Supreme Court of New Jersey

DOCKET NO. 085463

STATE OF NEW JERSEY, Plaintiff-Petitioner, v. COREY PICKETT, Defendant-Respondent,	Criminal Action On Motion for Leave to Appeal from an Interlocutory Order of the Superior Court of New Jersey, Appellate Division. Sat Below: Hon. Douglas M. Fasciale, P.J.A.D. Hon. Garry S. Rothstadt, J.A.D. Hon. Ronald Susswein, J.A.D.

BRIEF AND APPENDIX ON BEHALF OF THE ATTORNEY GENERAL AMICUS CURIAE

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OF COUNSEL AND ON THE BRIEF

TABLE OF CONTENTS

PAGE

TABLE TO APPENDIX

TABLE OF AUTHORITIES

PAGE

CASES

OTHER AUTHORITIES

PRELIMINARY STATEMENT

The Appellate Division’s published decision in this case is based on faulty logic, rejected science, and incorrect assumptions. While rejecting well-accepted validation studies and peer-reviewed articles, the Appellate Division inappropriately required the State to prove that TrueAllele is infallible.

The State provided defendant with a plethora of information concerning the reliability and validation of TrueAllele, a forensic science tool. But defendant challenged TrueAllele’s reliability on computer-science grounds and requested a review of TrueAllele’s proprietary source code. Although the trial court correctly denied defendant’s motion to compel the source code, the Appellate Division relied on errors found in software that was not TrueAllele, and a report that the forensic-science community has rejected, to question TrueAllele’s reliability and order source-code review.

The Appellate Division failed to appreciate that the errors relied were discovered by testing the software and that blind source-code review has never uncovered any errors in probabilistic genotyping software. Further, the panel dismissed the value of the decisions in other jurisdictions addressing the same issue as an “authority ‘house of cards,’” even though those courts had held testimonial hearings and properly exercised their gatekeeping functions.

Additionally, while relying on the independent testing standards advanced in a report that has been rejected, the panel diminished validation studies because they involved law enforcement crime laboratories and were therefore not independent. The Court did, however, not address that in the numerous cases where TrueAllele has been admitted in other jurisdictions, a defendant admitted it, resulting in not guilty verdicts or exonerations. If reliability was not an issue in those cases, it should not suddenly become an issue because it is the State that now seeks to introduce the very same evidence.

Although the Appellate Division's faulty logic must be addressed to allow reliable evidence in this case to be admitted, an overly broad reading of the panel’s holding must also be stopped. Indeed, the published decision in this case is already being invoked as authority for compelling source codes beyond probabilistic genotyping or DNA evidence. This Court’s guidance and intervention is necessary and leave to appeal should be granted.

STATEMENT OF PROCEDURAL HISTORY AND FACTS[1]

The Attorney General relies on the procedural history and facts outlined in the State’s brief and adds the following.

Following a shooting that occurred in Jersey City on April 16, 2017, defendant, Corey Pickett, and Jonathan Ferrara were indicted by the Hudson Grand Jury for first-degree murder and related crimes. (Pa1-6)[2].

Jersey City Police officers witnessed the incident in proximity and apprehended defendant and Ferrara after they fled. (Pa53). The paths on which they fled, police found a Colt .45 caliber semi-automatic handgun, a .38 caliber Smith and Wesson Revolver, and a ski mask. (Pa54). The items found were forwarded to the New Jersey State Police Office of Forensic Science for forensic analysis. Ibid.

On April 20, 2018, the State Police laboratory issued a report concluding that defendant was the major DNA contributor to the profiles obtained from two specimens from the ski mask. Ibid. The information collected from the laboratory was then sent to Cybergenetics Corp. Laboratory for analysis using its proprietary TrueAllele software. (Pa55).

On July 3, 2018, the results from TrueAllele showed that Ferrara’s DNA was not present on any of the items submitted for

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[1] The Statement of Procedural History and Statement of Facts have been combined for clarity.

[2] Pa refers to the State’s appendix.
Sb refers to the State’s brief.
Aa refers to the Attorney General’s Amicus appendix.

analysis, but defendant’s DNA was present on the Smith and Wesson revolver and the ski mask. Ibid.

On February 5, 2019, the State filed a motion to admit the DNA analysis results using the TrueAllele software. (Pa58).

A Frye[3] hearing was held in April 2019. The direct examination included two days of testimony from Dr. Mark W. Perlin of Cybergenetics. (Pa59). The State also introduced fifteen pieces of evidence that contained materials on validation papers and studies, forensic application of TrueAllele, regulatory approval, method reports, admissibility rulings, general acceptance, legal commentary, scientific development, and other related materials. (Pa24).

On July 1, 2019, the previous attorney for defendant filed a motion to withdraw as counsel, and the case was referred to the Office of the Public Defender (OPD). (Pa22-24). Defendant’s attorneys from the OPD submitted a notice to compel TrueAllele’s proprietary source code. (Pa59). The State and defendant tried to negotiate terms of a protective order, but the parties could not reach an agreement. (Pa64, 67).

On June 23, 2020, the Honorable Patrick J. Arre, J.S.C., entered an order denying defendant’s motion to compel the proprietary source code for TrueAllele. (Pa40-45). Defendant appealed the decision. The Attorney General appeared as amicus curiae in the Appellate Division.

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[3] Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).

On February 3, 2021, the Appellate Division reversed the trial court's denial of the motion to compel the source code and related materials in a published decision. (Pa46-119). The Court remanded the case to the trial court and directed the trial court to compel discovery of TrueAllele's proprietary source code under a protective order with the conditions and considerations discussed in its opinion. Ibid.

The State filed a motion for reconsideration of the Appellate Division decision, which was denied by an order entered March 2, 2021. (Pa120-24). The State then filed an emergent request for a stay to permit the filing of a motion for leave to appeal before this Court. This Court granted the stay on March 4, 2021. (Pa125-26). This Court also invited amicus curiae briefs in support or in opposition to the State's motion to be filed by March 22, 2021. (Pa125).

LEGAL ARGUMENT

POINT I

LEAVE TO APPEAL SHOULD BE GRANTED TO PREVENT IRREPARABLE INJURY TO THE STATE AND TO PREVENT AN INACCURATELY BROAD READING OF THE APPELLATE DIVISION'S PUBLISHED OPINION.

