

Overcoming Unscientific Opposing Arguments using Relevant Data

American Academy of Forensic Sciences
77th Annual Meeting
Baltimore, Maryland
February, 2025

Jennifer M. Bracamontes, MS
William P. Allan, MS
Mark W Perlin, PhD, MD, PhD



Cybergenetics © 2003-2025

Disclaimer and Disclosure

The views, statements, and content offered in this presentation are solely the work of the presenting author and any co-authors, and does not necessarily reflect any opinions, stances, standards, statements, or policies of the American Academy of Forensic Science. The content has not been reviewed or endorsed by the Academy, its staff, officers, or program leadership.

Cybergenetics created and sells TrueAllele® Casework technology and services. Jennifer Bracamontes and William Allan are employees of Cybergenetics. Dr. Mark Perlin is an owner/officer of Cybergenetics.

Non-contributor distribution

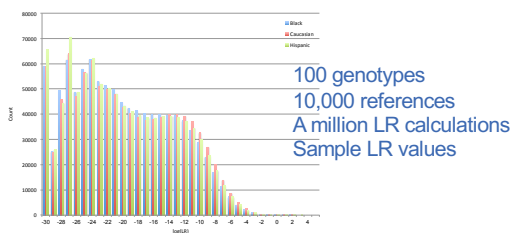
OPEN ACCESS [Freely available online](#)



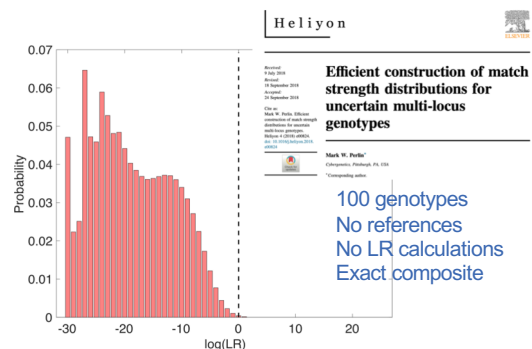
TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases

Mark W. Perlin^{1*}, Kiersten Dörner², Jennifer Hornyak¹, Lisa Schiermeier-Wood², Susan Greenspoon²

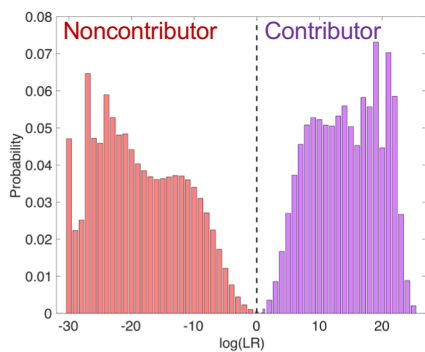
¹ Cybergenetics, Pittsburgh, Pennsylvania, United States of America, ² Department of Forensic Sciences, Richmond, Virginia, United States of America



Exact non-contributor distribution



Dual exact LR distributions

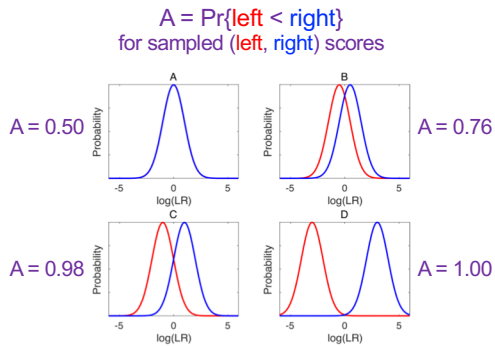


Opposition argument

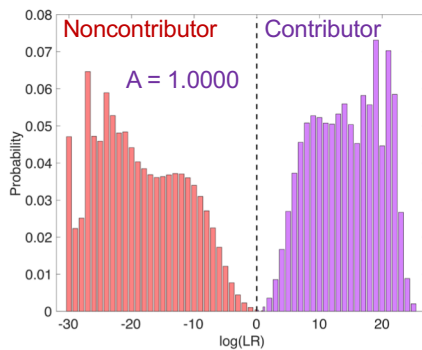
“Ground truth” laboratory data is needed to validate a probabilistic genotyping system (PGS).

