

Defeating opposition experts: winning with science

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Opposition Arguments

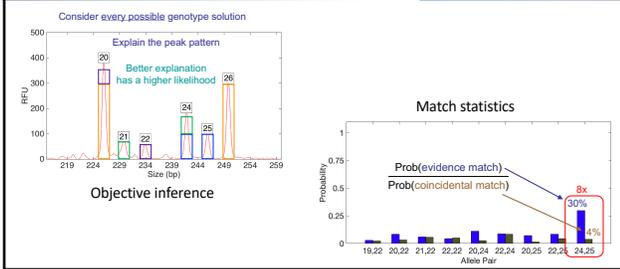


-  Method Reliability
-  Method Objectivity
-  Method Admissibility
-  Document Discovery
-  Irrelevant or Misconstrued Topics

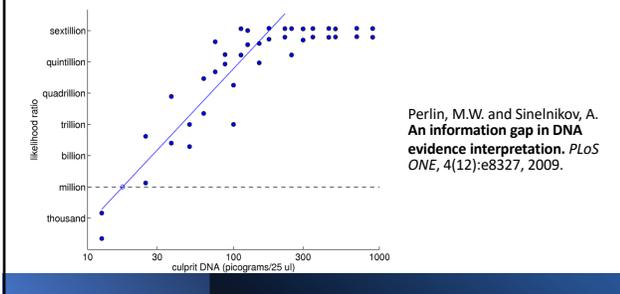
Admissibility Standards

<p>Frye (1920)</p> <ul style="list-style-type: none"> • general acceptance standard • "...while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs." 	<p>Daubert (1993)</p> <ul style="list-style-type: none"> • Whether the technique or theory in question can be, and has been tested; • Whether it has been subjected to publication and peer review; • Its known or potential error rate; • The existence and maintenance of standards controlling its operation; and • Whether it has attracted widespread acceptance within a relevant scientific community.
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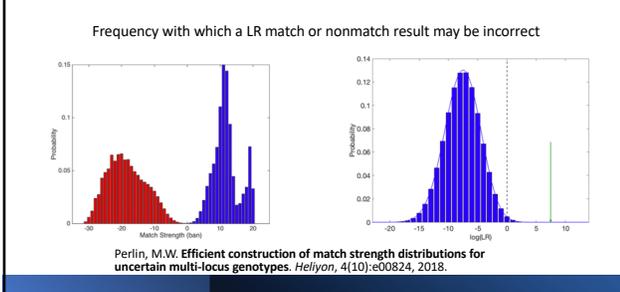
Probabilistic Genotyping (PG)



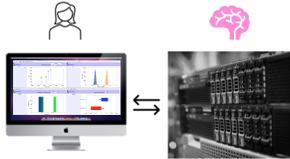
Likelihood Ratio (LR) Predictability



LR Error Rate



TrueAllele® Casework



- Uses all the data (no threshold)
- Limited human input/settings
- Parallel processing capability
- Can statistically include or exclude

TrueAllele Reliability

- Tested. 42 validation studies, 8 published
- Peer-reviewed. 8 validations, math, & methods
- Error rate. Established through validation and for reported LRs
- Standards. Complies with PG validation standards and guidelines
- Accepted. 46 states, 1,250 cases, 144 trials, 10 user labs
- Transparent. Documents, math, software provided
- Admissible. 41 rulings, 15 states and federal courts



Method Validation

False positives

In over 1,000,000 comparisons per group

- Empirically test method on data
- Calculate error rates (false inclusions, false exclusions)
- Stratify error rates

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)%

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

TrueAllele Validation

Study	1	2	3	4	5	6	7	8	SWGAM guideline
Sensitivity	1	1	1	1	1	1	1	1	3.2.1, 3.2.1.2, 4.1.13
False exclusions			1	1					3.2.1.1
Specificity			1	1	1		1	1	3.2.2, 3.2.2.2, 4.1.13
False inclusions			1	1			1		3.2.2.1
Reproducibility			1	1	1	1	1	1	3.2.3, 3.2.3.1, 4.1.13
Accuracy	1				1		1		3.2.6
Casework data						1	1	1	3.2.4, 3.2.4.1, 4.1.1
Known contributor data	1	1	1	1	1				4.1.1
Low-template DNA	1		1						4.1.6.2
Manual review comparison	1			1		1	1	1	3.2.6.1, 4.2, 4.2.1, 4.2.1.1
Peeling	1			1	1	1	1	1	4.1.2, 4.1.2.1
MCMC sampling				1	1				3.2.3.2
Contributor sufficiency				1	1				4.1.6.4
Invariant behavior				1					
Match statistic predictability	1			1	1				
Observed contributor number					1				

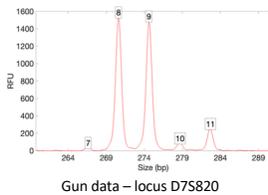
US v. Defendant

- 2020 shooting-related homicide in Washington, D.C.
- Gun and magazine recovered as evidence
- Defendant charged with crime



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US v. Defendant – Initial Analysis



Gun data – locus D7S820

Gun results

- At least 2 contributors
- Defendant excluded as major
- “Due to the possibility of allelic drop out, no conclusions can be made on the minor alleles.”