As set forth more fully in Point II, the decision that TrueAllele's proprietary source code is necessary for a finding of general acceptance exceeds the requirements under Frye and is based on broad assumptions and inaccurate information. But whatever this Court's ultimate conclusion on the merits, this motion presents an undeniably critical issue of statewide importance this Court needs to address. The Court should step in to prevent an impermissibly overbroad reading of the Appellate Division's decision that goes beyond this case's DNA context. The Attorney General thus urges this Court to grant the State's motion for leave to appeal so as to prevent the expansive application of a decision involving a specific software in a specific field and stop the potential chilling effect of the use of technology in New Jersey courts.

The State used reliable and widely accepted technology to determine that defendant's DNA was present on the handgun and ski mask discovered on his path of flight taken while being chased by police following a shooting. Defendant challenged the admissibility of those results and the general acceptance of the TrueAllele software because he did not have the opportunity to review the proprietary source code. The Appellate Division erroneously relied on misinformation while ignoring the precedent and standards of the relevant scientific community to determine that in order for TrueAllele to be generally accepted in New Jersey, its creator must turn over his proprietary source code despite twenty-one other states rejecting such a proposition, including when TrueAllele is used in exonerations.

While the Appellate Division’s decision has the potential to exclude reliable and highly probative evidence in this case mistakenly, there is also a risk that the decision may be wrongly expanded into other areas of technology and software. In the one month since the Appellate Division’s decision, the Division of Criminal Justice (DCJ) has received two requests from defense counsel invoking the Pickett decision to request source code for software wholly unrelated to this matter and DNA in general. Although the case involves child pornography with no DNA implications, defense counsel has wrongly read the Appellate Division’s opinion to mean that “the Defense should be able to meaningfully examine all relevant case materials by making the necessary technology accessible and understandable.” (Aa1-3).

Reading the opinion so sweepingly to include software that is not TrueAllele or even related to DNA and forensic science ignores the reasoning and concerns of the Appellate Division. The Court was heavily influenced by TrueAllele’s “profound shift in DNA forensics[,]” the “careful scrutiny” called for by the President's Council of Advisors on Science and Technology

(PCAST), and the errors found in other probabilistic genotyping software. (Pa49, 52-53). Further, the Appellate Division explicitly stated that “source code review is particularly crucial to evaluating the <u>unique</u> technology at issue here,” thus limiting its holding to TrueAllele. (Pa119) (emphasis added).

While this Court’s resolution of this appeal is critical to the State’s ability to present credible evidence and prevent New Jersey's technology from becoming stagnant, it is not the only issue requiring this Court’s review. As demonstrated by the defense counsel letters received just in DCJ within a month of the opinion, this Court must step in to limit the holding to TrueAllele and clarify that such a broad reading exceeds the bounds of the panel’s decision.

POINT II

LEAVE TO APPEAL SHOULD BE GRANTED BECAUSE THE APPELLATE DIVISION'S PUBLISHED DECISION WAS BASED ON MISINFORMATION AND THE SOURCE CODE IS NOT NECESSARY TO EVALUATE GENERAL ACCEPTANCE UNDER FRYE.

In its opinion, the Appellate Division disregarded and diminished the plethora of information the State provided concerning TrueAllele's general acceptance within the scientific community. Instead, the court relied on misinformation and presumptive reasoning to require the source code to prove general acceptance. Such a requirement exceeds Frye's requirements and changes the burden of proof from general acceptance to complete agreement and the impossibility of error.

"In New Jersey, the results of scientific tests are admissible at a criminal trial only when they are shown to have sufficient scientific basis to produce uniform and reasonably reliable results and will contribute materially to the ascertainment of truth." State v. Marcus, 294 N.J. Super. 267, 275 (App. Div. 1996) (quoting Romano v. Kimmelman, 96 N.J. 66, 80 (1984)). For criminal cases, New Jersey "has continued to rely on the Frye standard to assess reliability." State v. J.L.G., 234 N.J. 265 (2018). "The test requires trial judges to determine whether the science underlying the proposed expert testimony has 'gained general acceptance in the particular field in which it belongs.'" Ibid. (quoting Frye, 293 F. at 1014).

"[T]here are three ways to establish general acceptance under Frye: expert testimony, authoritative scientific and legal writings, and judicial opinions." Id. at 281. "Although we look for wide support within the relevant scientific community, complete agreement is not required for evidence to be admitted." Ibid. (emphasis added). "Proving general acceptance 'entails the strict application of the scientific method, which requires an extraordinarily high level of proof based on prolonged, controlled, consistent, and validated experience.'" State v. Harvey, 151 N.J. 117, 171 (1997) (quoting Rubanick v. Witco Chem. Corp., 125 N.J. 421, 436 (1991). "Essentially, a novel scientific technique achieves general acceptance only when it passes from the experimental to the demonstrable stage." Ibid.

In terms of general acceptance, this Court has said that it

> does not require complete agreement over the accuracy of the test or the exclusion of the possibility of error . . . . Neither is it necessary to demonstrate that the techniques, methodology, and procedures are infallible . . . . Nor is it necessary that acceptance within the scientific community be unanimous . . . . Every scientific theory has its detractors.
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> [Ibid. (citations omitted).]

Thus, at the Frye hearing the State needed to prove that the TrueAllele software and its results "were non-experimental, demonstrable techniques that the relevant scientific community widely, but perhaps not unanimously, accepts as reliable." Ibid.

To meet this burden, the State provided defendant and the court with the expert testimony of Dr. Perlin, validation studies, and peer-reviewed articles, as well as published and unpublished statements of reasons from other jurisdictions regarding the admissibility of TrueAllele. See J.L.G., 234 N.J. at 281. Despite this evidence, the Appellate Division instead relied on errors found in software that is not TrueAllele nor found by source-code review and standards from a report that has been discredited in the scientific community. Further, the Appellate Division failed to appreciate other jurisdictions' findings regarding TrueAllele's reliability and admissibility.

1. The Appellate Division placed improper emphasis on the errors found in STRmix and FST and without acknowledging how they were found.

