



April Newsletter

Better Justice Through Better Science™

Newsflash

- [*JFS Response Letter explains why TrueAllele*](#) works better than other DNA software
- [*How labs should report threshold-limited results*](#) on complex DNA evidence
- [*When you need to contact Cybergenetics*](#) for getting more DNA information

***TrueAllele connects victim to
basement concrete in cold case
homicide conviction***



Concrete DNA Evidence

In 2002, a man's burned remains were found in a metal locker near a Michigan blueberry field. Ten years later, police identified the remains as Roberto Caraballo. Other evidence suggested he was murdered in his basement. Detectives suspected the victim's wife, Beverly McCallum, and two others.

The Michigan State Police Crime Laboratory found possible blood under new concrete poured in the basement. They swabbed the concrete. DNA testing generated new evidence data. The crime laboratory couldn't draw conclusions from the concrete DNA evidence, due to the complexity of the mixture data.

On the same data, Cybergene's TrueAllele computer found the victim's DNA in the concrete. He was statistically present in the concrete bloodstain with a match number of 23.9 trillion.

On March 27, 2024, Cybergene's Casework Supervisor William Allan testified about the TrueAllele results before an Eaton County jury. After deliberating for two hours, the jury found McCallum [guilty of second-degree murder](#) and disinterment and mutilation of a body.

[Trial Page](#)

***TrueAllele solves uninterpretable
DNA in mother and daughter***

double homicide



On February 15, 2023, Allegheny County police found the bodies of Megan Campbell (39) and her 7-year-old daughter Lyla. Barricaded in their Swissvale apartment, the Pennsylvania women had been shot in the head at close range. The detectives saw signs of a struggle.

Investigators collected evidence: a pistol, two dumbbells (used to barricade the door), an overturned chair, a coat, and a t-shirt. The Medical Examiner's Office produced DNA data from the items. Fingerprints were found on the weapon, and ballistics matched the firearm.

On these probative DNA evidence items, the Crime Laboratory reported that "due to the data being uninterpretable, no comparison can be made to the reference samples." The District Attorney's Office then contacted Cybergenetics for assistance.

On the same "uninterpretable" DNA data, TrueAllele got answers. The computer unmixed the mixtures, which contained as many as five contributors. TrueAllele then compared the unmixed evidence with the two victims and suspect Kareef Easington. Some items showed DNA from all three people. TrueAllele found Easington's DNA on all six evidence items. His strong match statistics ranged from a trillion to two decillion (a 1 followed by 33 zeros).

On April 15, 2024, Cybergenetics Casework Manager Jennifer Bracamontes testified about the TrueAllele results at the Allegheny County Courthouse in Pittsburgh. The next day, the jury found Easington [guilty of two counts of](#)

Journal of Forensic Sciences publishes response Letter to Case Report

On April 26, the *Journal of Forensic Sciences* (JFS) published a *Letter* by Cybergenetics Chief Scientist Dr. Mark Perlin, Cuyahoga County Crime Lab's Dr. Nasir Butt, and George Mason University's Dr. Mark Wilson. The thousand-word [open-access article](#) is a "*Commentary on: Thompson WC. Uncertainty in probabilistic genotyping of low template DNA: A case study comparing STRmixTM and TrueAllele[®]. J Forensic Sci. 2023;68(3):1049–63.*"

Our [Letter](#) "briefly explains why the two software results differed" on drug package DNA evidence in a California criminal case. "Cybergenetics TrueAllele[®] probabilistic genotyping (PG) software found a strong exclusionary match statistic for the defendant of one over 1.2 million. ESR's STRmixTM PG program produced a weaker exclusionary match statistic of one over 24."

Why? Because "the two programs were given *different* amounts of STR **input data**. TrueAllele is a fully Bayesian system capable of looking at *all the peak data* without data thresholds." But STRmix "applies *peak height thresholds* to limit the amount of input data. TrueAllele used 210 data peaks" while "the STRmix program saw 24 peaks. The **88% reduction** in STRmix data peaks, relative to TrueAllele input, accounts for the observed likelihood ratio (LR) output differences."