Magazine results

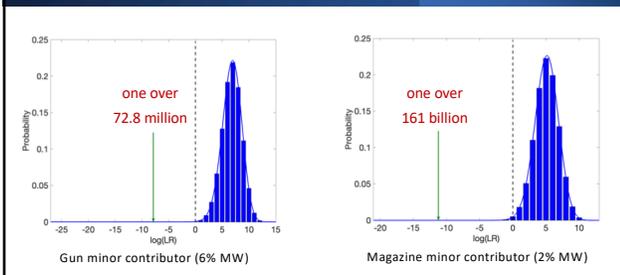
- 3 or more contributors
- Defendant excluded as major
- “Due to the limited data obtained, no conclusions can be made on the minor alleles that are not part of the major mixture.”

US v. Defendant – PG Analysis

- TrueAllele interpretation requested by defense attorneys
- PG analysis turned “inconclusive” data into informative results

Item	Description	Contributor	Defendant LR	LR Error Rate
5.1.1	gun	major	one over 36.1 duodecillion	1 in 1 googol people
		minor	one over 72.8 million	1 in 152 billion people
5.2.1	magazine	major	one over 24.3 undecillion	1 in 1 googol people
		middle	one over 145 nonillion	1 in 1 googol people
		minor	one over 161 billion	1 in 343 trillion people

US v. Defendant – LR Error Rate



US v. Defendant: Opposition Arguments

? Binary false exclusion rate

? Low-template DNA

? Contributor genotype separation

? Use of *match*

? Accreditation, validation, SWGDAM

Binary Error Rate

False exclusion percentage calculated from a few genotypes

TABLE 7.—Sensitivity varies with mixture weight. The true inclusion rate (one minus the false exclusion rate) based on positive log(LR) counts is shown for mixture weight ranges. There were a total of 280 observations, divided equally between the 1 ng and 200 pg DNA levels.

N=	Mixture Range, %	1 ng, %	200 pg, %
4	0-1	0	0
20	1-5	40	0
17	5-10	82	24
33	10-25	100	91
39	25-50	100	100
25	50-100	100	100
140			

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

Opposition Asserts

Opposition Fallacy

- TrueAllele has a very high false exclusion rate for minor contributors
- 60% false exclusion rate for 1-5% mixture contributors (magazine)
- 18% false exclusion rate for 5-10% mixture contributors (gun)
- High false exclusion rate applies to the reported minor contributors in this case
- PG report did not note the “unreliable” nature of the evidence

Binary Error Rate

Relevant binary error rate using case's software version

N=	Mixture Range %	count for LR<1	% for LR<1
20	1-5	7	35%
17	5-10	0	0%

With high template DNA, false exclusion error rate decreased from 60% to 35% for 1-5% mixture contributors (magazine)

Is binary error rate relevant?

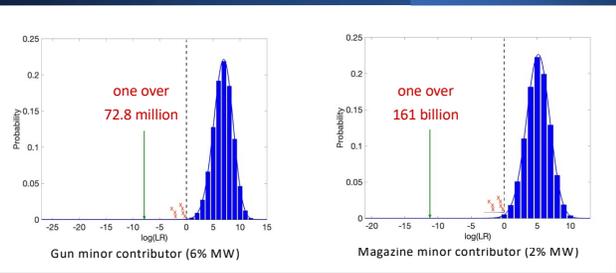


Stratified Error Rates

Source	Mixture Weight %	Exclusionary LR Statistic	log(LR)	Computed Exact LR Error Rate	log(PME)
Magazine	2.40	1 over 161 billion	-11.21	1 in 343 trillion	-14.54
Gun	5.89	1 over 72.8 million	-7.86	1 in 152 billion	-11.18
Validation	1.63	1 over 3,126	-3.49	1 in 1.21 million	-6.08
	1.08	1 over 412	-2.61	1 in 6.97 thousand	-3.84
	1.70	1 over 292	-2.47	1 in 23.3 thousand	-4.37
	1.32	1 over 25	-1.40	1 in 1.39 thousand	-3.14
	2.26	1 over 4	-0.60	1 in 490	-2.69
	1.65	1 over 3.5	-0.54	1 in 234	-2.37
	1.40	1 over 1.4	-0.15	1 in 341	-2.53

Error rate dependent on LR

LR Error Comparison



Stratified Binary Error Rates

(b) Contributor negative events

log(LR)	Observed contributor number				
	2	3	4	5	6
-2	0	0	0	0	1
-1	0	0	0	1	1
Total	0	0	0	1	2

Bauer, D.W., Butt, N., Hornyak, J.M., and Perlin, M.W. **Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors.** *Journal of Forensic Sciences*, 65(2):380-398, 2020.

Hornyak JM, Schmidt EM, Perlin MW. "Georgia Bureau of Investigation Forensic Biology Unit TrueAllele® Validation.", September 2016.

ncon	2	3	4	5
N =	8	12	16	20
False exclusions	0	0	0	6
min	3.386	1.357	0.968	-2.716
mean	11.991	5.513	5.002	2.356
max	15.643	12.150	13.383	13.186
std dev	4.095	3.194	3.575	3.671

Response to Opposition Motion Error Rate Statements

- ✘ Wrong LR software version study
- ✘ Wrong binary cutoff for false exclusion rate
- ✘ Considered too few genotype comparisons
- ✘ Ignored stratified error rates
- ✘ Misleading LR comparisons

Declaration Conclusion

"In conclusion, TrueAllele satisfies the Daubert prongs for the DNA mixture evidence in this case. The method clearly satisfies the error rate prong, with explicit reporting of low error rates for each reported LR statistic, using the best available error rate determination methods. There is no merit to the government's motion to preclude. TrueAllele should be admitted under the Daubert standard."



Admissibility Outcome

"The Court denies the government's motion to preclude evidence of a defense analysis that excluded the defendant as a contributor to the minor components of DNA obtained from a firearm and a magazine. The government's objections go to weight, not admissibility."



Questions?

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