The Appellate Division was persuaded that defendant needs to review TrueAllele's proprietary source code to prove reliability because of the errors found in other probabilistic genotyping software through source-code review. In its published opinion, the Court stated that in 2015, STRmix was forced to reveal its source code, which discovered coding errors leading to misleading results. The Court also noted that in 2017, a review of the Forensic Statistical Tool (FST) developed and used by the New York City Office of Chief Medical Examiner (OCME) revealed that the software "was unreliable, did not work as intended, and had to be eliminated." (Pa51). The panel found that these cases demonstrated that "software is not immune from human error." Ibid. The Court relied on defense expert

Nathanial Adams, who stated that any biases and errors might only be "conducive to detection only by a full examination and testing of the code and points to the consequential software error of STRmix and FST." (Pa96). The Appellate Division was also persuaded by the defense amici's assertion that TrueAllele's code likely contains the same errors and that the discontinuation of FST is a cautionary tale. (Pa97-98).

While the Appellate Division did acknowledge that the errors found in STRmix were first detected through testing rather than source-code review, it did not give value to the fact that it was testing and not source-code review that found all of the errors relied on by the defense. The statements made regarding STRmix by the court and the amici were so incorrect that STRmix issued a response to the decision entitled "Incorrect comments relating to STRmix in State of New Jersey v Corey Pickett."[4] (Aa4-7).

In its response, STRmix pointed out that it makes its source code available through its Defense Access Policy under an NDA, which includes similar restrictions as those requested by Cybergenetics. (Aa4). It highlighted that, although its source code had been inspected three times, there was never a miscode detected by independent source-code review that affected performance. Ibid. STRmix stated that "it is now known that

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[4] The Attorney General has included the response in its appendix for the Court's convenience but is publically available at https://www.strmix.com/news/incorrect-comments-relating-to-strmix-in-state-of-new-jersey-v-corey-pickett/.

some miscodes were present during those occasions causing intermittent and minor changes to the assigned [likelihood ration].” Ibid. STRmix further noted that of the fourteen miscodes found in STRmix, three were discovered in use when unusual results were detected and investigated by the STRmix team. Ibid. A parallel calculation of intermediate results discovered the other eleven errors. Ibid. STRmix emphasized that contrary to the Appellate Division’s assertion, “[n]one of the miscodes have been found by code review. None have been found as part of the judicial process.” Ibid.

STRmix also took issue with the Appellate Division and the defense amici for its reliance on the Courier Mail article “Queensland authorities confirm ‘miscode’ affects DNA evidence in criminal cases” from March 20, 2015, calling it a “tabloid newspaper” and noting its disappointment “to see the reliance on such an unreliable source in a serious judicial matter.” (Aa5)[5]. STRmix pointed out that out of 20,000 cases in South Australia and New Zealand, there were only twenty-two instances of a miscode firing. Ibid. But any changes to the likelihood ratio were made before the court case was heard. Ibid. And none of the changes were material or outcome-determinative. Ibid. Of note, though again, is that laboratory analysts discovered the miscode, not independent researchers. (Aa6).

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[5] A statement by the STRmix teams addressing the factual errors in the article is available at https://www.strmix.com/assets/STRmix/STRmix-PDFs/Statement-relating-to-STRmix-miscodes-180316.pdf.

Finally, STRmix noted that despite defendant’s assertion that an Illinois court compelled disclosure of its source code, that was not the case. (Aa6-7). It was disclosed under a negotiated protective order, but STRmix typically makes it available under a non-disclosure agreement (NDA), - the terms of which can be found on its website. (Aa7). STRmix also clarified the testimony Mr. Adams gave about his findings through his source-code review. Ibid. STRmix pointed out that in a testimonial hearing in State v. Fair, No. 10-1-09274-5 SEA (King County, WA, Superior Court Jan. 12, 2017), Mr. Adams admitted that he learned things that were important to his understanding of STRmix’s functioning that he would not have learned from another source.[6] Ibid. Although the statement ended up in the trial judge’s statement of reasons, Mr. Adams never stated that he “was able to identify potential issues in STRmix’s source code that negatively affected the functioning of the software and could not have been learned from any other source.” (Aa6).

There are similar issues with the Appellate Division’s reliance on FST errors. The Court referred to FST as a “discontinued program” and a “cautionary tale.” (Pa117). But FST’s reliability has repeatedly been upheld, and OCME did not end its use of the program because of any errors.

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[6] Mr. Adam’s testimony in Fair is available publically at https://johnbuckleton.files.wordpress.com/2018/08/09-21-16-nathaniel-adams-00400075xbe3c8.pdf.

As recently as last year, the Second Circuit determined that there was no error in determining that FST evidence was reliable and therefore admissible. United States v. Jones, 965 F.3d 149 (2d Cir. 2020). In that case, Dean Jones argued that the district court had abused its discretion in admitting DNA evidence and expert testimony based on FST. Id. at 153. DNA from a hat and glove that were found discarded from a fleeing robber was tested using FST. Id. at 154. The results showed that one of the sources of the DNA on the gloves was likely Jones. Ibid.

Before trial, Jones objected to the introduction of the DNA evidence, and the district court held a Daubert[7] hearing to determine the reliability of FST analysis. Ibid. The prosecution called Dr. Craig O'Connor, a Ph.D. in genetics who, at the time of his testimony, was the assistant director at the Department of Forensic Biology at OCME, and had previously served as a criminalist at OCME; and Dr. Adele Mitchell, a Ph.D. in human genetics and molecular biology who had helped develop FST for OCME. Ibid. Mr. Adams was also present in that case as a defense expert. Ibid. After reviewing the source code, Mr. Adams testified that FST was unreliable based on a post-validation allele cap. Id. at 158.

After the Daubert hearing, the district court denied Jones's motion to exclude FST's analysis. Ibid. The court was

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[7] Daubert v. Merrell Dow Pharm., Inc., 509 U.S. 579 (1993).

persuaded by “the procedures OCME used to determine the validity of its methodology,” “the external validation and peer review FST had undergone,” and OCME’s adherence to SWGDAM’s guidelines in its internal validation. Id. at 158-59. Regarding general acceptance, the court noted that while Jones was the first Daubert challenge to FST, more than forty New York state cases had rejected challenges to the admission of FST despite its more stringent standard for the admission of expert testimony. Id. at 160. On appeal, the Second Circuit found no error in the admission of the results. Id. at 162.