LR distributions show this isn't so.

Classification accuracy



Accuracy = 1, Perfect Classifier



Validate on casework data

“Since the [TrueAllele] method’s high *specificity* assures identification hypothesis H with considerable certainty, we can safely examine the $\Pr\{X=x \mid H\}$ *sensitivity* distribution of positive log(LR) values.”
- PLOS ONE 2014 Virginia validation study

Similarly, high *sensitivity* lets us safely examine the *specificity* distribution of negative log(LR) values.

PGS doesn’t need “ground truth”
to construct LR distributions.

United States v Curtis Johnson

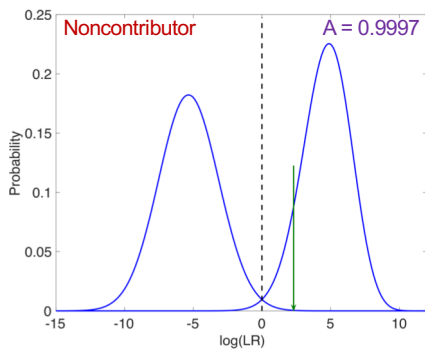
- In 2013, men robbed an armored truck outside a New Orleans bank, killing the truck guard in a shootout.
- A bandana was collected from the crime scene
- A 70 pg sample was a three-person mixture
- TrueAllele separated out bandana genotypes
- Comparing a 27% contributor with Johnson, **LR = 200**
- 2021 – *Daubert* hearing, TrueAllele admitted, first trial
- 2022 – Second trial, guilty verdict, 50-year sentence

Opposition argument

Low LR values are unreliable.

LR distributions show this isn't so.

Distribution gives LR error rate



Report LR error rate

A match between the bandana and Johnson
is 200 times more probable than coincidence.

For a match strength of 200, only 1 in 4.1
thousand people would match as strongly.

$$ER \leq 1/LR$$
$$1/4100 \leq 1/200$$

United States v Alejandro Sandoval

- Police collected a baggie containing methamphetamine
- Defense tested baggie, found a DNA mixture
- Two different PG software programs used
- Unsuccessful *Daubert* attempt to challenge OPG
- Plea agreement dropped the more serious charge
- JFS published a speculative “Case Report”



LETTER TO THE EDITOR | [Open Access](#) | CC BY-NC-ND 4.0

Commentary on: Thompson WC. Uncertainty in probabilistic
genotyping of low template DNA: A case study comparing
STRmix™ and TrueAllele®. J Forensic Sci. 2023;68(3):1049–63

Mark W. Perlin PhD, MD, PhD Nasir Butt PhD, Mark R. Wilson PhD

First published: 25 April 2024 | <https://doi.org/10.1111/1556-4029.15518> | Citations: 1

Opposition argument

TrueAllele and Other PG (OPG)
can give different LR results.
So PGS isn't reliable!

LR distributions show this isn't so.

Analytical thresholds

OPG

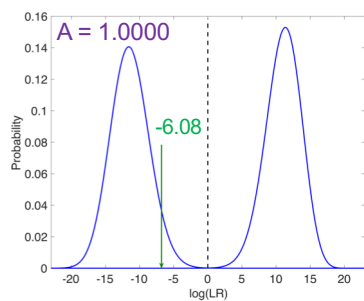
Threshold (rfu)	Data peaks	log(LR)
90	11	-0.53 ban
40	24	-1.38 ban (reported)
20	38	-7.48 ban