Threshold Sensitivity Study

Threshold (rfu)	CA v Defendant		NY v Hillary	
	LR	log(LR)	LR	log(LR)
90	1 over 3.35	-0.53		
80	1 over 4.75	-0.68	0	-Infinity
70	1 over 4.37	-0.64	30	1.48
60	1 over 4.90	-0.69	250	2.40
50	1 over 11.4	-1.06	15.5 million	7.19
40	1 over 13.9	-1.14	0	-Infinity
30	1 over 741	-2.87	0	-Infinity
20	1 over 30.5 million	-7.48		
10	1 over 4.8 million	-6.68		
0	0	-Infinity		

In two cases, STRmix results range over six orders of magnitude, depending on the threshold. Bold indicates the reported likelihood ratio (LR) match statistic.

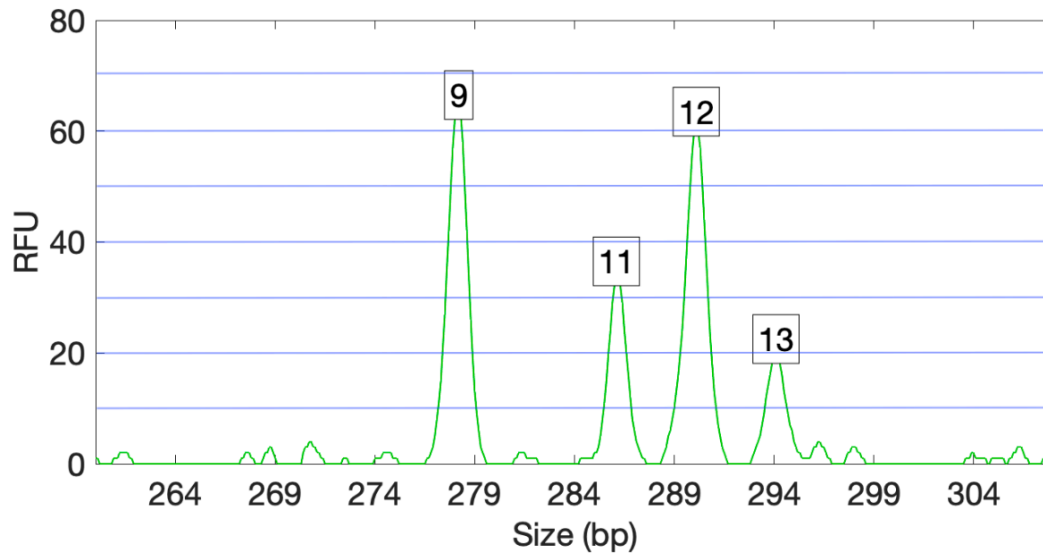
In the *Letter's* sensitivity study, “we tested STRmix on the STR data at *different thresholds*. The weakest STRmix LR value was 1 over 3.35 (using 11 peaks at a high 90 rfu threshold). The strongest LR was 1 over 30.5 million (38 peaks at a low 20 rfu threshold). Less STRmix input data gave less output identification information; more data yielded more information.” (See the table above.)

“At a 10 rfu threshold (54 peaks), the STRmix LR of one over 4.8 million was close to TrueAllele's reported one over 1.2 million. Given more data, STRmix got about the same LR results as TrueAllele. The difference in *data input* explains the difference between the reported TrueAllele and STRmix LR values in this case.”

“TrueAllele can use more data from low-template DNA than other programs because its hierarchical modeling obviates the need for peak height thresholds.” As is well known in science and statistics, “considering more STR data derives more LR information.”

Journal of Forensic Sciences

How to use threshold-based DNA software on low-level mixture evidence



The blue lines indicate different peak height data thresholds.
Higher data thresholds discard more DNA evidence data.

Our JFS [Letter's](#) threshold analysis above raises an interesting question. When can STRmix and other data-discarding threshold PG software be safely used on low-level DNA mixtures?

