Objective DNA Mixture Information in the Courtroom:
Relevance, Reliability & Acceptance

NIST International Symposium on Forensic Science Error Management:
Detection, Measurement and Mitigation
July, 2015
Washington, DC

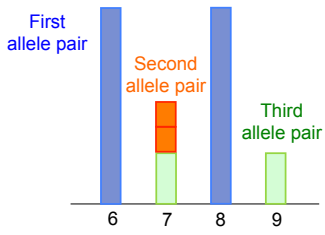
Mark W Perlin, PhD, MD, PhD
Cybergenetics, Pittsburgh, PA

Cybergenetics

Cybergenetics © 2003-2015

DNA mixture

Two or more people contribute their DNA to a sample



Forensic question

Did suspect Nelson Clifford contribute his DNA to the victim's clothing in a fifth case?

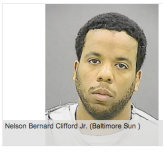
Man charged in multiple sexual assault cases acquitted a fourth time

Nelson Bernard Clifford, 35, remains in jail awaiting another set of charges

October 27, 2013 | By Jessica Anderson and Ian Duncan, The Baltimore Sun

A man charged in five sexual assault cases since 2010 based on DNA evidence was acquitted a fourth time Friday in Baltimore City Circuit Court, as prosecutors vowed to continue to try to convict him.

The acquittal is the latest move in a cat-and-mouse game between Nelson Bernard Clifford and the Baltimore state's attorney's office. As Clifford headed to trial on the most recent case, prosecutors refiled charges stemming from 2007 allegations, keeping him locked up without bail despite the result Friday.



Nelson Bernard Clifford Jr. (Baltimore Sun)

Bayes law

Use data to update belief (1762)

Prob(hypothesis | data) proportional to
Prob(data | hypothesis) x Prob(hypothesis)

New belief, **after** seeing data	How well hypothesis **explains** data	Old belief, **before** seeing data
posterior	*likelihood*	*prior*

Genotype modeling

Apply Bayes law to genetic identification

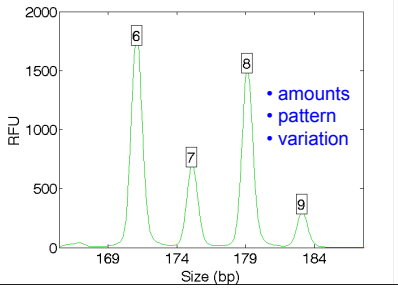
Prob(genotype | data) proportional to
Prob(data | genotype) x Prob(genotype)

New genotype probability, **after** seeing data	How well genotype choice **explains** data	Old genotype probability, **before** seeing data
posterior	*likelihood*	*prior*

Probabilistic genotyping

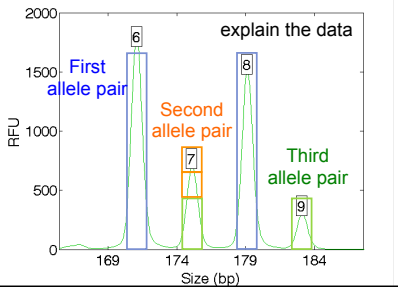
Genetic data

Quantitative peak heights at locus TH01



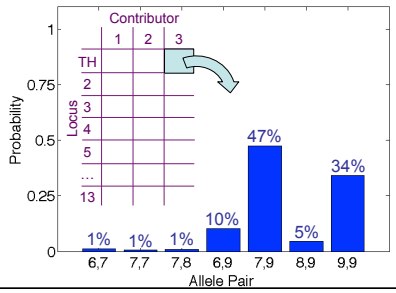
Separate genotypes

Consider *every possible* genotype (Bayes)



Separated genotype

Objective, unbiased – doesn't know suspect's genotype



Relevance (FRE 403)

