DECLARATION OF MARK W. PERLIN (US v. MILLS)

I, Mark W. Perlin, PhD, MD, PhD, declare I have personal knowledge of the following, and if called upon to do so, could and would testify competently to the matters contained herein:

I hold the following academic degrees: a B.A. in Chemistry from SUNY/ Binghamton, a Ph.D. in Mathematics from CUNY/Graduate School, an M.D. from the University of Chicago Pritzker School of Medicine, and a Ph.D. in Computer Science from Carnegie Mellon University. I have been issued thirteen patents. Prior to founding my own technology company, I was a senior research faculty member of Carnegie Mellon University's School of Computer Science. I have been qualified to testify as an expert in thirty-five jurisdictions. I am currently a scholar-in-residence faculty member in the Forensic Science and Law program at Duquesne University.

Cybergenetics is a Pennsylvania corporation located at 160 North Craig Street, Suite 210, Pittsburgh, PA 15213. Cybergenetics is the creator, developer, and owner of the TrueAllele® technology and software.

Declaration overview

This declaration begins with background information about the case and its DNA evidence. I describe the likelihood ratio statistic that numerically summarizes DNA match (or nonmatch) strength. I introduce error rates and their dependence on the likelihood ratio. I give an example of how LR-dependent error rates from validation studies are used in court.

I discuss the TrueAllele technology used in this case, expanding on the system's reliability and acceptance. I review the TrueAllele report provided in this case, showing the likelihood ratios and error rates. I discuss some problems with the government expert's claims about error rate, and why their analysis isn't relevant to this case.

Towards the end, I comment on the opposition motion, and offer some conclusions. There is a bibliography and two appendices, one listing about forty admissibility decisions and another presenting a mathematical proof for why strong likelihood ratios must have small error rates.

Background information

The Defendant Ravel Mills is accused of First-Degree Murder While Armed. The D.C. Department of Forensic Sciences (DFS) tested DNA swabbed from a gun (Item 5.1.1) and magazine (Item 5.2.1). DNA testing showed the gun to be a mixture of at least two contributors, and the magazine to have at least three contributors. In 2020, a DFS analyst using STRmix™ mixture software could not interpret the minor contributors. In 2022, Bode Technology's manual data review excluded Mills from the major contributors, but could not interpret the minors.

In 2022, the Public Defender Service (PDS) for D.C. asked Cybergenetics to examine the evidence. Running TrueAllele® technology on the same DNA data, the computer separated the mixtures into contributor genotypes, comparing them with Mill's DNA profile. TrueAllele statistically excluded Mills from the major contributors. Moreover, TrueAllele was able to interpret the minor components and compare them with Mills.

We reported two exclusionary nonmatch statistics (for the major and minor contributors) for Item 5.1.1 relative to Mills. We reported three exclusionary nonmatch statistics (major, middle, and minor contributors) for Item 5.2.1 relative to Mills. We calculated error rates and included them in our report. We provided a 159-page Case Packet containing supporting data and calculations. We sent the defenders a 4-gigabyte DVD containing considerable disclosure material.

The Daubert standard for reliable evidence (FRE 702) has four prongs, including one for error rates. Specifically, "whether there is a known or potential rate of error of the particular technique or theory." The error rate provides a frequency context for a trier of fact, indicating how often the technique may be wrong. There is no pre-determined error rate cutoff. A high error rate signals less useful evidence. The error rate goes to evidence weight, not admissibility.

A court may exclude relevant evidence (FRE 403) when its probative value is substantially outweighed by "unfair prejudice, confusing the issues, misleading the jury, undue delay, wasting time, or needlessly presenting cumulative evidence."

In 2023, the government submitted an opposition motion and expert statement to preclude the TrueAllele report, claiming some issue with error rates relative to the Daubert standard. This declaration shows why TrueAllele satisfies that standard, and why the government's arguments are baseless, confusing, and misleading.

Likelihood ratio

One or more people may contribute their DNA to biological evidence. PCR can amplify DNA molecules to make billions of DNA copies. A genetic analyzer can detect these copies to form DNA data. Interpreting this data produces genetic bar codes called *genotypes*, one for each person who contributed their DNA to the evidence. With complex DNA evidence (e.g., multiple contributors, small amounts of DNA) genotype uncertainty is represented using probability.

One can compare an evidence contributor genotype with a reference genotype (aka "DNA profile"), relative to a population, to calculate a DNA match statistic. The *likelihood ratio* (LR) match statistic number summarizes how much the data support the identification hypothesis that the reference person contributed their DNA to the evidence, versus the alternative that the contributor to the evidence was someone else.

An inclusionary LR greater than one (LR>1) supports the identification hypothesis, while an exclusionary LR less than one (LR<1) supports the alternative hypothesis. A larger LR *magnitude* indicates a stronger match (e.g., an inclusionary LR of a million, numerically written "1,000,000") or nonmatch (e.g., an exclusionary LR of a millionth, written "1 over 1,000,000"). A smaller LR magnitude indicates a weaker match (e.g., an inclusionary LR of ten "10") or nonmatch (e.g., an exclusionary LR of a tenth "1/10").

Error rate and the LR

An *error rate* (ER) is the frequency with which a LR match or nonmatch result may be incorrect. ER value is intrinsically related to LR magnitude. With simple DNA evidence from one person, the widely used random match probability (RMP) is both the error rate and the likelihood ratio. Mathematically, the inclusionary RMP equals 1/LR. That is, a large inclusionary LR over one automatically corresponds to a small ER under one.

With exclusionary nonmatch statistics, a strong LR is reciprocally written as a small number less than one. On simple exclusionary DNA evidence, ER = LR. A strong LR (small number) means a small ER number. With more complex DNA evidence, such as a mixture of two more people, the ER and LR relationship becomes an inequality, as discussed next.

A basic mathematical fact is that the likelihood ratio *error rate* (ER) must always be less than (or equal to) the LR (1). We write this fact as "ER ≤ LR". For example, if a strong exclusionary LR is one in a million, the ER for that LR cannot exceed one in a million. The true ER might be less (say, one in a billion) than the LR, but it can never be more (say, one in a thousand) than the LR. A short proof is given in the Appendix.

