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Mr. Robert M. Huston, BS
Laboratory Director and Manager of Administration
Office of the Allegheny County Medical Examiner
1520 Penn Avenue
Pittsburgh, PA 15222

Re: Inaccurate statements made to the Pittsburgh Post-Gazette

Dear Mr. Huston,

For eight years we have discussed TrueAllele® computer interpretation of DNA evidence. In over fifty criminal cases, Cybergenetics has re-analyzed DNA data after your lab couldn't find useful information. Our work has made Allegheny County safer. I was therefore disappointed to read your inaccurate statement in the Pittsburgh Post-Gazette on August 28, 2016.

As Laboratory Director for the Allegheny County Office of the Medical Examiner, you gave a "variety of reasons" why your lab never put TrueAllele to use, stating:

> "These include *reproducibility* of results, *time* of analysis, the availability of the *source code*, *general acceptance* by the scientific community, and *validation* of the system. Additionally, the *up-front cost* and *annual cost* ..."

DNA mixture interpretation (background)

Your crime lab analyzes biological crime scene evidence items. These unknown items are usually a mixture of two or more people. Your lab generates good data from those DNA items. However, your lab incorrectly interprets mixture data. Your analysts use a biased inclusion method that either gives no result, or calculates an inaccurate match statistic. Since criminal justice requires a match statistic, your lab often fails to produce useful identification information.

TrueAllele solves the DNA mixture problem. The computer objectively unmixes the data into genotypes; uncertainty is represented with probability. Afterwards, comparing an evidence genotype with a person's genotype yields an accurate match statistic. Unlike the lab's one-sided inclusion methods, TrueAllele can statistically exclude innocent people from DNA evidence.

"Validation of the system"

TrueAllele has undergone thirty-four validation studies. Seven of these TrueAllele studies have been published in peer-reviewed journals (Attachment A). Your laboratory conducted a TrueAllele validation study together with Cybergenetics, which was presented at a national forensics conference [1].

In contrast, the inclusion method employed by your laboratory is unvalidated. No developmental validation study has empirically established the method's accuracy or error rate. Your lab has not demonstrated the inclusion match statistic's reliability on county DNA mixtures.

There has been independent testing of the inclusion method on mixture data. My peer-reviewed paper "Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information" was published in 2015 [2]. Inclusion just counts how many tests an analyst chose to report. It puts a random number to a subjective choice. The statistic is unrelated to match information. It should not be used in court for identification purposes.

"Reproducibility of results"

Validation studies have measured and reported on TrueAllele's reproducibility (Attachment A). Empirical data show that the system's DNA match statistics are highly reproducible.

Your lab's inclusion method is not reproducible, however. The United States Department of Commerce (DOC) showed in 2005 that (single threshold) inclusion methods gave very different answers on the same DNA mixture data. Most labs in the study reported nothing. On the same data, the other labs gave incorrect match statistics ranging from ten thousand to a hundred trillion. A subsequent 2013 DOC study of newer (double threshold) inclusion methods showed most labs falsely implicating someone whose DNA wasn't even in the mixture.

"General acceptance by the scientific community"

TrueAllele has successfully withstood a dozen admissibility challenges in United States courts where general acceptance was considered (Attachment B). In 2012, the Pennsylvania Superior Court established appellate precedent for TrueAllele in *Commonwealth v. Foley*, according to the Frye general acceptance standard. In 2013, our county medical examiner Dr. Karl Williams published an article acknowledging that TrueAllele "computer analysis had met this general acceptance standard within the forensic scientific community" [3].

Over five hundred TrueAllele reports have been issued across thirty-eight states. Seven American crime labs routinely use the system on their own DNA mixtures. Extensive peer review publication and empirical testing have established TrueAllele's general acceptance by the scientific community.

However, the scientific community has consistently rejected your lab's inclusion method. Your lab's DNA mixture interpretation method has no scientific or mathematical basis. Empirical studies demonstrate the method's failure to produce accurate or objective match statistics [4].

Policy groups (e.g., the President's Council of Advisors on Science and Technology) recommend abandoning the inclusion approach entirely [5]. Your method has not been tested in court, and could fail a Frye admissibility test for general acceptance. The scientific community has moved on to better methods.

"Time of analysis"

On typical DNA mixtures, a standard TrueAllele system can solve eight evidence items in two hours. One day of TrueAllele processing can handle weeks of crime lab mixture data.

Your inclusion approach, however, wastes considerable human analyst time (and taxpayer dollars). DNA analysts either calculate an incorrect match statistic, or spend hours to days getting no result. Computers can instead perform that data analysis accurately and automatically, freeing up county employees for more productive work.

"Up-front cost"

There is no up-front TrueAllele cost because your crime lab already purchased a system – ten years ago. Cybergenetics has provided your lab with free validation and training over that time period, to help your analysts get started using their TrueAllele system.

"Annual cost of the system"

The annual TrueAllele maintenance charge is optional. So "free" is not a barrier.

Three years ago, Cybergenetics offered to process all your lab's DNA data (at no cost) to help the county fight crime [6]. This public service project would have protected county residents, while giving your lab time to start using TrueAllele. Prosecutors, defenders and judges welcomed the opportunity to use our technology for improving criminal justice. Your office stonewalled for eighteen months, thus avoiding outside scientific scrutiny of your longstanding DNA interpretation failure. Here again, "free" science was not a barrier.

"Availability of the source code"

Your crime lab does not have "source code" for the computer programs and equipment it regularly uses. Those systems include proprietary software and hardware (Attachment C). Scientists validate their software programs by empirical testing on actual data; they do not read source code text. If your lab truly required unavailable source code trade secrets from these companies, it would not be able to analyze DNA evidence. Your DNA lab would close.

