Blairsville, PA Dentist
Dr. John Yelenic

Murder Victim

April 2006: Death in home by exsanguination

State Trooper Arrested

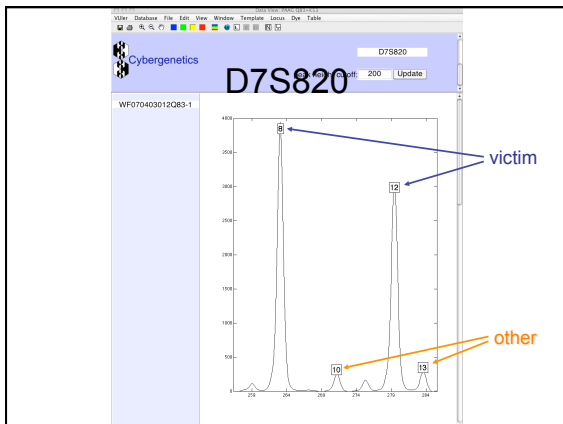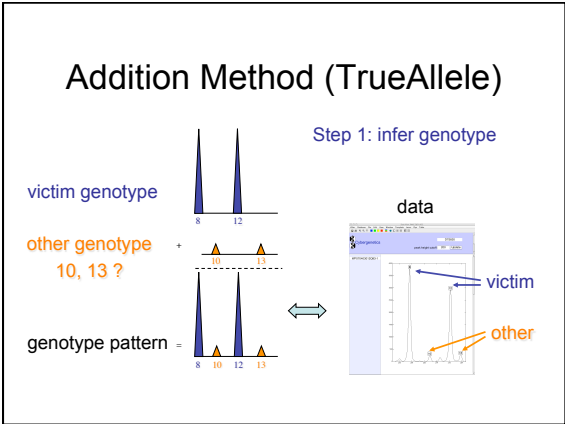November 2007: Kevin Foley charged with crime

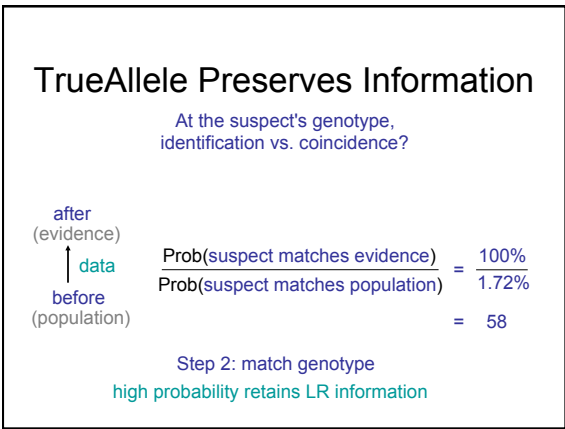## Fingernail DNA Evidence

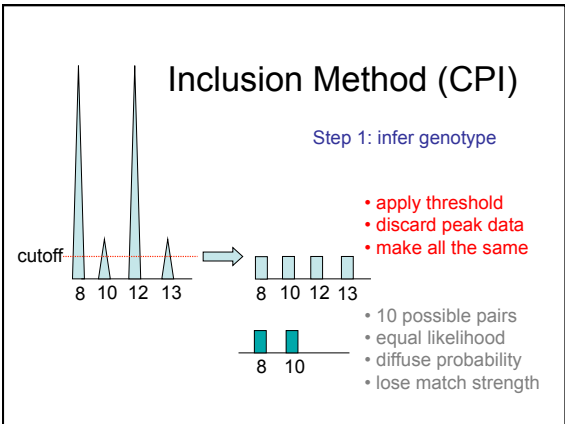93.3% victim + 6.7% DNA component

Three DNA Match Statistics

Score	Method
13 thousand	inclusion
23 million	subtraction
189 billion	addition

• Why are there different match results?
• How do mixture interpretation methods differ?
• What results should be presented in court?

