contextual bias?	yes	yes	no
<i>prepare</i>	People prepare input data?	yes	yes	no
<i>filtering</i>	People can discard input data?	yes	yes	no
<i>intervention</i>	People can adjust input data?	yes	yes	no
<i>subjective</i>	Human decision making?	yes	yes	no
<i>limits</i>	Follow human limitations?	yes	yes	no
<i>time</i>	Labor intensive process?	yes	yes	no
<i>error</i>	Human processing error?	yes	yes	no

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The weakest link



Nice try but no admissibility for New Zealand

Admissibility Rulings

Admissibility Rulings binder exhibit

- Have there been admissibility challenges to TrueAllele reliability?
 - How many challenges?
 - In how many states?
 - How often has TrueAllele been admitted as reliable evidence?
- What does this admissibility ruling binder contain?

Legal Commentary

Legal Commentary binder exhibit

- Have legal scholars and practitioners written about TrueAllele?
- What have they said?

Scientific Development

Scientific Development binder exhibit

- When did Cybergenetics scientists first publish how to solve PCR stutter?
- When did Cybergenetics first publish its mixture analysis methods?
- Does Cybergenetics regularly publish articles about DNA mixture interpretation?

Other Papers

Other Papers binder exhibit

- Is TrueAllele largely based on Bayesian probability modeling, Markov chain Monte Carlo computer methods, and the MATLAB programming language?
- Are these three methods generally accepted as reliable in the scientific community?

Daniels trial court ruling (2018)

This Court finds that the TrueAllele DNA test results in this case **meet the requirements of Frye**. The scientific methodology used will **assist the trier of fact**. The methodology has been subjected to peer review and publication, there is a known rate of error and standards controlling the technique's operation, **the methodology is generally accepted in the scientific community and the scientific principle being challenged is not new or novel**. All of the defense arguments in opposition to admission of the TrueAllele results are ripe for **cross-examination**.

The Palm Beach Post

COURTS

Jury finds man guilty in 2014 Wellington gas station fatal shooting

Hannah Winston hwinston@pbpost.com

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After two days of deliberations, a 12-person jury found Lajayvian Daniels guilty of first degree murder and robbery in the 2014 fatal shooting of 22-year-old Shihab Mahmud at a Wellington gas station.

Circuit Judge Joseph Marx sentenced Daniels, 25, to life in prison, the mandatory sentence for a first-degree murder conviction.

Appellate opinion (2021)

... we are satisfied that the trial court properly assessed and concluded that the DNA statistical interpretation performed by the **TrueAllele software program was reliable** after considering:

- (1) the theory or technique has been **tested**;
 - (2) the theory or technique has been subjected to **peer review and publication**;
 - (3) the known or potential **rate of error** for the program; and
 - (4) the **general acceptance** of the program.
- See *Daubert*, 509 U.S. at 593-94.

Appellate opinion (cont'd)

We are also satisfied that the trial court gave specific consideration to Appellant's argument regarding the **lack of internal validation** but concluded the argument and evidence did not merit excluding the TrueAllele evidence.

It is also particularly significant that the **defense expert** in this case was **not sufficiently familiar with the TrueAllele software** to effectively opine as to how the failure to internally validate the software using PBSO-generated test data compromised the reliability of the analysis of the DNA samples collected from clothing during the criminal investigation of this case.

More information

<http://www.cybgen.com/information>



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- Presentations
- Publications
- Webinars

<http://www.youtube.com/user/TrueAllele>
TrueAllele YouTube channel



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JUSTICE
THROUGH
SCIENCE
