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# **Opposition argument**

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

LR distributions show this isn't so.









## 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 | 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.

# 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







# 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 ≤ 1/LR** 1/4100 ≤ 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"

### FORENSIC SCIENCES

LETTER TO THE EDITOR I ⓐ Open Access i ⊕ ④ ⊙ ⊗ 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. Merin PD, MD, Pholog, Nast But Phol. Mark R. Wilson Pholog

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.

tical thr	esholds
Data peaks	log(LR)
11	-0.53 ban
24	-1.38 ban (reported)
38	-7.48 ban
Data peaks	log(LR)
210	-6.08 ban
	<b>Data peaks</b> 11 24 38 <b>Data peaks</b> 210











# 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(LR)= -7.86, log(ER)= -11.18
- Magazine: 2% component of a four-person mixture
  log(LR)= -11.21, log(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.

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# **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

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











# 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 LRs
- 4. Use LR distributions to report LR error rates
- 5. Respond to bad arguments with good LR science

**Cybergenetics** 