And the Appellate Division's suggestion that OCME discontinued FST because of errors is also incorrect. Testimony from a former lab official and former member of the New York State Commission on Forensic Science criticized FST and questioned its accuracy.[8] See Lauren Kirchner, Traces of Crime: How New York’s DNA Techniques Became Tainted, New York Times, September 4, 2017.[9] As a result, “a coalition of defense lawyers [asked] the New York State inspector general’s office . . . to launch an inquiry into the use of the disputed analysis methods in thousands of criminal cases.” Ibid. In response, the medical examiner’s office stood by its science, and the Chief of

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[8] The testimony was similar to the testimony of defense experts in Jones’s Daubert hearing in the district court. See Jones, 965 F.3d at 158.

[9] The article is available at https://www.nytimes.com/2017/09/04/nyregion/dna-analysis-evidence-new-york-disputed-techniques.html

Laboratories, Timothy Kupferschmid, said that “the discarded techniques were well-tested and valid, and that the lab was adopting newer methods to align with changing F.B.I. standards. He compared it to a vehicle upgrade.” Ibid.

Also, in response to the Legal Aid Society complaint, the DNA subcommittee, the governing body that regulates all forensic laboratories in New York, reviewed and evaluated the allegations. Ibid. The subcommittee ultimately found that there were no “significant malfunctions[,]” that “OCME used reasonable scientific methods[,] and that there was “no merit in the allegations regarding OCME’s scientific processes[.]” (Pa579). The ANSI-ASQ National Accreditation Board also submitted a letter to the Inspector General indicating that it found the Legal Aid Society and Federal Defenders of New York allegations to be unfounded. (Pa580-81).

The reasoning behind the Appellate Division’s decision is further flawed given the findings in the article, “What can forensic probabilistic genotyping software developers learn from significant non-forensic software failures?” In the article, the authors noted that “[w]ith regard to code review in forensic science we are not aware of any documented example of the discovery of a miscode.” (Pa568). Similar to the errors discovered in STRmix, the undocumented minor routine in FST, which was largely innocuous, was rediscovered by testing and then confirmed in the code. Ibid. The article noted that “testing identifies an unusual behavior in the software, the cause of which is subsequently found in the code once both a suitable test example is available, and a portion of the code comes under scrutiny." Ibid. The article confirmed that that had been the process for the miscodes found in STRmix and those found in Lab Retriever and EuroForMix, which were open-source software. Ibid.

The fact that even for open-source software, errors were not discovered until testing highlighted where to look in the code demonstrates that source-code review is not the starting point. The Appellate Division's decision to order source code review based on its concerns of errors that were only found by testing without defendant in this case ever testing the TrueAllele software or results cannot stand. Blind review of source code does not establish reliability but instead seeks to prove a technology is infallible.

2. The Appellate Division disregarded the numerous validation studies and peer-reviewed articles because of the PCAST report, which the scientific community has rejected.

The Appellate Division put inappropriate weight on the findings in President's Council of Advisors on Sci. & Tech., Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods 5 (2016) (PCAST Report). The Court pointed to the fact that PCAST found that "probabilistic genotyping programs should be independently evaluated to determine whether the methods are scientifically valid and, importantly, whether the software itself correctly implements the methods.” (Pa53). The Court then repeatedly, throughout its opinion, devalued TrueAllele’s validation studies involving Dr. Perlin because they were not the type of independent studies called for by PCAST. (Pa59, 99).

The panel correctly noted that there had been thirty-six validation studies conducted by Cybergenetics, law enforcement crime labs, or both, including the fact that seven of the studies have been published in peer-review journals. (Pa101). The Court then dismissed, however, the value of those validation studies and the process of peer-reviewed journals because Dr. Perlin, which PCAST explicitly noted as an impediment to reliable validation, authored six of the seven peer-reviewed publications. (Pa102). The Court took issue with the involvement of law enforcement agencies participating in the studies as they “likewise share an interest in the continued viability of the program.” (Pa103). Therefore, the Court found that for purposes of reliability in the criminal context, evaluations “should be performed by an expert working on behalf of someone in defendant’s shoes.” <u>Ibid.</u>

This Court should reject the notion that law enforcement crime labs' involvement in validation cuts against software reliability. Law enforcement crime labs are interested in the truth and accurate testing. As such, the reliance and emphasis on the PCAST report are misplaced as the forensic science and associated law enforcement community have denounced the report.

While the FBI agreed that because of the critical role forensic science plays in the criminal justice system, it needs to be held to high standards, the FBI disagreed with “many of the scientific assertions and conclusions of the report.” (Pa618). The FBI noted that the report created its own criteria for scientific validity in seven forensic-science disciplines without providing scientific support that those criteria are well accepted in the scientific community. Ibid. After PCAST’s release, the United States Department of Justice stated that it would not follow PCAST’s recommendations. (Pa583). DOJ felt that PCAST had overstepped its role as a science and technology advisory council by recommending forensic science's courtroom use. Hunt, Ted Robert (2017) “Scientific Validity and Error Rates: A Short Response to the PCAST Report,” Fordham Law Review Online: Vol. 86, Article 14.[10]

The conclusions found inside the PCAST report are an extremely narrow view that is not in line with mainstream scientific thought. Id. at 32. Instead, mainstream scientific thought believes that “all available information, evidence, and data derived from a multitude of studies—diverse and varied in experimental design—can be appropriately considered when assessing method accuracy, precision, and fitness for an intended use.” Ibid.

Given the forensic-science community's lack of support and trust in the PCAST study, the Appellate Division’s dependence on

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[10] The article is available at: https://ir.lawnet.fordham.edu/flro/vol86/iss1/1424.

its mandates and guidance to exclude peer-reviewed journals and well-accepted validation studies is troubling.

Whereas the PCAST report has mainly been criticized and rejected by the scientific community, probabilistic genotyping software has been validated in many peer-reviewed papers supporting general acceptance. These peer-reviewed articles have been the foundation for such software's admissibility in an overwhelming majority of court cases. The Journal of Forensic Sciences, whose mission is to advance forensic science research, education, and practice by publishing peer-reviewed manuscripts of the highest quality, recognized TrueAllele’s validation study as one of its 2020 noteworthy articles. See https://www.cybgen.com/information/newsroom/2021/jan/TrueAllele-validation-paper-chosen-as-a-2020-Noteworthy-Article-by-the-Journal-of-Forensic-Sciences.shtml.

