DNA Identification: TrueAllele® Testimony

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Continuing Legal Education
Allegheny County Courthouse
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Cybergenetics

Interpretion: Same Principle

DNA data

A. Infer genotype
   1. Data
   2. Model
   3. Compare
   4. Probability

B. Match genotype
   Likelihood ratio

Different Methods

Data Used	inclusion	subtraction	addition
victim profile	NO	YES	YES
original data	NO	NO	YES

Frye: General Acceptance in the Relevant Community

- Quantitative STR Peak Information
- Genotype Probability Distributions
- Computer Interpretation of STR Data
- Statistical Modeling and Computation
- Likelihood Ratio Literature
- Mixture Interpretation Admissibility
- Computer Systems for Quantitative DNA Mixture Deconvolution
- TrueAllele Casework Publications

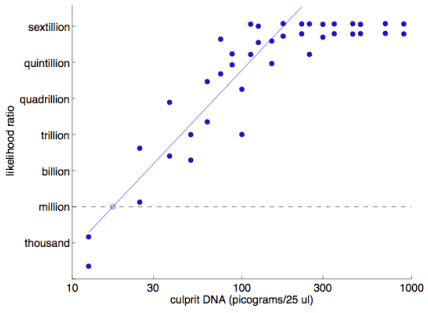
Validating Mixture Methods

Match Score = Information
- efficacy
- reproducibility

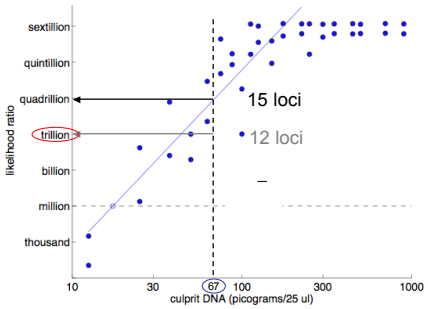
Perlin MW. *Scientific validation of mixture interpretation methods.* Promega's Seventeenth International Symposium on Human Identification, Nashville, TN. 2006.

Ranking:
1 Addition
2 Subtraction
3 Inclusion

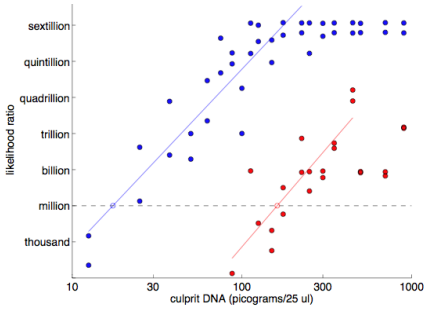
Validation Study



Expected Result



Addition vs. Inclusion



Threshold: all or none

Quantitative: shades of gray

Statistical Inference View

inclusion vs. likelihood ratio

"often robs the items of any probative value" - B. Weir

"usually discards a lot of information compared to the correct likelihood ratio approach" - C. Brenner

"does not use as much of the information included in the data as the LR approach but, conceptually, they are equivalent" - M. Krawczak

"Recommendation 1: The likelihood ratio is the preferred approach to mixture interpretation." - DNA commission of the International Society of Forensic Genetics (2006)

Relevant Scientific Community

- The forensic scientists who largely focus on DNA inference and statistics.
- Develop, discuss, publish, validate & assess DNA interpretation methods.
- Implement methods in computer software.
- Provide a pallet of interpretation methods for the practitioner to choose from.
- Lay the scientific foundation for practitioners.
- Give expert backup in court testimony.

Pennsylvania State Police

Mixtures with a known contributor
- genetic profile of the unknown can be inferred
- subtracting the contribution of the known donor
- peak height ratios can be used

Christine S. Tomsey, et al
Forensic DNA Laboratory
Croatian Medical Journal, 2001

Interpretation Differs

National Institute of Standards and Technology
Two Contributor Mixture Data, Known Victim

Some Differences in Reporting Statistics

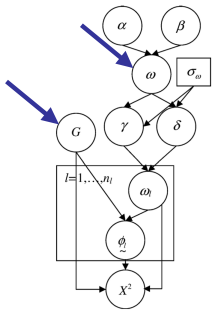
		Case1		
LabID	Kits Used	Caucasians	African-Americans	Hispanics
90	ProPlus/Cofiler	1.18E+15	2.13E+14	3.09E+15
34	ProPlus/Cofiler	2.40E+11	7.80E+09	9.80E+10
33	ProPlus/Cofiler	2.94E+08	1.12E+08	1.74E+09
6	ProPlus/Cofiler	40,000,000	3,500,000	280,000,000
9	ProPlus/Cofiler	1.14E+07	1.97E+07	1.54E+08
79	ProPlus/Cofiler	930,000	47,200	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Remember that these labs are interpreting the same MIX05 electropherograms

213 trillion (14)

31 thousand (4)

Other Methods are Similar



James Curran.
"A MCMC method for resolving two person mixtures."
Science & Justice.
2008;48(4):168-77.