I hope this letter has helped clarify your understanding. TrueAllele consistently succeeds at DNA mixture analysis, while your lab repeatedly fails at this task. The "reasons" you gave the newspaper apply to your own lab's failed methods, but not to the scientifically proven TrueAllele solution. When your crime lab is ready to embrace accurate and objective science, please contact Cybergenetics so that we can help you get started.

Sincerely,

Mark W. Perlin, PhD, MD, PhD
Chief Scientist and Executive

CC: Karl E. Williams, MD, MPH
Allegheny County Medical Examiner

References

[1] M.W. Perlin, K. Dormer, J. Hornyak, T. Meyers and W. Lorenz, "How inclusion interpretation of DNA mixture evidence reduces identification information." *American Academy of Forensic Sciences 65th Annual Meeting,* Washington, DC, February 22, 2013.

[2] M.W. Perlin, "Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information." *Journal of Pathology Informatics*, 6(1):59, 2015.

[3] K.E. Williams and M.J. Panella, "The continuing legal evolution of forensic DNA." *The Pennsylvania Lawyer*. January/February, 34-37, 2013.

[4] I.E. Dror and G. Hampikian. "Subjectivity and bias in forensic DNA mixture interpretation." *Science & Justice*. 2011;51(4):204-8.

[5] President's Council of Advisors on Science and Technology (PCAST). Report to the President on "Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods." *The White House*, Washington, DC, September, 2016.

[6] P.R. Ward, "Allegheny County crime lab vying to use more advanced DNA database; Technology developed by Cybergenetics gets conclusive results from DNA mixtures." *Pittsburgh Post-Gazette*, February 28, 2014.

Attachment A

Peer-reviewed TrueAllele validation studies

Perlin MW, Sinelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE*. 2009;4(12):e8327.

Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences*. 2011;56(6):1430-1447.

Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information. *Science & Justice*. 2013;52(2):103-14.

Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-66.

Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLoS ONE*. 2014:9(3):e92837.

Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences*. 2015; 60(4):857-868.

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276.

Attachment B

TrueAllele admissibility rulings

California trial court admitted TrueAllele into evidence in People v. Dupree Langston, Kern County, case number BF139247B, January 10, 2013. (Kelly-Frye)

Indiana trial court admitted TrueAllele into evidence in State v. Dugniqio Forest, Vanderburgh County, case number 82D03-1501-F2-566, June 3, 2016. (Daubert)

Indiana trial court admitted TrueAllele into evidence in State v. Malcolm Wade, Monroe County, case number 53C02-1411-F3-1042, August 3, 2016. (Daubert)

Louisiana trial court admitted TrueAllele into evidence in State v. Chattley Chesterfield and Samuel Nicolas, East Baton Rouge Parish, case 01-13-0316 (II), November 6, 2014. (Daubert)

Louisiana trial court admitted TrueAllele into evidence in State v. Harold Houston, Jefferson Parish, case 16-3682, May 19, 2017. (Daubert)

Massachusetts trial court admitted TrueAllele into evidence in Commonwealth v. Heidi Bartlett, Plymouth County, May 25, 2016. (Daubert)

New York trial court admitted TrueAllele into evidence in People v. John Wakefield, Schenectady County, indictment number A-812-29, February 11, 2015. (Frye)

Ohio trial court admitted TrueAllele into evidence in State v. Maurice Shaw, Cuyahoga County, case number CR-575691, October 10, 2014. (Daubert)

Pennsylvania trial court admitted TrueAllele into evidence in Commonwealth v. Kevin Foley, Indiana County, case number 1170 Crim 2007, March 2, 2009. Superior Court affirmed for statewide precedent, 2012 PA Super 31, No. 2039 WDA 2009, February 15, 2012. (Frye)

South Carolina trial court admitted TrueAllele into evidence in State v. Jaquard Aiken, Beaufort County, case number 20121212-683, October 27, 2015. (Jones)

Virginia trial court admitted TrueAllele into evidence in Commonwealth v. Matthew Brady, Colonial Heights County, case number CR11000494, July 26, 2013. (Spencer-Frye)

Washington trial court admitted TrueAllele into evidence in State v. Emanuel Fair, King County, case number 10-1-09274-5 SEA, January 12, 2017. (Frye)

Attachment C

Proprietary technology used by the Allegheny County DNA crime lab

Source code is not available for these standard DNA laboratory systems.

software (executable program only)

Applied Biosystems®	GeneMapper® ID v3.2	DNA analysis
Applied Biosystems®	GeneMapper® ID-X 1.2	DNA analysis
FBI	Popstats	DNA match
FBI	CODIS	DNA database
Microsoft®	Excel®	Spreadsheet
Porter Lee®	B.E.A.S.T.	LIMS system

hardware (with embedded software)

Applied Biosystems®	ABI Prism® 3130 Genetic Analyzer	DNA sequencer
Applied Biosystems®	ABI Prism® 3500 Genetic Analyzer	DNA sequencer
Applied Biosystems®	ABI 7500 RT-PCR	PCR machine
Applied Biosystems®	7500 FAST Real-Time PCR	PCR machine
Beckman Coulter	Biomek® 3000 Automated Workstation	Pipetting robot
Promega®	DNA39 Plexor® HY System	DNA quantification
Qiagen®	EZ1 Advanced XL Robot	DNA extraction
Thermofisher®	GeneAmp® 9700 Thermal cycler	PCR machine