TrueAllele’s methodology, which is made public, is also well accepted in the community. TrueAllele uses the Markov Chain Monte Carlo that is used routinely in computational biology, physics, engineering, weather prediction, and the stock market. Bruce Budowle, Probabilistic genotyping in forensic DNA analysis, American City & County, November 30, 2020, https://www.americancityandcounty.com/2020/11/30/probabilistic-genotyping-in-forensic-dna-analysis/.

Moreover, the State has provided documentation that TrueAllele is compliant with the Scientific Working Group's validation guidelines on DNA Analysis Methods (SWGDAM), which is a group of approximately fifty scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada. (Pa164-75). TrueAllele is also compliant with the standards set forth by the American National Standards Institute (ANSI) and AAFS Standards Board (ASB) for 2018, 2019, and 2020. (Pa402-95).

These forensic-science standards are based on the well-accepted scientific method of testing and validation, which should guide this Court instead of a report rejected by the relevant community. None of the standards for validation require analysis of source code.

3. The Appellate Division inappropriately dismissed the findings of other jurisdictions as an "authority 'house of cards.'"

The Appellate Division similarly disregarded the eighteen courts that have rejected source-code review to establish reliability. (Pa104). The Court wrongly stated, "prior determinations of reliability in other jurisdictions entailed no scrutiny of computer science or source code." (Pa104-05). Rather, the panel found that the courts depended in large part on Dr. Perlin's testimony and validation studies even though it was not independent or involved source code. (Pa105). Accordingly to the Appellate Division, therefore, the courts that followed the first admissibility determination in Commonwealth v. Foley, 38 A.3d 882 (Pa. Super. Ct. 2012), created "an authority 'house of cards.'" The Court inappropriately reasoned that by rejecting the need for source-code review to establish general acceptance, no court had considered whether TrueAllele's source code itself correctly implements its methods, which the Court stated, "can only be tested in the manner defendant and amici advocate for here." (Pa107).

It is, in fact, the opposite. When source code has been requested, or TrueAllele's reliability was challenged, the courts in those jurisdictions have held testimonial hearings where defense experts, including Mr. Adams, have made similar arguments to those made in this case. In those instances, it was not that there was a lack of scrutiny of computer science or the need for source code but rather that after hearing the testimony, the courts did not give weight to the argument that a computer-science approach was necessary to determine TrueAllele's reliability given the numerous and credible validation studies.

Regarding judicial opinions as evidence of general acceptance under Frye, TrueAllele has been used in over 750 criminal cases and has been accepted in courts in California, Florida, Georgia, Idaho, Indiana, Louisiana, Maryland, Massachusetts, Michigan, Nebraska, New Hampshire, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Texas, Virginia, Washington, West Virginia, Wyoming, United States (Middle District of Louisiana, Eastern District of Virginia), United States Marine Corps, Northern Ireland, and Australia. (Pa138).

TrueAllele has also been subject to over twenty-five admissibility decisions in the United States. Ibid. Courts presented with admissibility challenges to TrueAllele have universally rejected the need for source code and found TrueAllele sufficiently reliable to be admitted. Due to the validation studies and peer-reviewed articles, the courts have found that TrueAllele was generally accepted within the scientific community. Ibid.

For example, in a published case from the Supreme Court of Nebraska, defendant's expert Nathaniel Adams previously challenged TrueAllele's methodology. See State v. Simmer, 935 N.W.2d 167, 172 (Neb. 2019). Similar to the arguments here, "Adams's testimony and written report expressed concerns about the validity of TrueAllele's probabilistic genotyping program from a software engineering perspective." Id. at 176. His "primary objection to the software was that it had not been confirmed that the software does what Perlin says it does." Ibid. Therefore, as he does in this case, Adams requested that the source code be inspected to determine whether the software has been appropriately constructed. Id. at 177.

"Adams testified that TrueAllele had achieved only the 'illusion of validation' because it had not been validated in the domain of software engineering." Ibid. "Adams acknowledged the studies in the record validating TrueAllele, but claimed that there is a difference between the 'forensic DNA definition of validation and the software engineering definition of validation.'" <u>Id.</u> at 180. "In particular, Adams expressed concerns that the TrueAllele software source code had not been subjected to independent testing. He testified that without such a review, confirmation was lacking as to whether the TrueAllele software actually performs as described by Perlin." <u>Ibid.</u> Simmer also argued, "that the validation studies must be discounted because Perlin is a coauthor of some of the publications and, as the owner of the company that owns TrueAllele, has a financial interest in seeing it found reliable." <u>Ibid.</u>

The Supreme Court of Nebraska rejected both arguments. The court noted, "Perlin's part in the validation studies was not as pervasive or unchecked as Simmer suggests. Perlin was not involved in [ten] validation studies in the record. In addition, [six] of the studies in which he was listed as an author were published in peer-reviewed publications" and that "Perlin was not the lone author on any of the published, peer-reviewed validation studies. That is, other members of the scientific community also staked their reputations on the reliability of TrueAllele." <u>Ibid.</u>

Regarding source code, the court noted that although "a review of the TrueAllele source code might also have confirmed the reliability of TrueAllele, we cannot say that the district court abused its discretion by relying on the numerous validation studies confirming the reliability of TrueAllele by other means." <u>Id.</u> at 181. Contrary to the Appellate Division's assertion that previous courts had not addressed source code or computer science, the court in Simmer determined that it was not "required to find that TrueAllele had been validated 'from a software engineering perspective' to find it reliable." Id. at 180. Rather, the court relied on the State's presentation of "significant evidence that TrueAllele is reliable." Id. at 181. The evidence included "Perlin's testimony and copious documentary evidence describing TrueAllele's methodology," the fact that "SWGDAM has approved the use of validated and documented probabilistic genotyping software and provided guidelines for its validation," which "TrueAllele has complied with" and finally that "TrueAllele's methodology has been repeatedly tested and validated in peer-reviewed studies." Id. at 181-82.

Also, the courts relying on TrueAllele analysis are not limited to uses by the prosecution. In both guilt-phase trials and post-conviction relief cases, defense counsel and state innocence projects have sought introduction of TrueAllele testing results into courts without question to its reliability.[11] (Pa572-77). Cybergenetics contains lists of cases where TrueAllele has assisted in exonerations, was introduced by the defense, and even assisted the Legal Aid Society of New York.