Hypothesis = "suspect contributed his DNA"

likelihood ratio (LR) is Bayes law for a hypothesis

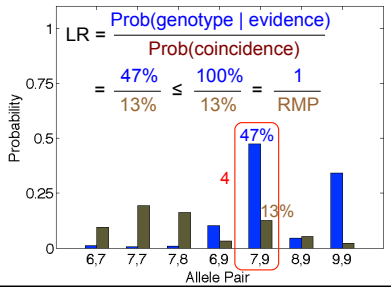
Probative ↓

$$LR = \frac{\text{Odds(hypothesis | data)}}{\text{Odds(hypothesis)}} = \frac{\text{Prob(genotype | data)}}{\text{Prob(genotype)}}$$

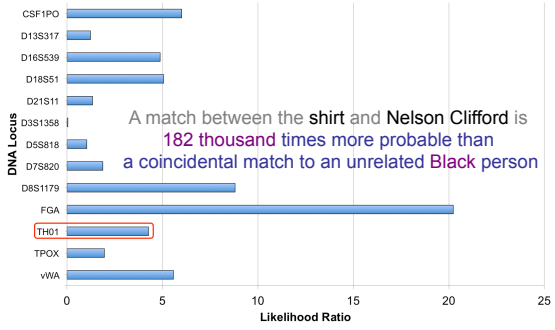
↑ **Non-prejudicial**

Match statistic is simple

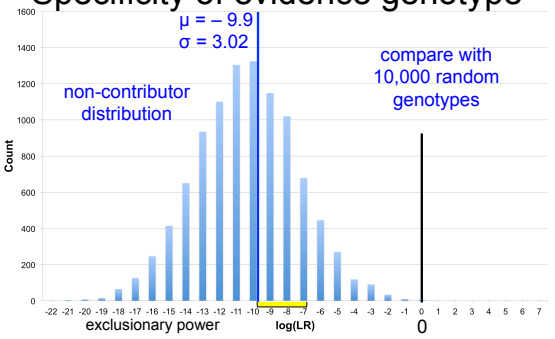
Suspect matches evidence more than random person



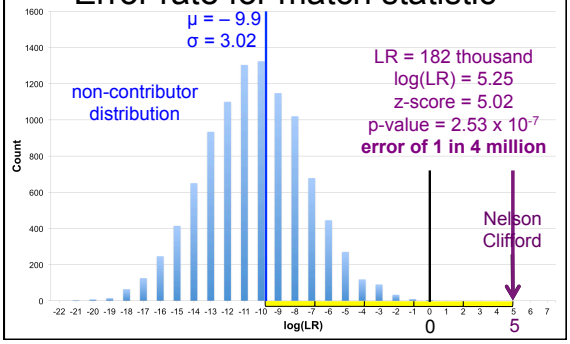
Match statistic at all loci



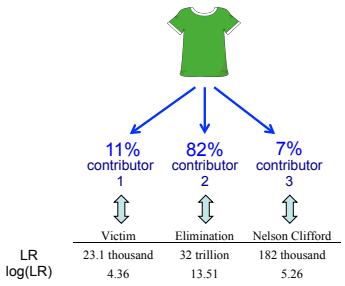
Specificity of evidence genotype



Error rate for match statistic



Separated DNA mixture



	Victim	Elimination	Nelson Clifford
LR	23.1 thousand	32 trillion	182 thousand
log(LR)	4.36	13.51	5.26

Case outcome

Jury convicts sex offender in fifth trial

By Justin George and Justin Fenton
The Baltimore Sun
contact the reporters

SHARELINES

- After four acquittals, jurors convicted Nelson Clifford of sex offenses in a fifth trial.
- Nelson Clifford faces life in prison after a jury convicted him of sex offenses Friday.
- Prosecutors view conviction of sex offender as a needed win against predatory behavior.

MAY 8, 2015, 8:42 PM

A Baltimore jury convicted a man Friday who had been acquitted in four previous sexual assault trials, a win for prosecutors who revived the discarded case in a bid to secure an elusive conviction.

Nelson Bernard Clifford, a convicted sex offender, was found guilty of two counts of third-degree sex offense. While the counts individually carry a maximum sentence of 10 years, prosecutors say Clifford faces an enhanced penalty — up to life in prison — because of prior convictions.

Validation papers

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

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;53(2):103-14.

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;*on-line*.

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;*in press*.

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):1430-47.