TrueAllele Users

Allegheny County Crime Lab (Forensic Identification)
Armed Forces DNA Identification Laboratory (Forensic Identification)
DeCode Genetics, Iceland (Genetic Discovery)
Forensic Science Service, UK (Forensic Identification)
Maryland State Police (Forensic Identification)
Marshall University, WV (Forensic Research)
Massachusetts State Police (Forensic Identification)
National Institutes of Health (Genetic Discovery)
New York City OCME (Mass Disaster Forensic Identification)
New York State Police (Forensic Identification)
Orchid Cellmark - Abingdon, UK (Forensic Identification)
Orchid Cellmark - Nashville, USA (Forensic Identification)
Puerto Rico Forensic Science Center (Forensic Identification)
SmithKline Beecham Pharmaceuticals, UK (Genetic Discovery)
University of Pittsburgh (Genetic Counseling, Genetic Discovery)

Other Mixture Systems

GeneMapper® ID-X (Applied Biosystems, California)

FSS I-3® I-STReam (Forensic Science Service, United Kingdom)

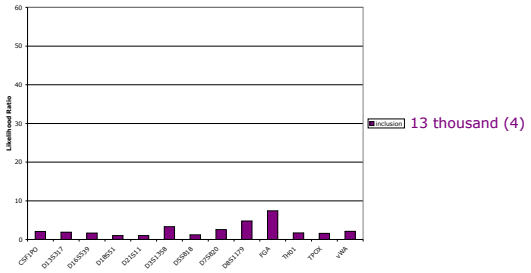
TrueAllele® Casework System (Cybergenetics, Pennsylvania)

Least Square Deconvolution (University of Tennessee)

MAIES (Universities of Oxford and Rome, Cass Business School, London)

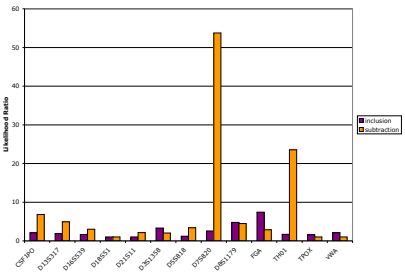
MCMC-Pendulum (University of Auckland, New Zealand)

Inclusion DNA Match



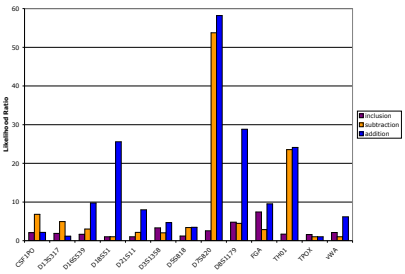
13 thousand (4)

Subtraction DNA Match



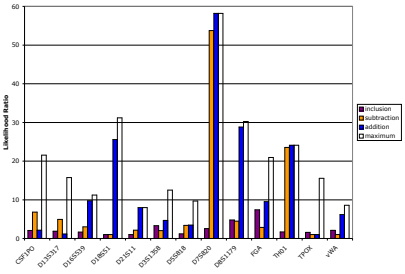
13 thousand (4)
23 million (7)

Addition DNA Match



13 thousand (4)
23 million (7)
189 billion (11)

Perfect DNA Match

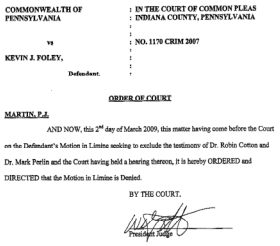


13 thousand (4)
23 million (7)
189 billion (11)
875 trillion (14)

Cross Examination

- How can reliable DNA give different statistics?
- Why doesn't the computer use thresholds?
- Has this method ever been used before in court?

TrueAllele Admitted



COMMONWEALTH OF PENNSYLVANIA : IN THE COURT OF COMMON PLEAS
: INDIANA COUNTY, PENNSYLVANIA
:
vs : NO. 1170 CRIM 2007
KEVIN J. FOLEY, :
Defendant. :

ORDER OF COURT

MARTIN, P.J.

AND NOW, this 2nd day of March 2009, this matter having come before the Court on the Defendant's Motion in Limine seeking to exclude the testimony of Dr. Robin Cotton and Dr. Mark Perlin and the Court having held a hearing thereon, it is hereby ORDERED and DIRECTED that the Motion in Limine is Denied.

BY THE COURT,

President Judge

Trial Testimony

- *one principle*: infer genotype, then match
- methods make *different use* of the data
- better data use gives *more information*
- MIX05: *huge variation* in interpretation
- validation study *predicts* match result

Trial Cross Examination

- Why are there different statistics?
  how method uses data, ethnic population, …
- Shouldn't the same data give the same answer?
  microscope analogy for examining same slide
- Don't computers need thresholds?
  that is a human limitation, and is not relevant

"John Yelenic provided the most eloquent and poignant evidence in this case," said the prosecutor, senior deputy attorney general Anthony Krastek. "He managed to reach out and scratch his assailant," capturing the murderer's DNA under his fingernails.

www.cybgen.com/information/newsletters/CybgenNews1.pdf