Last year, the Georgia Innocence Project, with assistance

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[11] If the court excludes TrueAllele evidence for the State if the source codes are not provided that also excludes exculpatory evidence for Ferrara.

from the Idaho Innocence Project, arranged for DNA testing using TrueAllele on a bathrobe belt and necktie used to bind the victim of a homicide in 1977. State v. Gates, 840 S.E.2d 437, 439-40 (Ga. 2020); Georgia Supreme Court Affirms Right to a New Trial Based on TrueAllele Evidence, Forensic Mag (March 24, 2020) (available at https://www.forensicmag.com/562235-Georgia-Supreme-Court-Affirms-Right-to-a-New-Trial-Based-on-TrueAllele-Evidence/). Initial testing of the newly discovered items "showed the presence of at least three individuals' DNA on the belt and one of the ties but that the [Georgia Bureau of Investigations] was 'unable' to conduct further analysis of the results with the methods then in use by the GBI." Gates, 840 S.E.2d at 446. Gates was then permitted to analyze the results and comparison through TrueAllele which was able to "exclude[] Gates as a contributor to the DNA mixture found on the belt and tie." Ibid. The Court acknowledged, "TrueAllele had the ability to interpret that which human interpretation methods could not." Id. at 448. Because of the results, the Georgia Supreme Court granted Gates a new trial. Id. at 456.

The Washington Supreme Court has stated that the appropriate standard is "'general acceptance in the appropriate scientific community', that is, acceptance by the community of scientists familiar with the challenged theory." State v. Russell, 882 P.2d 747, 761 (Wash. 1994). The out-of-state decisions admitting TrueAllele while rejecting source-code review were not an echo chamber of authority repeating itself but rather trial courts holding testimonial hearings to exercise their gatekeeping function to accept the authority of the forensic-science community.

Based on the information provided, the State met its burden under Frye and established that TrueAllele is reliable after considering that the technique has been tested, subjected to peer review and publication, and generally accepted by the forensic community.

POINT III

IF THIS COURT IS NOT SATISFIED THAT TRUEALLELE IS GENERALLY ACCEPTED, THEN A REMAND FOR TESTIMONY CONCERNING SOURCE CODE IS NECESSARY.

If this Court believes that the validation studies, peer-reviewed articles, and judicial opinions are insufficient to determine general acceptance, it should also find that the record is incomplete to decide whether the source code must be disclosed. The State should be permitted to re-open Dr. Perlin’s direct examination on the limited issue of source code, and Mr. Adams should testify in support of the defense position to meet its burden as the moving party.

Defendant raised the issue of source code after Dr. Perlin’s direct examination had been completed. If the issue had been raised before or during Dr. Perlin’s testimony, it could have been explored during direct examination. As a result, the record does not contain his expert opinion on source code and its relation to the scientific-validation process. Also, defendant’s request for the source code came in the form of a certification from his expert. That expert should be put under oath to have his credentials assessed and his credibility determined and subjected to cross-examination necessary for the court to perform its gatekeeping function properly.

The Appellate Division inappropriately relied on the declarations and certification of the experts without subjecting them to cross-examination. (Pa60). Although the experts' declarations established their positions and the experts were unlikely to change, they were not sufficiently scrutinized through the adversarial process of cross-examination. Many courts in other jurisdictions held testimonial hearings about the admissibility of TrueAllele and the production of source codes. But unlike in this case, those courts had the opportunity to hear the testimony from both sides and cross-examination. In its brief, the State highlights those cases and the experts who testified for each side. (Pb21 to 26).

For example, in Fair, the court heard testimony from the same defense expert here. During his direct examination, he discussed his concerns with Dr. Perlin's process and development of TrueAllele. But in that case, the prosecutor was then able to cross-examine Mr. Adams about his lack of experience and knowledge in critical areas that relate to understanding TrueAllele. For instance, Mr. Adams admitted he did not have any statistics, math, or biology experience and was only knowledgeable of computer science, whereas Dr. Perlin has Ph.D.s in math and computer science, a Bachelor's degree in Chemistry, and a medical degree. The prosecutor was also able to highlight a bias that Mr. Adams has only ever worked for a company from which defense attorneys only hire. While the Attorney General does not suggest that the testimony from an out-of-state case be used here substantively, it is included here to highlight the importance of actual testimony from the experts where credibility can be questioned instead of just presumed.

CONCLUSION

The broad reading and faulty reasoning of the Appellate Division’s published decision must be addressed; thus, the Attorney General urges this Court to grant the State’s motion for leave to appeal and reverse the Appellate Division decision.

Respectfully submitted,

GURBIR S. GREWAL
ATTORNEY GENERAL OF NEW JERSEY
AMICUS CURIAE

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APPELLATE BUREAU

OF COUNSEL AND ON THE BRIEF

DATED: March 22, 2021

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Respond to:
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February 11, 2021

Via Ecourts

Re: State v. Michael Nieves
Indictment No.: 19-10-00115-S

Dear DAG Danielle Counts:

Please see enclosed preliminary forensic report from Tino Kyprianou of Axiana Computer Forensics LLC. As you can see from the report, there are many issues regarding the distribution of the discovery materials. I want to explore filing an additional discovery motion in regards to what Mr. Kyprianou states is missing from the investigative report. As mentioned in Conclusions (d) and (e), the Defendant was provided little information about the investigative software used to download contraband and the reliability of such software. This is in contradiction to State v. Pickett (2021),[i] which states that the Defense should be able to meaningfully examine all relevant case materials by making the necessary technology accessible and understandable.

Please review this report with the relevant law enforcement officials. I am hoping to resolve this case amicably. Due to the conclusions drawn by Mr. Kyprianou and the dated nature of this case, I kindly request that this matter be resolved to a 3rd degree possession of child pornography charge, with no necessary registration under Megan's Law and instead, enter Mr. Nieves into non-custodial probation. I will be on the call with Judge Bucca tomorrow at February 12, 2021, at 10 am.

Thank you for your time and consideration regarding the matter.

Very truly yours,
LAW OFFICES OF ERIC B. MORRELL

By: ERIC B. MORRELL

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[i] *State v. Pickett*, No. A-4207-19T4 (N.J. Super. Ct. App. Div. Feb. 3, 2021).