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.

Latest peer-reviewed study

JOURNAL OF FORENSIC SCIENCES

J Forensic Sci, 2015
doi: 10.1111/1556-4029.12788
Available online at: onlinelibrary.wiley.com

Get PDF (1343K)

Share

PAPER

CRIMINALISTICS

Mark W. Perlin,[1] Ph.D., M.D.; Jennifer M. Hornyak,[1] M.S.; Garett Sugimoto,[2] M.S.; and Kevin W.P. Miller,[2] Ph.D.

TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors*

ABSTRACT: Computer methods have been developed for mathematically interpreting mixed and low-template DNA. The genotype modeling approach computationally separates out the contributors to a mixture, with uncertainty represented through probability. Comparison of inferred genotypes calculates a likelihood ratio (LR), which measures identification information. This study statistically examined the genotype modeling performance of Cybergenetics TrueAllele® computer system. Highly- and low-template DNA mixtures of known randomized composition containing 2, 3, 4, and 5 contributors were tested. Sensitivity, specificity, and reproducibility were established through LR quantification in each of these eight groups. Covariance analysis found LR behavior to be relatively invariant to DNA amount or contributor number. Analysis of variance found that consistent solutions were produced, once a sufficient number of contributors were considered. This study demonstrates the reliability of TrueAllele interpretation on complex DNA mixtures of representative casework composition. The results can help predict an information outcome for a DNA mixture analysis.

KEYWORDS: forensic science, DNA mixture, genotype modeling, validation study, likelihood ratio, probabilistic genotyping

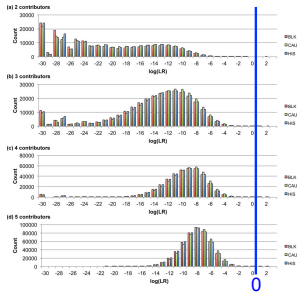
Specificity

2

3

4

5

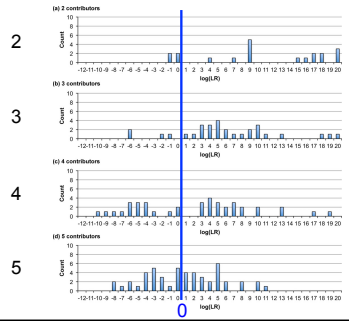


- low-template DNA
- compare millions

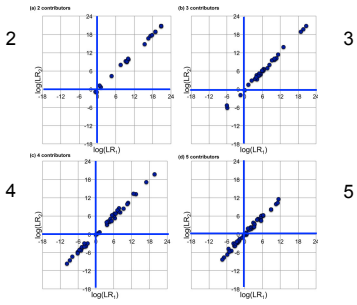
- exclusionary power
- contributor number

- false positive table
- error rate in court

Sensitivity



Reproducibility



Reliability (FRE 702)

- based on sufficient facts or **data**
- product of reliable principles and **methods**
- expert has reliably **applied methods** to **data**

Daubert factors:
(1) methods centered upon a **testable** hypothesis
(2) **error rate** associated with the method
(3) method has been subject to **peer review**
(4) **generally accepted** in relevant scientific community
(Frye criterion)

Acceptance is widespread

Admitted after Daubert or Frye challenge in:
California, Louisiana, New York, Ohio, Pennsylvania, Virginia, Australia & United Kingdom

Used in hundreds of criminal cases in most of the United States, for both prosecution and defense

Crimes labs use TrueAllele® system in California, South Carolina & Virginia; others starting soon

TrueAllele brings DNA mixture evidence back into the case, with *guilty plea* the most common outcome

Conclusions

- Objective genotyping eliminates examination bias
- Identification information for cases and validations
- Validation establishes accuracy and error rates
- Courts need solid science – empirically proven

- Criminal justice
- Societal safety
- Conviction integrity

Learning about genotyping

http://www.cybgen.com/information

- Courses
- Newsletters
- Newsroom
- Presentations
- Publications
- Webinars

http://www.youtube.com/user/TrueAllele
TrueAllele YouTube channel

Cybergenetics

YouTube

perlin@cybgen.com