Interpretation: Same Principle

DNA data

A. Infer genotype
1. Data
2. Model
3. Compare
4. Probability
B. Match genotype
   Likelihood ratio

Different Methods

<table>
<thead>
<tr>
<th>Data Used</th>
<th>inclusion</th>
<th>subtraction</th>
<th>addition</th>
</tr>
</thead>
<tbody>
<tr>
<td>victim profile</td>
<td>NO</td>
<td>YES</td>
<td>YES</td>
</tr>
<tr>
<td>original data</td>
<td>NO</td>
<td>NO</td>
<td>YES</td>
</tr>
</tbody>
</table>
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


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.
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

<table>
<thead>
<tr>
<th>Genotype</th>
<th>100% User</th>
<th>ForensicCel</th>
<th>ForensicCtrl</th>
<th>Siemens 1</th>
<th>Siemens 2</th>
<th>Maxima 1</th>
<th>Maxima 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.30 G</td>
<td>1.28 G</td>
<td>1.29 G</td>
<td>1.31 G</td>
<td>1.32 G</td>
<td>1.34 G</td>
<td>1.35 G</td>
</tr>
<tr>
<td>2</td>
<td>1.10 G</td>
<td>1.08 G</td>
<td>1.09 G</td>
<td>1.11 G</td>
<td>1.12 G</td>
<td>1.14 G</td>
<td>1.15 G</td>
</tr>
<tr>
<td>3</td>
<td>2.20 G</td>
<td>2.18 G</td>
<td>2.19 G</td>
<td>2.21 G</td>
<td>2.22 G</td>
<td>2.24 G</td>
<td>2.25 G</td>
</tr>
<tr>
<td>4</td>
<td>3.30 G</td>
<td>3.28 G</td>
<td>3.29 G</td>
<td>3.31 G</td>
<td>3.32 G</td>
<td>3.34 G</td>
<td>3.35 G</td>
</tr>
</tbody>
</table>

213 trillion (14)
31 thousand (4)

Remember that these labs are interpreting the same MXML electropherograms.

Other Methods are Similar

James Curran.
"A MCMC method for resolving two person mixtures."
Science & Justice.
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®-STREAM (Forensic Science Service, United Kingdom)
TrueAllele® Casework System (Cybergenetics, Pennsylvania)
Least Square Deconvolution (University of Tennessee)
MCMC-Pendulum (University of Auckland, New Zealand)

Inclusion DNA Match

![Inclusion DNA Match Chart]

Note: 13 thousand (4)
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

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

Jury convicts trooper of dentist slaying

Published: Thursday, March 14, 2008 10:46 AM EDT

An Indiana County Court jury this evening convicted state trooper Kevin Foley of first degree murder in the April 13, 2008, slaying death of Banker's dental 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.