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March 4, 2021

***Via Email:* CountsD@njdcj.org**
Danielle Counts
Deputy Attorney General

Re: State v. Michael Nieves
Indictment No.: 19-10-00115-S

Dear DAG Danielle Counts:

This letter is in response to the State's refusal to grant a meeting between the forensic examiners. Regardless of what would have been said in the meeting between Mr. Kyprianou and the State's forensic expert(s), the State's argument against Mr. Nieves is weak. Specifically, in reference to the charge of distribution outlined in N.J.S.A. 2C:24-4B (1). As detailed in the preliminary report, I submit that the State cannot prove beyond a reasonable doubt that Mr. Nieves, "did knowingly distribute" any items depicting the sexual exploitation or abuse of a child. Some weaknesses in the case against Mr. Nieves include, but are not limited to:

1. The inability to directly connect Mr. Nieves' personal computer to the implicated IP address 67.83.21.116.

The IP address was assigned to the house at 407 Pleasant Avenue, Piscataway, NJ 08854, not Mr. Nieves' personal computer or cell phone. According to the discovery provided by the police, at least five other individuals could have been using that same IP address via their own personal computers or cellular devices.

2. The inconsistencies in the police records available in the discovery materials.

In the Affidavit, Detective Thomas stated that of the seventeen files downloaded from IP address 67.83.21.116 on February 11, 2018, five appeared to depict child pornography. In fact, only one file allegedly contained child pornography downloaded on this date. A similar numerical inconsistency persists on July 28, 2018.
Furthermore, the report signed by Detective Thomas from May 4, 2018, and the report by Detective Donlan from the same date, provide different facts than those outlined by the Affidavit.

3. The fact that the contraband files downloaded by the State were not found on Mr. Nieves' computer.

The contraband was found on a loose drive (Enterprise3TBHDD-472E). Nothing in the discovery materials or investigative reports indicates that the loose drive was connected to

Mr. Nieves' personal computer. Additionally, the contraband found on the drive (Enterprise3TBHDD-472E) have different MD5 hashes than those listed in the report, indicating that these files could not have been the same files as those downloaded by the state.

4. The ambiguity surrounding the chain of custody of the evidence.

Both the Affidavit and the State's investigative reports do not clearly identify which law enforcement officer operated the investigative software and downloaded the suspected child pornography files. Additionally, it remains unclear how the law enforcement officers were able to download the alleged pornography files from BitTorrent. If necessary, my offices will file a motion to allow us to test the investigative software to confirm that it is possible to download files on Peer to Peer software from a single source. Used as foundational support in State v. Pickett (2021), and relevant here, State in the Interest of A.B. (2014) found that "[a] criminal trial where the defendant does not have 'access to the raw materials integral to the building of an effective defense' is fundamentally unfair."

Based on the points made above, I submit there is reasonable doubt that Mr. Nieves knowing distributed child pornography.

Once my offices received the appropriate hard drives, my staff, Mr. Kyprianou, and I put a lot of time and effort into reviewing and analyzing the materials. I am pursuing all available avenues for the defense of my client and am continuing to work on the formal discovery motion. In light of the above-listed defenses and the fact that Mr. Nieves has no prior criminal record and has been gainfully employed for the last 20 years, I am requesting non-custodial probation for Mr. Nieves. If necessary, please speak with your supervisor to pursue this resolution. We had discussed a jury trial previously, but I am considering a bench trial, as Judge Bucca stated he had tried cases like this previously.

Very truly yours,
LAW OFFICES OF ERIC B. MORRELL

By: ERIC B. MORRELL

Incorrect comments relating to STRmix in State of New Jersey v Corey Pickett

February 16, 2021

Summary

In the case of State of New Jersey versus Corey Pickett a ruling was made preventing the admissibility of some of the forensic DNA evidence until release of the source code underlying the probabilistic genotyping software TrueAllele for review by the defense. Supporting this opinion were briefs from six amicus curiae; Drs Heimdahl and Matthews, the Innocence Project, American Civil Liberties Union, Upturn Inc, The Legal Aid Society, and The Association of Criminal Defense Lawyers of New Jersey. A number of these briefs refer to STRmix. Some of this information is incorrect and we take this opportunity to correct the record. In view of the risk of a repeat of these misstatements, we offer the correct information here.

We make no comment on detail in this ruling outside of the direct comments relating to the software STRmix™. The STRmix team supports Corey Pickett's 6th Amendment right to confront the witnesses against him.

STRmix makes its code available through its Defence Access Policy (https://strmix.com/assets/STRmix/STRmix-PDFs/Access-to-STRmix-Software-by-Defence-Legal-teams-April-2020.pdf) under an NDA. This code has been inspected three times. In no case was a miscode detected by independent code review that affected performance although it is now known that some miscodes were present during those occasions causing intermittent and minor changes to the assigned *LR*.

1. No miscodes in STRmix have been identified by independent code review

Incorrect or misleading statement: Heimdahl and Matthews (H&M) state "*Flaws have been discovered in other PG programs including STRmix and Forensic Statistical Tool ("FST") and in much simpler technologies such as breathalyzers. Those flaws which called into question thousands of convictions frequently went undiscovered until the source code was reviewed as part of the judicial process*". …

Response: None of the miscodes in STRmix have been found by code review and none have affected a conviction.

Of the 14 post production miscodes found in STRmix (https://strmix.com/news/summary-of-miscodes/) three were noticed in use (two by users and one by the STRmix team) where unusual results were detected and investigated by the STRmix team. Eleven (three by one user and eight by the STRmix team) were detected by parallel calculation of intermediate results. The three found by a user were during internal validation. The eight by the STRmix team were often associated with developmental validation of a successor version but existed in earlier versions. None of the miscodes have been found by code review. None have been found as part of a judicial process.

This is further discussed in Buckleton, Curran, Taylor, Bright, What can forensic probabilistic genotyping software developers learn from significant non-forensic software failures? WIREs Forensic Science, 2020, https://doi.org/10.1002/wfs2.1398 .