D7S820

victim

other

Addition Method (TrueAllele)

Step 1: infer genotype

victim genotype

other genotype
10, 13 ?

genotype pattern =

data

victim

other

TrueAllele Preserves Information

At the suspect's genotype,
identification vs. coincidence?

after
(evidence)

data

before
(population)

$$\frac{\text{Prob}(\text{suspect matches evidence})}{\text{Prob}(\text{suspect matches population})} = \frac{100\%}{1.72\%}$$

$$= \quad 58$$

Step 2: match genotype
high probability retains LR information

Inclusion Method (CPI)

Step 1: infer genotype

• apply threshold
• discard peak data
• make all the same

cutoff

8 10 12 13   8 10 12 13

• 10 possible pairs
• equal likelihood
• diffuse probability
• lose match strength

8   10

CPI Loses Information

At the suspect's genotype,
identification vs. coincidence?

after
(evidence)

↑ data

before
(population)

$$\frac{\text{Prob(suspect matches evidence)}}{\text{Prob(suspect matches population)}} = \frac{4.42\%}{1.72\%}$$

= 2.57

Step 2: match genotype

lower probability loses LR information

Interpretation: 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

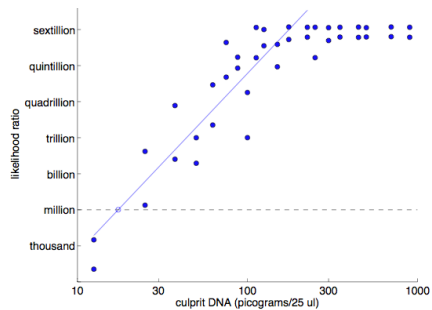## Validating Mixture Methods

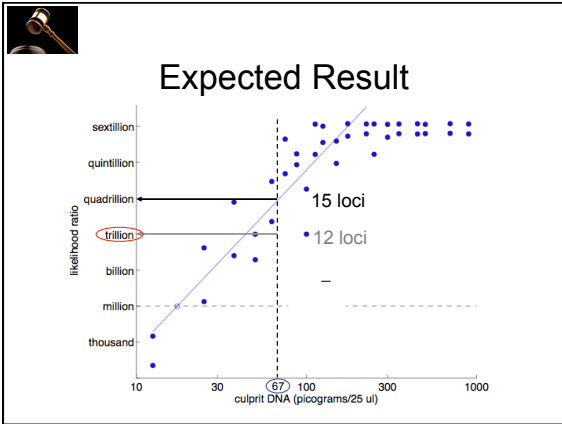Match Score = Information
- efficacy
- reproducibility

Perlin MW. *Scientific validation of mixture interpretation methods.* Promega's Seventeenth International Symposium on Human Identification, Nashville, TN. 2006.
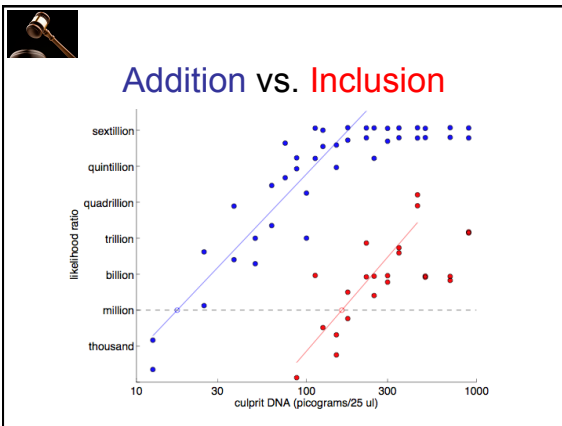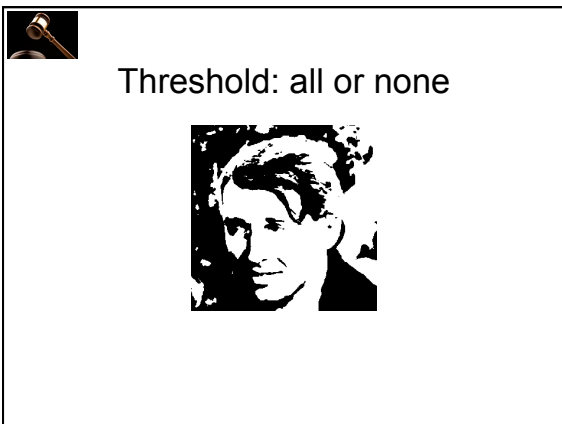
Ranking:
1 Addition
2 Subtraction
3 Inclusion

Validation Study

Expected Result

15 loci

12 loci

likelihood ratio — sextillion, quintillion, quadrillion, trillion, billion, million, thousand

culprit DNA (picograms/25 ul) — 10, 30, 67, 100, 300, 1000

Addition vs. Inclusion

likelihood ratio — sextillion, quintillion, quadrillion, trillion, billion, million, thousand

culprit DNA (picograms/25 ul) — 10, 30, 100, 300, 1000

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

| 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	7.00E+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	47,900	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Case1

213 trillion (14)

31 thousand (4)

Remember that these labs are interpreting the same MIX05 electropherograms

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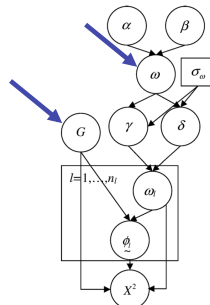
James Curran.
"A MCMC method for resolving two person mixtures."
Science & Justice.
2008;48(4):168-77.

