



All mixed up: responding to flawed opposition case reports on complex DNA evidence

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Abstract

Low-level DNA mixtures can be important forensic evidence. In a recent federal case, a California man was accused of drug possession. The defense lawyer requested DNA testing. Cybergenetics' TrueAllele® system found strong exclusionary likelihood ratios (LR) of a millionth. STRmix™ software found weak LR values near one tenth. The prosecutor retained opposition expert William Thompson, who used the numerical discrepancy to harshly criticize TrueAllele. Who was right?

Fully Bayesian TrueAllele examined all the DNA mixture data to find reproducible match statistics. Probabilistic genotyping (PG) STRmix software only saw about 10% of that data, insufficient for a conclusive answer. Both programs were right, based on different methods and data. Thompson's case report raised many irrelevant claims, but it ignored the data amounts and betrayed little understanding of PG methods. His report was completely wrong.

The scientific portion of this poster corrects Thompson's mischaracterizations, presenting the PG methods accurately. A STRmix sensitivity study of peak height thresholds shows how different data inputs yield LR values spanning 12 orders of magnitude.

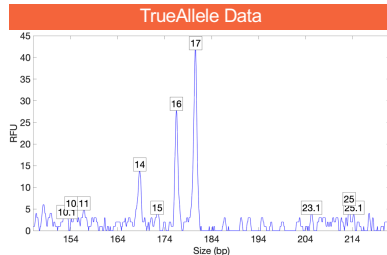
The response portion builds on this science to explain why Thompson is mistaken. The poster examines many of his conceptual errors, drawing from a rebuttal of 120 assertions.

Poster highlights include:

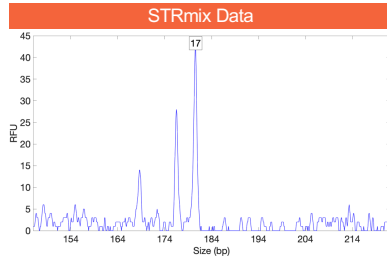
- TrueAllele and STRmix probabilistic genotyping software both analyzed the same low-level two-person mixtures at a defendant's request.
- Both programs found exclusionary results, with Cybergenetics reporting TrueAllele LR values around one millionth, and a lab reporting STRmix LR values near one tenth.
- TrueAllele used all data at 21 STR loci, while STRmix was limited to 24 peaks over 14 loci, a density of 1.7 peaks per locus, insufficient for informative mixture analysis.
- A sensitivity study on varying data thresholds found STRmix LR values ranging over 12 orders of magnitude, far greater than any difference with TrueAllele.
- Thompson's case report was unfounded and inaccurate. 120 of his statements warranted response.

Defendants are entitled to meaningful DNA evidence. With low-level mixtures, entering more data and updating more variables can potentially deliver more exculpatory LR information. Thompson advised crime labs to "punt" when they can't interpret DNA. But using more effective software, they can go for the goal of truth.

Data



At locus vWA, TrueAllele considers 10 data peaks applying no threshold. In total, TrueAllele considered 210 data peaks across all 21 loci.



At locus vWA, STRmix considers only 1 data peak above the 40 rfu threshold.

STRmix analysis applied a 40-rfu peak height threshold to the mixture of two people. Just 24 data peaks were input for 14 loci (1.7 peaks per locus). But a two-person mixture can have up to 4 allelic peaks per locus.

Locus	Allele	Height	Size
D1S1656	15	106	184.1
D1S1656	15.3	52	187.1
D2S441	11	140	88.99
D2S441	14	87	101.1
D2S1338	23	51	328.5
D3S1358	15	170	121
D3S1358	18	113	133.1
D5S818	10	68	150.6
D5S818	12	126	158.9
D8S1179	11	54	138.4
D8S1179	14	50	150.8
D10S1248	13	191	105.6
D10S1248	14	56	109.6
D10S1248	16	185	117.5
D12S391	22	62	247.7
D13S317	12	107	226.9
D19S433	14.2	102	150.9
D19S433	15.2	124	154.9
D21S11	29	77	202.9
D21S11	30	83	206.9
D22S1045	15	276	109.3
FGA	21	48	255.8
FGA	26	44	275.9
vWA	17	46	180.6

Data peak table showing the 24 peaks considered by STRmix across 14 loci.