With large magnitude LR statistics, there may be no need to report an error rate explicitly. That is because the error rate is implicitly bounded above by the LR. For example, with an inclusionary LR of a million (LR = 1,000,000), the error rate must be less than or equal to a millionth (ER ≤ 1/LR = 1/1,000,000). And with an exclusionary LR of a millionth (LR = 1/1,000,000), the error rate must be under one over a million (ER ≤ LR = 1/1,000,000).

Since LR error rate depends on the LR value, error rates are reported relative to the actual LR. If an exclusionary LR for a suspect is some small number 1/N, it makes sense to report the small LR error rate as, "For the suspect's likelihood ratio of 1/N, only 1 in N people would be excluded as strongly as the suspect." Reporting LR error rate independently of a suspect's LR makes no sense, since we want to know how often an LR as strong as the reported suspect's LR value would occur by chance. The relevant context is how strongly the evidence matches (or doesn't match) the suspect – the suspect's LR value – not an arbitrary *binary* cutoff level.

Using LR-dependent error rate

TrueAllele validation studies typically stratify error rates by LR value. This LR stratification is helpful when testifying about DNA in order to quantify LR error rates. For example, in a peer-reviewed TrueAllele validation paper published in 2014 with the Virginia Department of Forensic Science (2), the Figure 5 specificity histogram showed an empirical LR distribution, stratifying event counts (y-axis) by LR value (x-axis). The paper's corresponding Table 6 stratified false positive event counts by LR value (LR = 1, 10, 100, or 1000).

I testified for the prosecution on TrueAllele results for DNA mixture evidence in *California v. Billy Ray Johnson*. During the December 2013 Grand Jury hearing, when asked about error rates I referred to the Virginia study's LR distributions. The prosecutor asked me about the reliability of TrueAllele match statistics based on their LR value:

> Q. So anything above 1,000 you consider to be a reliable statistic?"

Referring to the stratified LR levels from the validation study, I could respond based on the determined LR-dependent false positive error rates:

> A. Once you're beyond 1,000 or 10,000, you're -- in the studies we do, it was a study that we had talked about, it was a Virginia study where we did millions of comparisons between evidence items and random samples, and we were able to measure the extent of false positives, and going beyond a match statistic of 1,000 we just -- it's one in a million, and then beyond that you just don't see it at all.

The validation study's LR-stratified error rates scientifically supported this testimony about LR match strength:

> Q. For the last item of [mixture] evidence in that particular group from that case number, were you able to find some matches?
> A. Yes, we were.
> Q. What is the first one?
> A. The first is a positive match statistic to [victim name deleted] which is a likelihood ratio of 4.99 million.
> Q. What is the second?
> A. That's to [victim name deleted], the likelihood ratio is 272 quadrillion.
> Q. Okay. And the third?
> A. Is to [defendant] Billy Ray Johnson, with a likelihood ratio of 740 million.
> Q. And would you consider those all to be strong match statistics regarding this mixture?
> A. Knowing the TrueAllele system, those would be extremely unlikely to be a false positive, correct.

Validation papers contain many tables that summarize various findings. However, for reporting error rates, the most useful results are error frequencies stratified by LR value.

TrueAllele technology

DNA mixtures were a long-standing unsolved problem in forensic science. Manual methods and older software were unable to use biological mixture evidence to produce reliable DNA match statistics. Cybergenetics solved the problem over twenty years ago (3), with foreign products appearing about ten years later (e.g., STRmix, EuroForMix, likeLTD). Our TrueAllele

software “unmixes” data from mixed DNA items into genotypes, one for each contributor to the mixture. Genotype uncertainty is represented as probability, exploiting the natural variation in PCR amplification. This technology is sometimes called “probabilistic genotyping”.

After TrueAllele separates out the genotypes, each contributor can be compared with a reference profile to calculate a likelihood ratio. The LR provides the “weight of evidence” for how much a person did or didn’t contribute their DNA to an evidence item. TrueAllele is a software tool for accurately measuring LR weight.

There is a natural error rate for an LR, since the ER is always bounded above by the LR. However, some more advanced statistical computer programs for forensic biology can go beyond this automatic inequality bound. Such software further analyzes a probabilistic genotype to find an exact LR error rate.

TrueAllele’s Distribution module can find the exact error rate for any reported LR. TrueAllele calculates this exact LR error rate by considering all trillion trillion possible reference genotypes (4). We report this exact ER by saying, “For an exclusionary statistic of one over (a number), only 1 in (another number) people would be excluded as strongly.”

A DNA match statistic considers the relatedness of people in a human population. This co-ancestry correction reduces the LR magnitude. In 2014, Cybergenetics improved its LR calculation by better accounting for co-ancestry relatedness (5).

TrueAllele reliability

At least 42 validation studies have been conducted, establishing TrueAllele accuracy. Eight of these studies were published in peer-reviewed scientific journals (columns in the table below). The table lists 16 validation axes (rows), showing their relevance to the SWGDAM 2015 validation guidelines for probabilistic genotyping (last column).