In both the *Letter's* California case and [New York v. Hillary](#), varying the threshold changed STRmix LR values a million-fold (see table). The STRmix results that were reported at only one threshold level were unhelpful to the defendants. Yet at lower thresholds (that used more data) other STRmix LR values were exculpatory. STRmix contradicted itself.

TrueAllele, which has no threshold parameter, simply *used all the data* to accurately exclude the defendants from the DNA evidence. No threshold, no contradiction. Just science.

Clearly one preset threshold is not enough. STRmix needs to have a *threshold sensitivity study* conducted whenever it is used on low-level DNA mixtures. A court needs to know how changing STRmix input data affects its LR information output.

Disclosing only one of many self-contradictory results is unfairly prejudicial, potentially confusing, a waste of time, and can mislead a jury. A STRmix prosecutor or defender should reveal the full spectrum of LR results over a range of threshold parameter values. Or [contact Cybergenetics](#) for an accurate TrueAllele answer.

[Free Screening](#)

***When you need to contact
Cybergenetics for***

a DNA reassessment

Crime labs can get [the wrong DNA answer](#). Following their protocols, some labs won't test small amounts of DNA. Or won't interpret mixtures containing more than several contributors. Other labs use DNA interpretation software whose threshold parameters discard crucial DNA data. The result can be an inaccurate match statistic, or unreported DNA evidence.

The [pioneering](#) TrueAllele technology gives an accurate unbiased answer to hard DNA questions. Our advanced math means no thresholds, just using all the data all the time. Multi-level modeling accounts for all relevant variables, without needing calibration. TrueAllele corrects the interpretation mistakes that other DNA programs make.

Contact Cybergenetics for [free TrueAllele screening](#) when a crime lab:

1. Reports DNA evidence as “uninterpretable”, “uninformative”, draws “no conclusions”, or calls the data “too complex”.
2. Says there is “insufficient DNA”, “too many contributors”, or that “no comparison can be made”.
3. Uses limited FBI PopStats software for [inaccurate](#) DNA mixture interpretation.
4. Applies peak height thresholds to their DNA data, discarding probative evidence.
5. Runs limited probabilistic genotyping software (e.g., STRmix, LRmix, EuroForMix) to get small DNA match numbers, “inconclusive” results, or no result at all.
6. Cannot process DNA data from older, unfamiliar, or multiple STR kits.

In over a thousand criminal and civil cases, Cybergenetics' better TrueAllele science has overcome these artificial limitations.

[Contact Cybergenetics](#)

***Cybergenetics makes available
a new TrueAllele Reliability
web resource***



Supporting information about TrueAllele reliability.

Jump to a section:

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Background Readings

Glossary: A glossary of terms

Newspaper articles

- [How TrueAllele is used for forensic DNA evidence \(June, 2011\)](#)
- [TrueAllele was used in a terrorist case \(February, 2012\)](#)

In dozens of successful admissibility challenges, Cybergenetics has provided over a hundred documents that help establish the reliability of TrueAllele evidence. This month, we posted those documents on our website in a new [TrueAllele Reliability](#) webpage.

You can download most of the documents directly from the Reliability page. When there is a copyright restriction, we provide a link to the publisher.

Our [Reliability](#) webpage makes TrueAllele's foundational reliability available to forensic scientists and the general public. We hope you find this new resource helpful and informative.

[TrueAllele Reliability](#)

Cybergenetics to present three talks at MAAFS Annual Meeting in Pittsburgh

Cybergenetics will be attending the 2024 *Mid-Atlantic Association of Forensic Scientists* (MAAFS) conference at the Sheraton Station Square in Pittsburgh, Pennsylvania held May 6th to 10th. Cybergenetics scientists will be presenting three talks:

Defeating opposition experts: winning with science (Jennifer Bracamontes)

An opposition expert's argument may confuse a judge or jury. In a recent criminal case, the DNA opponent undermined probabilistic genotyping error rates. They misread a published validation study to incorrectly find a high error rate. This talk shows our successful response to the flawed attack.