TrueAllele

Threshold (rfu)	Data peaks	log(LR)
none	210	-6.08 ban

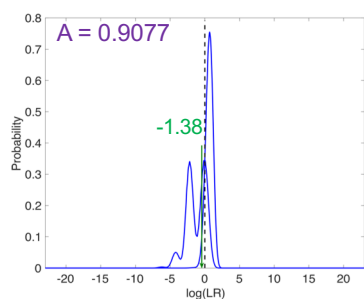
TrueAllele distribution pair

No AT, 210 data peaks



OPG distribution pair

AT = 40 rfu, 24 data peaks



United States v Ravel Mills

- 2020 shooting-related homicide in Washington, D.C.
- Gun and magazine recovered as evidence
- Gun: **6% component** of a **three-person** mixture
 - $\log(\text{LR}) = -7.86$, $\log(\text{ER}) = -11.18$
- Magazine: **2% component** of a **four-person** mixture
 - $\log(\text{LR}) = -11.21$, $\log(\text{ER}) = -14.54$
- Federal prosecutor requested *Daubert* hearing
- Typical defense expert attack: old-style binary logic
- TrueAllele won "on the papers", no hearing needed

Opposition argument

TrueAllele's own validation study
shows high LR error rates.
Thus the PGS isn't reliable!

LR distributions show this isn't so.

TrueAllele validation study

JOURNAL OF FORENSIC SCIENCES
J. Forensic Sci., July 2015, Vol. 60, No. 4
doi: 10.1111/1556-4029.12788
Available online at: onlinelibrary.wiley.com

PAPER
CRIMINALISTICS

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

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

Opposition argument

Binary error rate (LR < 1 or LR > 1)
in the case's actual software version

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

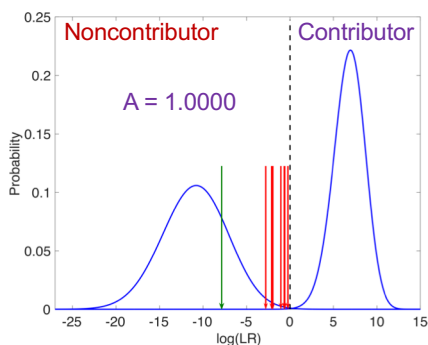
Binary error rates are simplistic and irrelevant

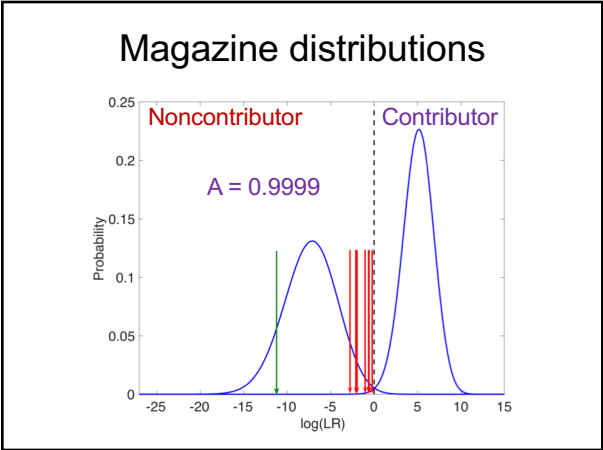
1. The likelihood ratio is quantitative
2. Error rate depends on LR magnitude

Error rate depends on LR

Source	Mixture Weight %	log(LR)	log(ER)
Gun	5.89	-7.86	-11.18
Magazine	2.40	-11.21	-14.54
Validation	1.63	-3.49	-6.08
	1.08	-2.61	-3.84
	1.70	-2.47	-4.37
	1.32	-1.40	-3.14
	2.26	-0.60	-2.69
	1.65	-0.54	-2.37
	1.40	-0.15	-2.53

Gun distributions





Conclusions

How to rebut unfounded PGS opposition arguments

1. Use fully Bayesian PGS on all STR data (no threshold)
2. Separate mixtures into accurate contributor genotypes
3. Report all inclusionary and exclusionary LR
4. Use LR distributions to report LR error rates
5. Respond to bad arguments with good LR science

 Cybergenetics