Study	2	3	4	5	6	7	8	9	SWGDAM guideline
Sensitivity	1	1	1	1	1	1	1	1	3.2.1, 3.2.1.2, 4.1.13
False exclusions			1		1				3.2.1.1
Specificity			1	1	1		1	1	3.2.2, 3.2.2.2, 4.1.13
False inclusions			1		1			1	3.2.2.1
Reproducibility			1	1	1	1	1	1	3.2.3, 3.2.3.1, 4.1.13
Accuracy	1				1			1	3.2.6
Casework data						1	1	1	3.2.4, 3.2.4.1, 4.1.1
Known contributor data	1	1	1	1	1				4.1.1
Low-template DNA	1		1						4.1.6.2
Manual review comparison	1			1		1	1	1	3.2.6.1, 4.2, 4.2.1, 4.2.1.1
Peeling	1			1	1	1	1	1	4.1.2,4.1.2.1
MCMC sampling				1	1				3.2.3.2
Contributor sufficiency			1		1				4.1.6.4
Invariant behavior			1						
Match statistic predictability	1		1		1				
Observed contributor number					1				

The table column numbers correspond to the numbered references listed on page 4 of our TrueAllele case report (studies 2 through 9):

1. Perlin MW, Szabady B. Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *J Forensic Sci.* 2001;46(6):1372-7.
2. Perlin MW, Sinelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE.* 2009;4(12):e8327.
3. 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. *Sci Justice.* 2013;53(2):103-114.
4. Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *J Forensic Sci*. 2015;60(4):857-868.
5. Greenspoon SA, Schiermeier-Wood L, Jenkins BA. Establishing the limits of TrueAllele® Casework: a validation study. *J Forensic Sci.* 2015;60(5):1263-1276.
6. Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors. *J Forensic Sci*. 2020;65(2):380-398.
7. Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *J Forensic Sci.* 2011;56(6):1430-1447.
8. Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *J Forensic Sci.* 2013;58(6):1458-1466.

9. 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.
10. Kadash K, Kozlowski BE, Biega LA, Duceman BW. Validation study of the TrueAllele® automated data review system. *J Forensic Sci.* 2004;49(4):1-8.
11. Perlin MW. Efficient construction of match strength distributions for uncertain multi-locus genotypes. *Heliyon*. 4(10):e00824, 2018.
12. SWGDAM. Guidelines for the validation of probabilistic genotyping systems. 2015; https://www.swgdam.org/publications
13. ANSI/ASB. Standard for Validation of Probabilistic Genotyping Systems (ANSI/ASB Standard 018). 2020; http://www.asbstandardsboard.org/wp-content/uploads/2020/07/018_Std_e1.pdf

TrueAllele is objective, because it (a) doesn't see the suspect's DNA profile while deriving genotypes from DNA data, and (b) can statistically exclude as well as include suspects. TrueAllele's results are predictable, with a straight-line relationship between DNA amount and LR match strength (studies 2, 4 & 6) – more DNA generally gives a higher LR, while less DNA gives a lower LR.

The JFS 2015 and 2020 validation papers (studies 4 & 6) report false inclusion and false exclusion frequencies and error rates. The error rate data are stratified by LR value in the papers' figures and tables. That is how validation papers are used to report error rate – for a given LR value, they can provide the error rate.

TrueAllele acceptance

TrueAllele has been used in tens of thousands of cases. It helped identify victim remains in the World Trade Center disaster. Ten crime labs have automated their DNA mixture interpretation process with TrueAllele, for greater productivity, accuracy, and information. Cybergenetics has worked on over 1200 cases, assisting police (290 cases), prosecutors (400), defenders (over 200), innocence groups (65), and crime laboratories (over 200). TrueAllele has helped exonerate 10 wrongfully convicted men.

TrueAllele is used more by prosecutors than defenders. For example, crime labs have issued TrueAllele reports in tens of thousands of cases, almost all for prosecution or police. When defendants have challenged TrueAllele reliability, the evidence has been admitted almost

every time. To my knowledge, the government has never before challenged a defendant's introduction of TrueAllele. An Appendix lists the admissibility rulings.

TrueAllele has withstood over 35 Daubert and Frye defense challenges. TrueAllele has been used in 8 federal cases, withstanding 3 Daubert challenges in federal court: *United States v. Lenard Gibbs*, No. 1:17-CR-207 (N.D. Ga. 2019); *United States v. Curtis Johnson*, No. 17-201 (E.D. La. 2021); and *United States v. Hunter Anderson*, No. 4:21-CR-00204, 2023 WL 3510823 (M.D. Pa. 2023). TrueAllele reliability has been affirmed by 6 state appellate courts (Florida, Georgia, Nebraska, New York, Pennsylvania, Tennessee).

TrueAllele report

The PDS sent the DFS case data to Cybergenetics, along with the forensic question, "Is Ravel Mills' DNA present in the DNA mixtures recovered from the gun (5.1.1) or magazine (5.2.1)?" Cybergenetics conducted TrueAllele analysis on the mixture data, developing genotypes from the gun and magazine, and comparing them with Mills profile. We calculated LR match statistics in TrueAllele using our Visual User Interface (VUIer™) software, version 3.3.8343.1R20b (26-Aug-2022).

Report and case packet

On December 1, 2022, Cybergenetics sent the PDS a TrueAllele case report containing DNA nonmatch statistics comparing the gun and magazine items with Mills, along with error rates. On January 23, 2023, Cybergenetics sent the PDS a TrueAllele disclosure Case Packet that has supporting information for the TrueAllele calculations performed in the Mills case, including notes, data, genotypes (evidence, reference, population), LR statistics, and error rates.

On January 24, 2023, Cybergenetics sent the PDS a Dropbox link to a TrueAllele 4 GB DVD with disclosure materials for the case, including documents on:

- TrueAllele's reliability: background reading, over thirty validation studies and publications, regulatory approvals, general acceptance, and admissibility rulings.
- The mathematical model used by the software.
- Tutorial videos of TrueAllele methods, how the system works, and CLE courses.

• Installers and manuals for VUIer™ software to examine TrueAllele results.

• Case-specific files for reviewing results from this case.

• Instructions for opposing counsel on how to test the system free of charge.

Item 5.1.1 (gun)

Cybergenetics reported the TrueAllele results shown in the table below. The TrueAllele-inferred minor contributor to the gun (bold row) had a mixture weight of 5.9%, and an expected LR value over 12 million, indicating an informative genotype.