Getting more from less: low-level DNA mixtures on cartridges (Kari Danser)

How much identification information can be recovered from firearm cartridges? Our study examined DNA data from different casing materials and collection methods. On the same STR data, we compared TrueAllele[®] computer interpretation with simple allele counting. TrueAllele measured more information and found previously unidentified contributors.

The same DNA answer: everything everywhere all at once (William Allan)

The objective TrueAllele[®] genotyping computer gets the same DNA match statistics, regardless of laboratory or analyst. The identification information doesn't depend on sequencer or STR kit. TrueAllele learns lab parameters from evidence data without calibration. Our multi-center study shows that analysts everywhere get everything at once from all their DNA data.

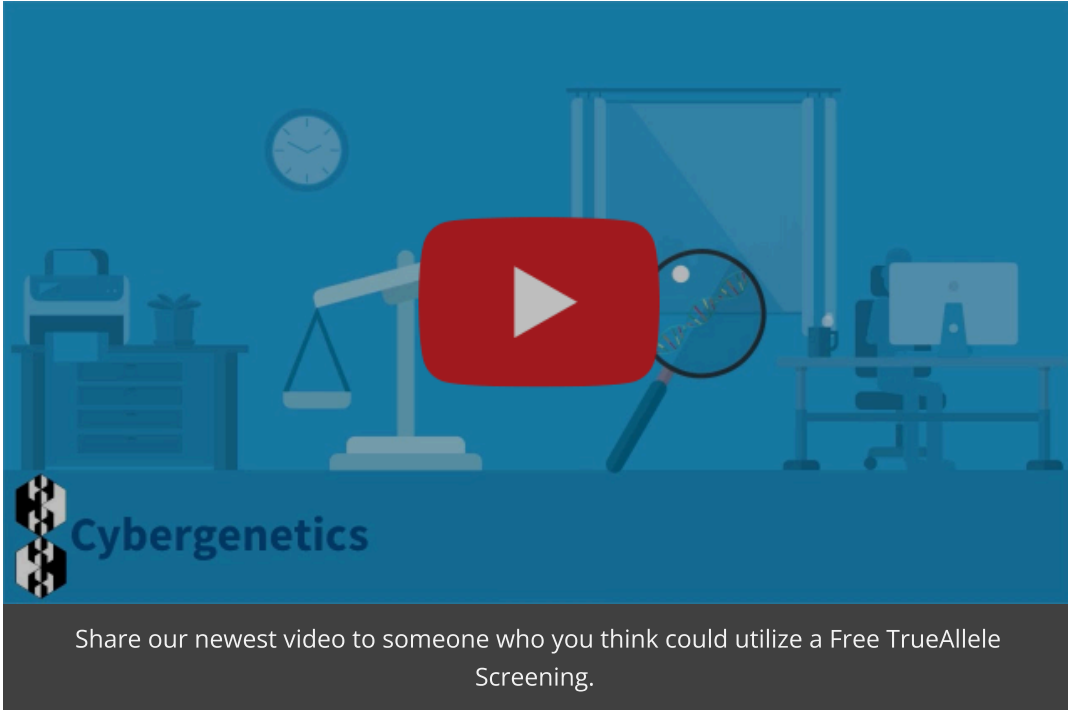
Presentations

Upcoming Conferences

This month, Cybergenetics attended the *Wisconsin Association of Homicide Investigators* conference in the Wisconsin Dells, Wisconsin. We spoke with hundreds of crime investigators about how TrueAllele technology and services can help them solve their toughest cases.

Next month, Cybergenetics will be attending the *New Jersey Homicide Investigators Association* conference in Princeton, New Jersey, June 10th to 14th. Stop by our trade booth to learn how TrueAllele technology can help solve your most complex DNA cases.

Free Screening



The banner features a blue background with a white play button in the center. Behind the play button are faint icons of a clock, a scale of justice, a magnifying glass, and a computer workstation. The Cybergenetics logo is in the bottom left corner. Below the banner, a dark grey bar contains the text: "Share our newest video to someone who you think could utilize a Free TrueAllele Screening."

 Share  Tweet  Forward

Free TrueAllele Screening

Contact Cybergenetics today, making the impossible routine™

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