2. No miscodes in STRmix have affected a criminal trial

Incorrect or misleading statements:

H&M state "*In total, at least thirteen "coding faults" have been found in STRmix, TrueAllele's chief competitor. In one notable example, the miscode impacted 60 criminal cases, requiring new likelihood ratios to be issued in 24 cases. David Murray, "Queensland Authorities Confirm 'Miscode Affects DNA Evidence in Criminal Cases" , Courier Mail Mar. 20, 2015 9 https://bit.ly/34DBlZy."*

Innocence project states "*Indeed, doubts about TrueAllele's accuracy are plausible—a competing program, STRmix, that performs the same type of analysis as TrueAllele, was found to have coding errors that impacted the data presented in court. David Murray, Queensland Authorities Confirm "Miscode" Affects DNA Evidence in Criminal Cases, Courier Mail (Mar. 20, 2015).*"

Innocence project: "*Genotyping software in particular has also been found error-prone—source code errors impacting the reliability of STRmix, a competitor to TrueAllele, materially altered match statistics in DNA mixture analysis in over sixty cases. David Murray, Queensland Authorities Confirm "Miscode" Affects DNA Evidence in Criminal Cases, Courier Mail (Mar. 20, 2015)."*

Innocence project: "*For example, STRmix was found to have errors that tainted numerous criminal proceedings*."

Upturn states: *"And in 2015, investigators in Australia encountered an error in their use of STRmix, a probabilistic genotyping software program intended to resolve mixed DNA profiles similar to TrueAllele. David Murray, Queensland Authorities Confirm 'Miscode' Affects DNA Evidence in Criminal Cases, The Courier Mail (Mar. 20, 2015). The error produced incorrect results in at least sixty criminal cases, including a high-profile murder case. Ibid."*

Upturn: "*For probabilistic genotyping in particular, STRmix and FST have both been revealed to have outcome-determinative errors*."

American Civil Liberties Union (ACLU) state *"Likewise, when STRMix (another probabilistic DNA tool similar to TrueAllele) was analyzed by independent researchers, they found programming errors that created false results in 60 cases in Queensland, Australia."*

Response: The reference is to a tabloid newspaper. It is disappointing to see the reliance on such an unreliable source in a serious judicial matter. The factual errors in the Courier Mail article were addressed at the time by the STRmix team. A statement is available at https://www.strmix.com/assets/STRmix/STRmix-PDFs/Statement-relating-to-STRmix-miscodes-180316.pdf. A review of over 20,000 cases in South Australia and New Zealand only identified 22 instances of this miscode firing.

In Queensland, the 24 statements were amended with a minor change to the *LR* in some cases. In all instances this change was before the court case was heard. The changes were minor not "material" or "outcome-determinative" and affected only a subset of the 60 cases. For example, Australia round all *LR*s down to 10^{11} (one hundred thousand million or one hundred billion) and hence in some of the 24 reissued statements the *LR* was exactly the same.

The miscode was discovered in use by the laboratory analysts and not investigators or independent researchers, it did not affect the result in all 60 cases, and the reissued *LR* in what we assume was the "high profile murder case" (the subject of the Courier Mail article) was identical. This is even stated in the Courier Mail article itself:

"*Joan Ryther, who was eight weeks pregnant, was raped and murdered while walking to work in May 2013. Mr Bosscher was advised the case had been affected by the STRmix coding error and was sent a replacement witness statement. The DNA likelihood ratios in both the new and original statements appear to be the same*."

3. Comparing non-equivalent scientific methods as equal is misleading.

Incorrect or misleading statement: ACLU brief *"Furthermore, the sample analysis is dictated by the assumptions programmed into the software. This creates the worrisome reality that softwares like STRMix and TrueAllele provide divergent probability calculations from one another—a discrepancy that can mean the difference between exculpation and inculpation. See Commonwealth v. Foley, 38 A.3d 882, 887, 890 (Pa. Super. Ct. 2012) (noting that TrueAllele calculated a match statistic of 189 billion, compared to a competitor's estimate of 13,000—a more than 14-million-fold difference)."*

Response: This is inappropriately deceptive. The comparison was between TrueAllele and CPI (termed the inclusion method in the reference to follow) and not between TrueAllele and STRmix. CPI is a non-computer based technique that precedes probabilistic genotyping and routinely returns lower values for a comparison to a true donor. We quote from the Cybergenetics webpage[1] "*For the 7% minor unknown contributor, the inclusion method produced a genotype having a 13 thousand match score, obligate allele analysis one of 23 million, and TrueAllele computer interpretation a score of 189 billion. The difference was entirely attributable to how well each method preserved the identification information present in the mixture data. TrueAllele's quantitative interpretation used more of the data, while the other methods ignored peak heights and inclusion further ignored the victim's genotype*." CPI is known to be wasteful of information.

4. Access to the STRmix source code is available as per our Defence Access Policy

Incorrect or misleading statements: Defense brief "*An Illinois court has compelled the disclosure of the source code that runs STRMix, another probabilistic genotyping program, pursuant to a similar protective order."*

Defense brief: "*Mr. Adams reviewed STRMix's computer code in 2014 and found errors that impacted the reliability of the results. This review is discussed in State v. Fair, No. 10-1-09274-5 SEA (King County, WA, Superior Court). The review cited in Fair was pursuant to a strongly worded protective order that prevented Adams from disclosing exactly what is included in STRMix's code. Id. However, the Fair court observed Adams "was able to identify potential issues in STRMix's source code that negatively affected the functioning of the software and could not have been learned from any other source.*" *Id.*

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[1] https://www.cybgen.com/information/presentations/2010/AAFS/Perlin_Three_match_statistics_one_verdict/page.shtml

Response: No compulsion is required. As per our Defence Access Policy, STRmix offers to disclose its code to representatives of the defense under an NDA. In this case, the code was released under a negotiated protective order and not an NDA.

Adams actual testimony in Fair[2] was "*Let me ask you this question and see whether you can answer it without running afoul of your agreement with STRmix. Did you learn things from your review of STRmix's source code that you could not learn from any other source? A. Yes. Q. Those things that you learned from STRmix's source code that you could not learn from any other source, were they important in understanding STRmix's functioning? A. Yes*.."

The defense do correctly quote the ruling in Fair. However, in this instance the ruling is not based on the actual testimony which does not include the statement "*negatively affected the functioning of the software"* The transcript is in the public domain and should have been consulted by defense before offering incorrect opinions to a court.

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[2] https://johnbuckleton.files.wordpress.com/2018/08/09-21-16-nathaniel-adams-00400075xbe3c8.pdf