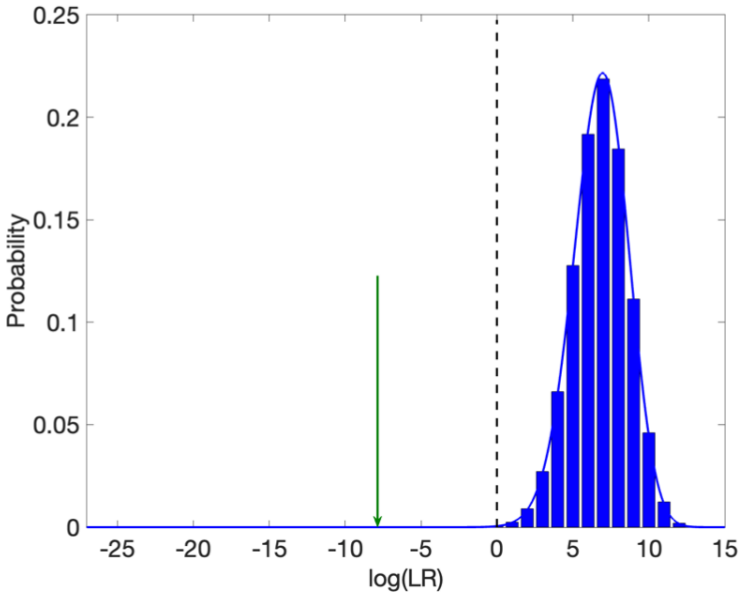
Comparing with Mills, the *exclusionary LR* was 1.374×10^{-8} (**one over 72.8 million**), and the *error rate* was 6.570×10^{-12} (**1 in 152 billion**). Note that this result satisfies the inequality law ER ≤ LR, since $6.570 \times 10^{-12} \leq 1.374 \times 10^{-8}$.

Item	Description	Contributor	Ravel Mills LR	LR Error Rate
5.1.1	gun	major	one over 36.1 duodecillion	1 in 1 googol people
		minor	**one over 72.8 million**	**1 in 152 billion people**

The error rate calculation for the gun LR was provided on page 156 of the Case Packet. The figure of the minor contributor's genotype LR distribution is reproduced below.

The figure's x-axis shows the LR in scientifically standard "powers of ten" log(LR) units, where "5" means 5 powers of ten, with 5 zeros after the 1, or 100,000; "0" means no powers of ten or 1; and "–5" means one over 5 powers of ten, or 1/100,000. The y-axis gives the relative frequency (i.e., probability) of LR values occurring at the x-axis LR value.

The figure shows a blue bell-shaped curve. The curve is the probability distribution of LR values for the (still unknown) person who left his DNA as the minor contributor to the gun mixture. The curve is centered around 7 log units (LR=10,000,000, ten million), which means that the expected LR value of the true DNA contributor is around ten million. The curve appears to the right of 0 (LR=1) and to the left of 12 (LR=1,000,000,000,000, a trillion). Since that is where virtually all the LR probability resides, it is extremely unlikely that the true DNA contributor would have an LR that is less than zero or greater than a trillion.



To quantify the exact false negative error rate of the defendant's exclusionary LR, we look at his nonmatch statistic of 1 over 72.8 million, located around –8 log units on the figure (green arrow). The area under the curve to the left of this arrow is way of measuring how far away the defendant is from the mass of probable LR values (blue contributor bell curve). The computer calculated an area of one in 152 billion to the left of the defendant's green arrow. This is the exact *false negative error rate* for a true contributor to the minor gun mixture component when their LR value is 1 over 72.8 million or less.

Item 5.2.1 (magazine)

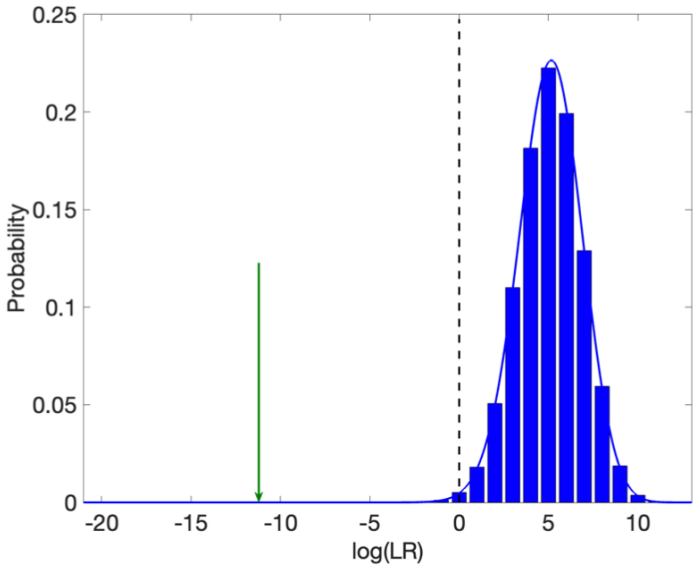
Cybergenetics reported the TrueAllele results shown in the table below. The TrueAllele-inferred minor contributor to the magazine (bold row) had a mixture weight of 2.4%, and an expected LR value of 420 thousand, indicating an informative genotype.

Comparing with Mills, the *exclusionary LR* was 6.217×10^{-12} (**one over 161 billion**), and the *error rate* was 2.910×10^{-15} (**1 in 343 trillion**). Note that this result satisfies the inequality law ER ≤ LR, since $2.910 \times 10^{-15} \leq 6.217 \times 10^{-12}$.

Item	Description	Contributor	Ravel Mills LR	LR Error Rate
		major	one over 24.3 undecillion	1 in 1 googol people
5.2.1	magazine	middle	one over 145 nonillion	1 in 1 googol people
		minor	**one over 161 billion**	**1 in 343 trillion people**

The error rate calculation for the gun LR was provided on page 158 of the Case Packet. The figure of the minor contributor's genotype LR distribution is reproduced below.

The blue bell-shaped curve is the probability distribution of LR values for the (still unknown) person who left his DNA as the minor contributor to the magazine mixture. The curve is centered around 5 log units (LR=100,000, a hundred thousand), which means that the expected LR value of the true DNA contributor is around a hundred thousand. The curve appears to the right of –2 (LR=1/100, a hundredth) and to the left of 12 (LR=1,000,000,000,000, a trillion). Since that is where virtually all the LR probability resides, it is extremely unlikely that the true DNA contributor would have an LR that is less than a hundredth or greater than a trillion.