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)

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,

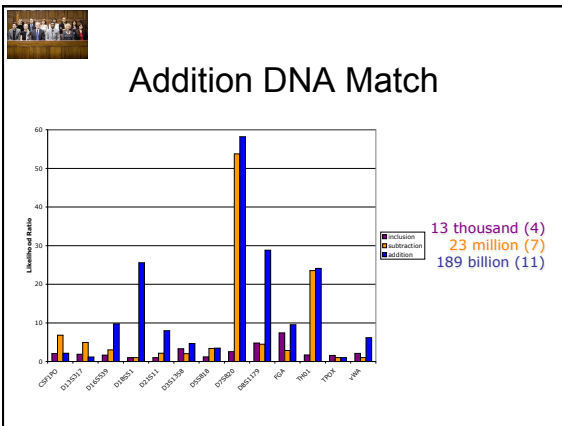_____
President Judge

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
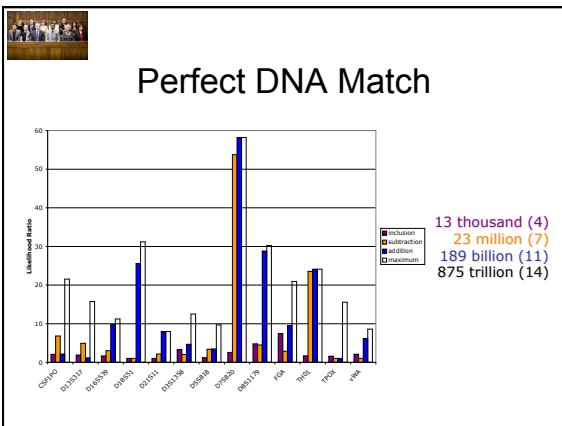- validation study *predicts* match result

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Inclusion DNA Match

inclusion 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)

Cybergenetics © 2007-2010
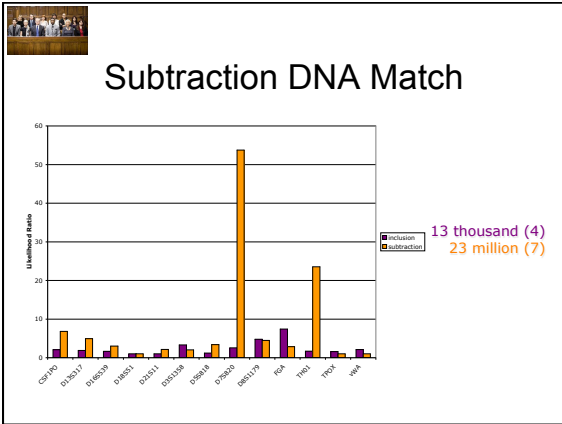
Trial Cross Examination

- 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

Microscope Metaphor

"The less informative methods ignored some of the data, while the TrueAllele computation considered all of the available DNA data."

"A scientist may look at the same slide using the naked eye, a magnifying glass, or a microscope. A computer that considers all the data is a more powerful DNA microscope."

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Jury convicts trooper of dentist slaying

Published: Thursday, March 19, 2009 12:46 AM EDT

An Indiana County Court jury this evening convicted state trooper Kevin Foley of first degree murder in the April 13, 2006, slashing death of Blairsville dentist John Yelenic.

"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.

Pennsylvania Precedent

TrueAllele in Pennsylvania

5 trials, 2 exonerations

Crime	Evidence	Defendant	Outcome	Sentence
murder	fingernail	Kevin Foley	guilty	life
murder	clothing	Glenn Lyons	guilty	death
rape	clothing	Ralph Skundrich	guilty	awaiting
murder	gun, hat	Leland Davis	guilty	23 years
rape	clothing	Akaninyene Akan	guilty	32 years
murder	shotgun shells	James Yeckel, Jr.	guilty plea	25 years
murder	fingernail	Anthony Morgan	stipulation	life
weapons	gun	Thomas Doswell	guilty plea	1 year
drugs	gun	Derek McKissick & Steve Morgan	guilty pleas	2 1/2 years
murder	wood	Sherman Holes	guilty plea	10 years