Match Statistics

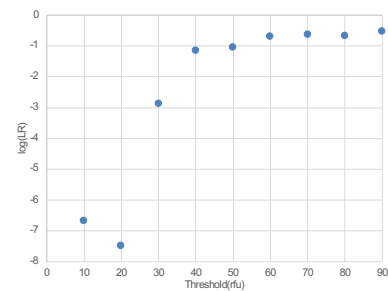
Evidence	Contributor	Weight	Std Dev	-KL (nom)	KL (con)	log(LR)
3_ncon2_dgrd_100K	1	0.8	0.33	-15.36	13.25	-9.60
3_ncon2_dgrd_100K	2	0.4	0.33	-9.78	8.26	-3.96
3_ncon2_dgrd_100K_rep1	1	0.45	0.27	-11.64	9.45	-5.49
3_ncon2_dgrd_100K_rep1	2	0.55	0.27	-13.97	12.07	-7.72
3_ncon2_dgrd_100K_rep2	1	0.54	0.56	-11.63	11.38	-6.68
3_ncon2_dgrd_100K_rep2	2	0.46	0.56	-11.35	9.19	-4.92

TrueAllele Match Table. This table displays the TrueAllele results showing both the inferred mixture weight and log(LR) match statistics. TrueAllele uses all of the peak data.

Threshold	Data Count	log(LR)
90	8	11
80	9	13
70	9	14
60	10	16
50	12	21
40	14	24
30	16	29
20	18	38
10	19	54
0	21	210

STRmix Sensitivity Study. STRmix was provided peak data at 10 different thresholds ranging from 0 to 90 rfu. Once STRmix was provided all of the peak data its exclusionary statistic decreased and produced similar results to TrueAllele's match statistic.

When given enough data, STRmix produced a similar answer to TrueAllele. For example, at a lower threshold of 10 rfu, the STRmix sub-source log(LR) is -6.68. This value is close to TrueAllele's average log(LR) of -6.29 across 6 genotypes.



STRmix Sensitivity Study. The scatterplot shows rfu threshold vs. STRmix sub-source log(LR).

Analogy

Fuel Tank Analogy: A Car Without Gas

Which goes further, a car with gas or a car without gas?

Two cars being tested for distance. The blue car has a full tank while the red car's gas tank is almost empty. Is this a meaningful comparison?



Full tank
All data peaks



Empty tank
10% data peaks

An analogy can provide context for this complex issue. In this case, one can compare data to fuel. Is it a fair comparison to test two cars for distance when one has a full tank of gas, while the other has a nearly empty tank? Of course not; a car running on empty is at a disadvantage.

This analogy is similar to comparing TrueAllele and STRmix in this case, where TrueAllele uses all of the data, but a threshold limits STRmix data. With far fewer peaks, STRmix would not be expected to reach the same answer. Just as a car without gas would not travel as far as a car with a full tank.

Conclusions

- TrueAllele and STRmix both reached exclusionary results in this case.
- Their difference in match statistics is largely accounted for by the amount of data used.
- When given more peak data, STRmix found more exclusionary results.
- Mixture weight can not be accurately determined from insufficient peak data.
- The opposition report lacks scientific merit – it does not take into account the differences in input data.
- Cybergenetics responded to over 120 points in an SSRN paper. This poster focused on the vastly different data input amounts.
- For more details, please refer to the SSRN report cited below.

Reference

[1] Perlin, Mark W., Allan, William P., Bracamontes, Jennifer M., Danser, Kari R., and Legler, Matthew M. Reporting Exclusionary Results on Complex DNA Evidence, A Case Report Response to 'Uncertainty in Probabilistic Genotyping of Low Template DNA: A Case Study Comparing STRmix™ and TrueAllele® Software (May 18, 2023). Available at SSRN: <https://ssrn.com/abstract=4449313> or <http://dx.doi.org/10.2139/ssrn.4449313>