To quantify the exact false negative error rate of the defendant's exclusionary LR, we look at his nonmatch statistic of 1 over 161 billion, located around –11 log units on the figure (green arrow). The area under the curve to the left of this arrow is way of measuring how far away the defendant is from the mass of probable LR values (blue contributor bell curve). The computer calculated an area of one in 343 trillion to the left of the defendant's green arrow. This

is the exact *false negative error rate* for a true contributor to the minor gun mixture component when their LR value is 1 over 161 billion or less.

Opposition Report

Wrong LR statistic software version

The opposition motion purports to develop TrueAllele false negative error rates from a published JFS2015 validation study (6) that used our *pre-2014* co-ancestry LR method. This is the wrong LR statistic calculation, relative to Cybergenetics *US v. Mills* report.

Our case report calculated DNA LR statistics using VUIer™ version 3.3.8343.1R20b (26-Aug-2022). This TrueAllele version calculates LR values using our *post-2014* co-ancestry relatedness method (5). Validation results using the post-2014 LR calculation may be relevant to this case, whereas the opposition motion's pre-2014 LR results are definitely not.

The case-relevant part of JFS2015 sensitivity Table 7 is for mixture weight ranges of 1-5% and 5-10%, using a 1 ng high-template DNA level. We recalculated this table using the post-2014 VUIer software. The resulting LR-independent measure of false negative error rate for LR values less than 1 (i.e., LR < 1) at 1 ng is shown in the correct post-2014 software sub-table:

N=	**Mixture Range %**	**count for LR<1**	**% for LR<1**
20	1–5	7	35%
17	5–10	0	0%

Using the correct software version, the opposition motion's claimed binary false negative error rates become lower. With a fixed LR<1 criterion, the 1 to 5% mixture range now has a 35% rate (from N=20 events) and the 5 to 10% range has a 0% rate (from N=17 events). These LR-independent binary measures are of limited utility, as elaborated below.

Wrong LR cutoff for false negatives

The error rate depends on the likelihood ratio. That crucial fact is implicit in the mathematical error rate law ER ≤ LR that says error rate cannot ever exceed the LR statistic. That is how the long-standing random match probability (RMP) error rate for simple DNA

evidence from one person has been calculated in millions of crime lab reports for decades. That is how we reported our error rates in this case (e.g., with the gun item, "for an exclusionary statistic of *one over 72.8 million*, only 1 in 152 billion people would be excluded as strongly" explicitly states the relevant LR of "*one over 72.8 million"*). And that is how error rate software, like the TrueAllele VUIer Distribution module, calculates relevant error rates in cases and validation studies.

The correct error rate cutoff is the reported LR value. The error rate should be given relative to the suspect's LR, showing the chance of the true minor contributor being excluded as strongly. However, the government used a fixed universal cutoff of 1 for a *binary* error rate. Their measure is independent of the relevant continuous LR value. That is not how forensic DNA false negative rates are calculated or reported. Error rates depend on the LR.

Misleading comparison with weak LR values

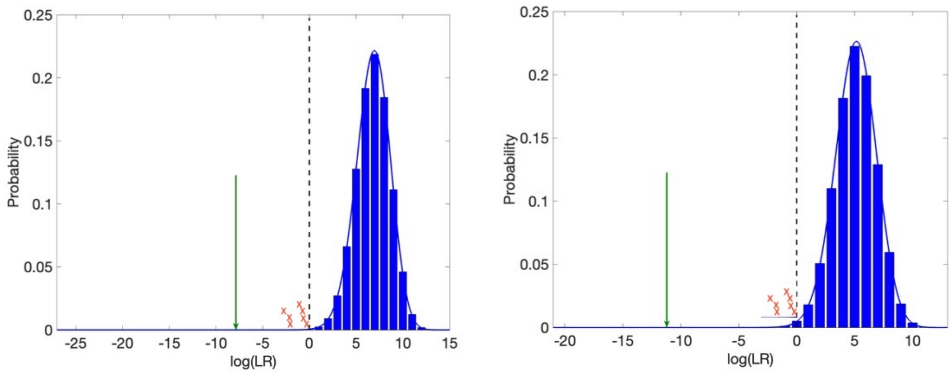
The opposition motion ignores the crucial dependence of error rate on LR in their binary analysis. An LR statistic of one tenth usually has far less weight than an LR of one millionth precisely because the stronger one millionth LR must have an error rate of 1 in a million or less. We list the two exclusionary LR values from our *US v Mills* report, along with the seven LR<1 values from the JFS2015 study in the 1 to 5% mixture range (1 ng DNA), sorted by LR.

Source	**Mixture Weight %**	**Nonmatch Statistic LR**	**Maximum LR Error Rate**	**Computed Exact LR Error Rate**
Item 5.2.1	2.40	1 over 161 billion	1 over 161 billion	1 in 343 trillion
Item 5.1.1	5.89	1 over 72.8 million	1 over 72.8 million	1 in 152 billion
JFS2015	1.63	1 over 3,126	1 over 3,126	1 in 1.21 million
JFS2015	1.08	1 over 412	1 over 412	1 in 6.97 thousand
JFS2015	1.70	1 over 292	1 over 292	1 in 23.3 thousand
JFS2015	1.32	1 over 25	1 over 25	1 in 1.39 thousand
JFS2015	2.26	1 over 4	1 over 4	1 in 490
JFS2015	1.65	1 over 3.5	1 over 3.5	1 in 234
JFS2015	1.40	1 over 1.4	1 over 1.4	1 in 341

The two LR<1 minor contributor results from our *US v Mills* TrueAllele report have large LR magnitudes. These magnitudes are around 70 million for the gun, and 160 billion for the magazine. Indeed, the strong LR values have extremely low computed false negative error rates of 1 in 152 billion and 1 in 343 trillion, respectively.

However, the seven LR<1 events from the JFS2015 validation study have much smaller LR magnitudes. Six of the LR values are weaker than one in a thousand. The distance between the weakest case LR (1 over 72.8 million) and strongest study LR (1 over 3,126) is a factor of 23 thousand, i.e., 4 powers of ten. The relatively weaker nonmatch study statistics would be expected to have higher error rates. They aren't relevant to the stronger LR values in the case report, and shouldn't be compared with them.

These seven red herring values are shown below (red crosses) on the contributor distribution figures from the Case Packet for both the gun (left) and magazine (right). These LR values are relatively weak, unlike the strong exclusionary nonmatch statistics for the defendant (green arrow). The weak values lie much closer to the contributor distribution bell curve (blue) for a true contributor than they do to the defendant's LR value (green arrow). They are not relevant to the defendant's strong exclusionary LR values, or their error rates.



The opposition motion set up a straw man by making an inappropriate comparison, trying to use weak LR validation values to undermine strong LR case report values. However, the large case LR magnitudes and small error rates (4) show that the government's comparison attempt is irrelevant to the facts of this case.

Published validation study using relevant software

The peer reviewed JFS2020 TrueAllele validation paper on mixtures containing up to ten people used the relevant post-2014 LR calculation (7). This work was cited in our *US v. Mills* case report, though glossed over in the government expert's report.

In the Supplemental Materials published alongside the validation paper, Supplemental Table S1(b) shows counts for the observed contributor negative events. The table (shown below) reveals that there were **zero contributor negative events** for 2, 3 or 4 observed contributors. That is, the *false negative error rate* in this study was zero for conditions relevant to the case.

(b) Contributor negative events

	Observed contributor number				
log(LR)	2	3	4	5	6
-2	0	0	0	0	1
-1	0	0	0	1	1
Total	0	0	0	1	2

Internal validation study mentioned in expert report

The opposition motion referred to an internal TrueAllele validation study conducted by the Georgia Bureau of Investigation (GBI) in 2017. Their expert report (paragraphs 44–46) stated, "It is clear that the same observation of high levels of false exclusion are evident using TrueAllele with two other STR kits." However, looking at the LR-stratified false inclusion rates in the GBI study, that statement isn't true.

Sensitivity Table 2(a) of the GBI study (page 6) for high DNA template amounts is reproduced below. It shows that for the 2 and 3 contributor mixtures relevant to this case, there were **zero false exclusions** in N=20 events. The smallest LR value seen for 2 contributors was LR = 2,400 (minimum log(LR) of 3.386); the smallest observed LR for 3 contributors was LR = 22. The GBI study cited by the government showed a *zero binary false exclusion error rate*.

ncon	2	3	4	5
N =	8	12	16	20
False exclusions	0	0	0	6
min	3.386	1.357	0.968	-2.716
mean	11.991	5.513	5.002	2.356
max	15.643	12.150	13.383	13.186
std dev	4.095	3.194	3.575	3.671

Too few genotype comparisons for error rates

The opposition motion relied on validation studies that estimated false negative error rates using only dozens or hundreds of LR comparisons. While pioneering at the time, there are now exact error rate methods consider a trillion trillion LR values (4). These distribution convolution methods give accurate exact LR error rates for a single casework genotype, and can also be used in validation studies for groups of genotypes.

This exact error rate work was cited in our *US v. Mills* report, though entirely ignored in the opposition motion. Cybergenetics holds two patents on this innovative and useful method for determining LR error rates from evidence genotypes (8, 9).

Using the best available methods for computing highly accurate error rates is highly relevant to case reporting. Older binary error rate methods using little data and inapposite LR values are not relevant to the evidence in this case.

Limitations of other interpretation methods

The opposition motion refers to earlier government case reports in *US v Mills* that used less capable mixture interpretation methods. The limitations of limited methods are not relevant to TrueAllele's proven capabilities.

Bode Technology's manual review of the gun and magazine DNA data would not be expected to handle small mixture components under 10%. The failure of such manual mixture interpretation approaches in these situations is well known (10).

The DFS lab failed to produce results on the minor components of the gun and magazine mixtures using their in-house STRmix software. That is unsurprising, given that STRmix fails to

get much information from small mixture components (11), and the software may not be reliable at such low levels (12).

Opposition Motion

The opposition motion concludes with four main points. All are wrong.

1. "First, there can be no dispute that these error rates apply to the minor contributors in this case."

Given the information we have provided above about relevant error rates, this assertion is clearly incorrect. Error rates depend on the LR. Their preset binary error rates are irrelevant.

2. "Second, this evidence is well outside the purpose of adopting Daubert and Rule 702 in presenting reliable information to a jury to improve decision-making."

The government's wishful thinking is not supported by TrueAllele's documented reliability, court acceptance, and the accurate error rates relevant to this case.

3. "Third and relatedly, the evidence should be precluded because Cybergenetics concealed the unreliable nature of the evidence by not noting it in the report."

This false assertion has no basis in fact. Cybergenetics' report gave accurate and relevant error rates, and disclosed the relevant peer reviewed papers. The government ignored the highly accurate error rate methods and results. They instead devised misleading arguments from the material we provided them that are entirely irrelevant to the facts of this case.

4. "Fourth, where the likelihood ratios favoring exclusion are so high as in this case, any cross examination or presentation of evidence by the government to expose the high likelihood the results are false, allows the defendant to argue that the government's assertions are biased and part of an effort to minimize evidence that is inconsistent with its theory of the case."

The LR values are high because that is what accurate computer weighing of the DNA data show. The government's assertions are irrelevant and incorrect. The defense has a right to present its case, even if the scientific evidence doesn't support the government's arguments.

In fact, this fourth point shows why the government's motion should be denied. They concede that "the likelihood ratios favoring exclusion are so high [in magnitude] in this case." A high exclusionary LR *magnitude* (much greater than 1) means a low LR *value* (much less than 1). But the science of the likelihood ratio requires that the error rate must be just as low, if not

lower, by the mathematical law ER ≤ LR. A "high" likelihood ratio favoring exclusion means a commensurately low error rate.

The government's ignorance of the (mathematical) law is no excuse. Since they agree that the exclusionary LR values in this case are "so high," one must logically conclude that the associated LR error rates are "so low" that they are not an issue. There is no need for a hearing to debate this mutually agreed upon Daubert point about TrueAllele's low error rate.

Conclusions

TrueAllele is an accurate computerized technology for measuring the weight of evidence in complex DNA mixture evidence. The software has been extensively tested, published in peer reviewed journals, has a testable error rate, follows national standards, and is generally accepted in the scientific community. Three federal courts have accepted TrueAllele as reliable after Daubert challenge, along with dozens of other courts.

Cybergenetics TrueAllele report in *US v. Mills* provides strong nonmatch statistics, and commensurately low error rates. These exact LR error rates were computed using the most complete technology available for complex DNA evidence, accounting for over a trillion trillion reference genotypes. The error rate method has been published in a peer reviewed journal (4). The TrueAllele technique, both as a method and as applied in this case, clearly meets the Daubert prong for error rates, since "there is a known or potential rate of error."

The government's opposition motion fails to convince. The strong TrueAllele LR statistics in this case are clearly distinguished from the weak LR values in their cited validation paper. Since error rate is bounded by likelihood ratio, their irrelevant LR values are concomitantly irrelevant to the correct error rates given in our case report. Ignoring science is not an argument.

The "Opposition Motion" subsections above describe the major flaws in the government's motion. The government and their expert relied on a study that used the wrong software version (pre-2014) for this case, applied the wrong cutoff of one (instead of the LR value) for determining a false negative error rate, made misleading comparisons of the strong case LR values with irrelevant weak LR values, glossed over more applicable validation studies that used case-relevant LR software (post-2014) and undermined their argument, considered too

few comparisons relative to modern error rate determination methods, and didn't disclose the well-known limitations of the other interpretation methods used in this case. The opposition motion is irrelevant, confusing, has no scientific merit, and is not applicable to the TrueAllele results and error rates reported this case. Their motion should be denied.

In conclusion, TrueAllele satisfies the Daubert prongs for the DNA mixture evidence in this case. The method clearly satisfies the error rate prong, with explicit reporting of low error rates for each reported LR statistic, using the best available error rate determination methods. There is no merit to the government's motion to preclude. TrueAllele should be admitted under the Daubert standard.

I declare the above is true and correct under penalty of perjury under the law of the Commonwealth of Pennsylvania, executed this 20th day of July 2023 in Pittsburgh, Pennsylvania.

By: _____

References

1. Perlin MW. Genotype likelihood ratio distributions and random match probability: Generalization, calculation and application. Cybergenetics; 2017.
2. 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 March 25;9(3):e92837.
3. Perlin MW, inventor Method and system for DNA mixture analysis. United States patent 09/776,096. 2002 October 17.
4. Perlin MW. Efficient construction of match strength distributions for uncertain multi-locus genotypes. Heliyon. 2018;4(10):e00824.
5. Perlin MW. Likelihood Ratio Calculation Application Note. TrueAllele® VUIer™: Cybergenetics; 2014.
6. Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors. J Forensic Sci. 2015;60(4):857-68.
7. Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® Interpretation of DNA Mixtures Containing up to Ten Unknown Contributors. J Forensic Sci. 2020;25(2):380-98.
8. Perlin MW, inventor Method, apparatus and computer software program for determining probability of error in identifying evidence. US patent 10489233. 2019.
9. Perlin MW, inventor Method, apparatus and computer software program for determining probability of error in identifying evidence patent 11,385,955. 2022.
10. Perlin MW. Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information. J Pathol Inform. 2015;6(1):59.
11. Perlin MW, Allan WP, Bracamontes JM, Danser KR, Legler MM. 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. SSRN. [Preprint]. 2023 May 18.
12. Perlin MW. Suspect-centric bias in DNA mixture interpretation. Forensic Magazine. 2018:10-3.

Appendix A. Admissibility Rulings

In all the following cases, a defendant challenged the government's introduction of TrueAllele evidence. TrueAllele was admitted over defense challenge almost every time.

To my knowledge, the government has never before challenged a defendant's introduction of TrueAllele.

Federal (3 challenges in 3 districts)

• Federal district court admitted TrueAllele into evidence in United States v. Lenard Gibbs, Northern District of Georgia, case number 1:17-CR-207, May 30, 2019. (Daubert)

• Federal district court admitted TrueAllele into evidence in United States v. Curtis Johnson, Eastern District of Louisiana, case number 17-201, July 14, 2021. (Daubert)

• Federal district court admitted TrueAllele into evidence in United States v. Hunter Anderson, Middle District of Pennsylvania, 4:21-CR-00204, 2023 WL 3510823 (M.D. Pa. 2023).

Appellate (6 state affirmations)

• Florida Fourth District Court of Appeals *affirmed* TrueAllele admissibility in State v. Lajayvian Daniels, No. 4D19-822, February 24, 2021. (Frye and Daubert)

• Georgia Supreme Court *affirmed* TrueAllele admissibility in State v. Thaddus Nundra, South Georgia Circuit, S23A0043, March 21, 2023. (Harper)

• Nebraska Supreme Court *affirmed* for statewide precedent TrueAllele admissibility in State v. Charles Simmer, 302 Neb. 369, November 1, 2019. (Daubert)

• New York Supreme Court *affirmed* for statewide precedent TrueAllele admissibility in People v. John Wakefield, 2019 N.Y. App. Div. LEXIS 6153, August 15, 2019. (Frye)

• New York Court of Appeals *affirmed* New York Supreme Court decision for TrueAllele admissibility in People v. John Wakefield, 38 N.Y.3d 367 (2022), April 26, 2022. (Frye)

• Pennsylvania Superior Court *affirmed* for statewide precedent TrueAllele admissibility in Commonwealth v. Kevin Foley, 2012 PA Super 31, No. 2039 WDA 2009, February 15, 2012. (Frye)

• Tennessee Criminal Appeals Court *affirmed* TrueAllele admissibility in State v. Demontez Watkins, No. M2020-00035-CCA-R3-CD, December 16, 2021. (Daubert)

State (39 challenges in 15 states)

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

• Florida trial court admitted TrueAllele into evidence in State v. Lajayvian Daniels, Palm Beach County, case number 2015CF009320AMB, October 31, 2018. (Frye)

• Georgia trial court admitted TrueAllele into evidence in State v. Adedoja Bah, Douglas Judicial Circuit, case number 17CR00938, October 22, 2019. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Alexander Battle, Ben Hill County, case number 16-CR-082, May 22, 2019. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Monte Baugh and Thaddeus Howell, Coweta County, case number 2017-CR-618, March 11, 2019. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Bryan Byers, Dekalb County, case number 19CRI780-3, April 8, 2022. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Rahul Joseph Das, Western Judicial Circuit, case number 2020-CR-125-S, August 16, 2021. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Nathaniel Day, Tifton Judicial Circuit, case number 2018CR141, October 23, 2019. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Zarren Garner, Western Judicial Circuit, case number SU-19-CR-0586-S, April 26, 2021. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Thaddus Nundra, South Georgia Circuit, case number 18-CR-134, January 21, 2019. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Lashumbia Session, Cobb County, indictment number 18-9-4511-58, December 30, 2021. (Harper)

• Georgia trial court admitted TrueAllele into evidence in State v. Guy Sewell, Floyd County, case number 17-CR-1675 JFL004, August 7, 2019. (Harper)

• Indiana trial court admitted TrueAllele into evidence in State v. Randal Coalter, Perry County, case number 62C01-1703-MR-192, August 2, 2017. (Daubert)

• 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. Vaylen Glazebrook, Monroe County, case number 53C02-1411-F1-1066, February 16, 2018. (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 did not use TrueAllele evidence in State v. Shawn Briscoe and Lance McIntyre, Jefferson Parish, case number 16-5524, September 20, 2022. (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. Corlious Dyson, Fifteenth Judicial District, case number 2013-CR-140554, June 2, 2023. (Daubert)

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

• Louisiana trial court admitted TrueAllele into evidence in State v. Dermell Lewis, Corey Major and Gerald Parker, Orleans Parish, case number 541-690, May 12, 2022. (Daubert)

• Louisiana trial court admitted TrueAllele into evidence in State v. Kyle Russ, East Baton Rouge Parish, case number 01-14-0566, April 30, 2019. (Daubert)

• Louisiana trial court admitted TrueAllele into evidence in State v. James Tabb, Fifth Judicial District, case number F-2018-216, June 1, 2022. (Daubert)

• Maryland trial court admitted TrueAllele into evidence in State v. Tyrone Harvin, Baltimore City, case number 118261014, October, 2021. (Daubert)

• Maryland trial court did not use TrueAllele evidence in State v. Gregory Jones, Montgomery County, Criminal No. 136661, November 30, 2021. (Daubert standard not applied)

• Massachusetts trial court admitted TrueAllele into evidence in Commonwealth v. Heidi Bartlett, Plymouth County, case number PLCR2012-00157, May 25, 2016. (Daubert)

• Nebraska trial court admitted TrueAllele into evidence in State v. Charles Simmer, Douglas County, case number CR16-1634, February 2, 2018. (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)

• New York trial court admitted TrueAllele into evidence in People v. Casey Wilson, Chemung County, indictment number 2013-331, May 1, 2019. (Frye)

• Ohio trial court admitted TrueAllele into evidence in State v. David Mathis, Cuyahoga County, case number CR-16-611539-A, April 13, 2018. (Daubert)

• 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. (Frye)

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

• Tennessee trial court admitted TrueAllele into evidence in State v. Abdullah Powell, Stewart County, case number 2017-CR-155, January 15, 2021. (Daubert)

• Tennessee trial court admitted TrueAllele into evidence in State v. Demontez Watkins, Davidson County, case number 2017-C-1811, December 17, 2018. (Daubert)

• 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)

Appendix B. ER ≤ LR: An exclusionary error rate is bounded by the likelihood ratio

This short mathematical proof was adapted from the technical report Cybergenetics provided on "Genotype likelihood ratio distributions," pages 9 through 13.

Definitions

• X is the set of all genotypes.

• $p(x)$ is the *prior probability* $Pr\{X = x\}$ of genotype x appearing in the population.

• $q(x)$ is the *posterior probability* $Pr\{X = x|data\}$ that an item contributor has genotype x, after examining DNA data from an evidence item.

• The *likelihood ratio* (LR) $f(x)$ is the posterior to prior genotype probability ratio $q(x)/p(x)$.

• The exclusionary *error set* E_α is the subset of genotypes $\{x \in X | f(x) \leq \alpha\}$ for which the LR $f(x)$ is less than or equal to a fixed LR α. Taking reciprocals, $E_\alpha = \{x \in X | 1/f(x) \geq 1/\alpha\}$.

• The exclusionary *error rate* (ER) is $Pr\{x \in E_\alpha\}$, the sum $\sum_{x \in E_\alpha} q(x)$ of posterior probabilities $q(x)$ taken over all genotype values in error set E_α.

Proposition. An exclusionary ER ≤ LR.

Proof

Markov's Inequality implies that the ER $\sum_{x \in E_\alpha} q(x)$ is bounded above by

$\frac{1}{1/\alpha} \sum_{x \in E_\alpha} [1/f(x)] \cdot q(x)$, which equals $\alpha \cdot \sum_{x \in E_\alpha} [1/f(x)] \cdot q(x)$, since $\alpha = \frac{1}{1/\alpha}$.

But summand $\frac{1}{f} \cdot q = \frac{p}{q} \cdot q = p$, so the upper bound becomes $\alpha \cdot \sum_{x \in E_\alpha} p(x)$.

The partial sum $\sum_{x \in E_\alpha} p(x)$ cannot exceed probability one, so $\sum_{x \in E_\alpha} q(x) \leq \alpha$. Since $\alpha = LR$, we have shown that $ER \leq LR$.

To recap, ER = $\sum_{x \in E_\alpha} q(x) \leq \alpha \cdot \sum_{x \in E_\alpha} p(x) \leq \alpha \cdot (1) = \alpha = LR$.

Therefore, an exclusionary *ER* cannot exceed its *LR*. **QED**